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Protein encoded by sequence Rat C-terminal amidating enzym

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A_Geneseq_36:R20026
A_Geneseq_36:R95016
A_Geneseq_36:W68387
A_Geneseq_36:W35856
A_Geneseq_36:P93323
                                                                                                                                                                                                                                   A_Geneseq_36:R59926
A_Geneseq_36:R12452
A_Geneseq_36:R10500
A_Geneseq_36:R106400
A_Geneseq_36:R106379
A_Geneseq_36:R74171
A_Geneseq_36:R74171
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A_Geneseq_36:W10653
A_Geneseq_36:W15326
A_Geneseq_36:W16326
A_Geneseq_36:W13009
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A_Geneseq_36:W13825
A_Geneseq_36:R99462
A_Geneseq_36:R05159
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A_Geneseq_36
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A_Geneseq_36:W44941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database: A_Geneseq_36:*
Database sequences: 188963
Database length: 23686106
Search time (sec): 139.200000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search information block: Query: US-09-323-427-1
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                                                                                   A_Geneseq_36
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A_Geneseq_36
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A_Geneseq_36:P81184
A_Geneseq_36:R87953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-323-427-1 to: A_Geneseq_36:*
                                              : W44941
: R88912
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software, version
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                                                                                                                                                            Lambda gt10ch2 encoded C-termin Lambda gt10ch101 encoded C-term i Lambda gt10ch201 encoded Dept i Protein encoded by sequence whi Protein encoded by sequence whi I Type B alpha-amidating enzyme i Bacillus thuringiensis PS167P i Nematode toxin 167P protein. B i Nematode toxin 167P new B Segment of desmosomal cadherin, C-terminal amidation enzyme. Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Documentation .. i AE-III (peptidylhydroxyglycine
                                                                   C. difficile toxin A. Fusion F
Clostridium difficile toxin A.
Human CD45 for use in T lymphod
Bovine peptidyl-glycine alpha-a
Newcastle disease virus immunog
Newcastle disease virus glycopi
Haematopoietin receptor Hu-Bl. 2
Haematopoietin receptor Hu-Bl. 2
                                                                                                                                                                                                                                                                                                                                                              Human neurotrophic biglycan. Pt Expression plasmid pUCPLC1799 H C-terminal prepro-C-terminal all Peptidyl C-terminal alpha-amidal Peptidyl C-terminal alpha-amidal Yeast transcription regulatory Biosynthetic enzyme of icosape
                     Haematopoietin receptor Hu-Bl.2
Oat phytochrome A apoprotein
Carbamoyl-phosphate-synthetases
Candida albicans histidine kir
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E. coli colitose or glucose tra
GAP protein Ira2. Blocking Ras
Enzyme involved in eicosapenta
S. putrefaciens EPO biosynthes
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat neurotrophic biglycan. Pro
 protease-activated secreted protein c
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A_Geneseq_36:R11110
A_Geneseq_36:R10322
A_Geneseq_36:R80530
                                                                                                                                         313
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                                                                                           ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                       Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                           AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
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alignment_scores:
Quality:
Ratio:
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US-09-323-427-1 x R20112
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08-JAN-1992.

27-MAY-1991;

01-JUN-1990;

10-AUG-1990;

30-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                               peptide(s) e.g. human calcitonin.
Claim 4; Page 18; 28pp; English.
The sequence was deduced from a cDNA insert from pAE-III-202-4
(FERM BP-3172). The vector serves as a source for a DNA fragment encoding PHL for the construction of an expression vector for the prepn. of recombinant PHL. The protein may be truncted to comprise only residues 383-706 or 383-713. The PHL catalyses the reaction: R-GlyOH -> R-NH2. It can be used to produce peptides wit amidated C-termini, e.g. calcitonin, growth hormone, LH-RH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CIBA) CIBA GEIGY AG.
Iwasaki Y, Shimoi H, Suzuki K,
Kawahara T, Kangawa K;
WPI; 92-010570/02.
N-PSDB; Q20269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel DNA encoding peptidyl hydroxy:glycine N-C lyase (PHL) used to prepare PHL which can be used in the amidation of peptide(s) e.g. human calcitonin.
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AE-III (peptidylhydroxyglycine N-C
Amidation; PHL.
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lAlaAspGlyTyr.....
                                             AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                               CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                       TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 312
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JP-210535.
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1243 CTCAATGTTTATGGGTTTAAGCATTGCATTGATT...GCTGCCGTCATTA 1289
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                                                                                                                                                                                                                                                                                           TGATATCAACACCCTTGAA.....ATTAGCGATGATAATCAAGCTT 1142
                                                                                                                                                                                                                                                                                                                                                                                            GCA......GAACCGGAGAATATCATT...GATGTACGAAC 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisArgSerValLysLysAlaGlyIleGluValGluGluIleThrGluTh
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                                                                                                   GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT
                                                                                                                                                                                                                                                                                                                                                 alGluLysGlnThrGlnGluLysGlnGlnLys.....GlnLysAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCG 1019
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                                                                                                                                                                                                                                                a \verb|GlyValProThrGlnGluLysGlnAsnValValGlnGluSerSerAlaG|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eAspMetProHisAspIleAlaAlaAlaAspAspGlyThrValTyrValG
                                                   ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVa
                                                                                                                                                                                                  TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV
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                                                                                                                                                 lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...ATTACCATTAAAGAACCAAAT.....AGCGAATGTGTTCGACC 969
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alignment_scores:
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US-09-323-427-1 x P81184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1290 TTACCATTTCGTTTAAATTTCGT 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydrophobic character and presumably comprise a cleavable signal peptide. The extreme carboxy-terminal part comprises a region of 20 hydrophobic AAs, which presumably serves as a transmembrane anchor. The FIPV peplomeric protein has 35 potential glycosylation sites, of which 22 are in the N-terminal part (pos. 1-790) which corresponds to the S-part of the IBV E2 (see P81183). N.B. IBV = infectious bronchitis virus. "X" in the AA sequence denotes the translation of a stop codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful as antigenic protein for vaccine
Disclosure; Fig 1; 13pp; English.

cDNA was prepd. from FIPV straim 79-1146. N81533 gives the sequence
of the peplomeric gene in three reading frames. The top reading
frame is an open reading frame of 4356 nucleotides and has a coding
capacity for a precursor polypeptide having a mol. wt. of 160,470
(1452 AAs). The beginning and the end of the E2 gene are indicated
in the FT of N81533. The first 18 N-terminal AAs have a strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoded by the 2nd reading frame of FIVP strain 79-1146.

Vaccine; peplomeric protein; E2 gene. Feline infectious peritonitis virus. Ep-264999-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUIN ) DUPHAR INT RES BV.
DE GROOT RJ, Spaan WJM, Van Der Zeijst BAM;
WPI; 88-114147/17.
N-PSDB; N81533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-1987; 201657.
05-SEP-1986; NL-002244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P81184 standard;
                                                                                                                                                                                                                                                                                                                                                         194 ACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-1988.
                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                uAspThrProLysPheLysCysArgCysAsnAsnAlaLeuIle.ValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leAlaIleAlaIlePheIleArg
                                                                                                                                                                                                                                                                                                                     SerThrIleMetAlaLeuSerHis
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                                                                                                            CAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTC 393
                                                                                                                                                     LeuLysGluLysGluLeuAsnGluMetVal......ValGlyLeuLe
                                                                                                                                                                                             ATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGAT 343
                                                                      uArgLysGlyLysLeuLeuIleArgAsnAsnGlyLysLeuLeuAsnPheG
                                   ACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCAC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for feline infectious peritonitis virus - and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1594 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.00
0.376
45.783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 18.
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N81533 gives the sequence
                                                                                                                                                                                                                                                                                                                     .AsnSerValLe 62
.ValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   840
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396	0 etTy	380
1109	8crgcagaaccgg	106
380		36:
1067		1019
363	::: ::: :::	349
1018	9 CACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGT	969
348	3 laLeuLeuProG	33
968	8 CAGTATTACCATTAAAGAACCAAATAGCGAATGTO	921
333	rSer	316
927	AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGA	887
316	:	313
888	ATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTAI	837
312	8 erGlyMetMetThrLeuLeuGlnLeuIleLeuValValValLeu	298
836	GGAAATTCTAAATGCTGATGG	787
298	eLeuSerTeuSerTyrProArgThrMetGluGlnLysSerMetVall	281
786	TTGTCCAFTCCTGCTTTGTCGATGATGGTAACGGTGAI	744
281	SerProProThrSerGlyIleProHisValArgValLe	265
743		743
264	snMetGly***CysAla***LeuLysIleAlaIleLeuThrMetAsnA	248
743	2AATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCG	70:
248	lLeuI	231
701	CATA	698
231	<pre>metHisValValAsnHisTyrTyrPheMetCysMetValSe</pre>	215
697	GACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC	648
214	leTyrMetProPheIleLeuLeuTrpLysProTrpLysIleAlaLeuVal	198
647	TGGATGG	639
198	YThrThrAlaLeuGluGlnLeuGluLeuLeuProPheSerIleLeuIle	181
638	CAGTATGCCGTTATGAAATTT	618
181	LysLysGluVal***LeuLeuValValIleThrLeuGlnArgCysGl	165
617	AAATCACAA	579
164	snTrpLeuAlaMetLysThrLeuSerGluIlePheCysLeuValThrLeu	148
578	CATGGAAGC	535
148	н	131
534	TATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTT	489
131		115
488	GTGGTATTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCAT	444

Hasenoehrl R, Huston J, Junghans U, Mueller HW; WPI: 95-03938/51. Proteoglycan cpds., partic. chondroitin for maintain structural and function of memory deficit(s) in the elderly and pat	/label= Hypervariable_reg.l; E01479; W0-E01479. HRINGER MANNHEIM GMBH.	learning. Bos taurus. Location/Qualifiers Key region 7. 23	20-MAR-1996 (first entry) Bovine neurotrophic biglycan. Biglycan; proteoglycan; chondroitin sulp neurotrophic; central nervous system; CN	q_documentation_ R87953 standa	seq_name: A_Geneseq_36:R87953	1602 TTATCAACTTGTCCTATTTTATTCTAACAGTTTATCAT ::: ::: :::	1577ATAGTTTCGTTTC ::: 537 l***ArgLysLeuLeuLeuValSerGLyAlaIlePhe	1530 ATCTTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCCATG	TTTATAGCTTCTGAAA. ::::::::::::::::::::::::::::::::::	CTGTAATACAATAAGTG ::: .valSerLeuValLeuT	1380 GTTTCTTCTTATCATCCTTCTAATAACTAATTTTAGCTAAC :::::::: 495 ThrGln***	1330 AAAATAATGTTAGAATCATCGAAGCAATAATAAAACTGCCA ::: 478 heHis***IleGlnGlnValValSerPheLeuLysPheHis	1283 GTCATTATTACCATTTCGTTTAAATTTCGTCCAAA ::: ::: ::::::: ::: 461 rThrLeuIleSerLeuGlnMetTyrAsnLeuValTrpV	1239 GCTTCTCAATGTTTATGGGTTTAAGCATTGCZ ::: 445 AlaAsnValMetValCysLeu***IleThrGlnTrpMe	1192 TGTAATACTTGCTGCAGTACAAAATGGAATCTGCA	1142 TTGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACA	1110 ACACCCTTGAAATTAGCGAA
s U, K roitin ion of and pat	ble_re	, w	sul m; C			GTTTATCATTTG 1642 ValTyrLeuLeu 567	a .	TTCATCATTAGGCCATGA 1576 ::::::: e***GluHisTyrHisProVa 537	AAGCTTATTCATTATTCAGTA 1529 ASpThrValMetTyr 521	CATCAA :::: tValLy	ATTTTAGCTAACAAATATATA 1429	ATAAAACTGCCATATATATTC 1379 ::: ::: LeuLysPheHisValIleVal 494	TCGTCCAAATCAGAAGGCATA 1329 :: ::: ::::: euValTrpValLeuGlnTyrP 478	AGCATTGCATTGATTGCTGCC 1282 rGlnTrpMetLeuLeuAspSe 461	GAATCTGCATGTCACCATTTG 1238 	TCTGCAACATAATGGACAACC 1191 ::: aCysGlyGlnCysProVall 430	AAATTAGCGATGATAATCAAGCT 1141

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alignment_block:
US-09-323-427-1 x R87953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: R87953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1005 AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA 1054
                                                                                                                                                1423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 8; 60pp; English.
Bovine biglycan (R87953) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function
                                                                                                                                                                                                                                            1373 TATATTCGTTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                               160 GluAsnSerGlyPheGluProGlyAlaPheAspGlyLeuLysLeuAsnTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAA 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC
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                                                ATCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sAsnHisLeuValGluIleProProAsn.........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euValLeuValAsnAsnLysIleSerLysIleHisGluLysAlaPheSer 99
                                                                                                                                              ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC
                                                                                                                                                                                                 rLeuArgIleSerGluAlaLys....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAAATCAGAAGGCATAAAAATAATGTTAGA.....ATCA 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT 1312
LeuAspHisAsnLysIleGlnAlaIleGluLeuGluAspLeuLeuArgTy
                                                                                              lyIle.....ProLysAspLeuProGluThrLeuAsnGluLeuHis
                                                                                                                                                                                                                                                                                                                                                                                             heSerGlyLeuArgAsnMetAsnGluIleGluMetGlyGlyAsnProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lGluLeuArgIleHisAspAsnArgIleArgLysValProLysGlyValP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ........LeuProSerSerLeu........Va
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0.798
40.468
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Gaps: 13
Percent Identity: 20.401
                                                                                                                                                                                            ......................LeuThrG
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6
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       216
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alignment_block: US-09-323-427-1 x R87951

Align seg 1/1

to: R87951

from: 1

to: 369

1005 AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA 1054

alignment_scores: Quality:

Percent Similarity:

Ratio:

95.50 0.789

40.468

Percent Identity:

20

Length: Gaps:

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seq_documentation_block:
ID R87951; standard; Prot
AC R87951; cfirst e
DT 20-MAR-1996 (first e
DT 20-MAR-1996 (first e
DT 20-MAR-1996 (first e
DT 20-MAR-1996 (central
KW Biglycan; proteoglyca
KW learning.
OS Rattus Sp. Locat
FT peptide 1.3
FT peptide 1.3
FT region 44.
FT PANAY-1994; E01479.
PR 09-MAY-1994; WO-E01479
PR 09-MAY-1994; WO-E01479
PR (BOEF) BOEBHRINGER MA
PI Hasenoehrl R, Huston
PI Mueller HW;
PR WP50B; T08788.
PT proteoglycan cpds., p
PT for maintain structur
PT memory deficit(s) in
PS Claim 1; Page 44-45;
CC neurotrophic activity
Obtd. by expression o
CC cells, can be used to
CC and function of CNS n
pathological and/or t
CC degenerative diseases
CC in the elderly and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: A_Geneseq_36:R87951
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                                                                                                 Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia Claim 1; Page 44-45; 60pp; English.
Rat biglycan (R87951) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. Recombinant biglycan, obtd. by expression of encoding cDNA (708768) in eukaryotic host cells, can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat neurotrophic biglycan.
Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
neurotrophic; central nervous system; CNS; memory Loss; dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-1995.
09-MAY-1994; E01479.
09-MAY-1994; WO-E01479.
(BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                  be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAR-1996 (first entry)
          in the elderly and in patients with dementia.
Sequence 369 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Huston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Hypervariable_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Sig_peptide
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ID R87952 standard; Protein; 369 AA C R87952;

DT 20-MAR-1996 (first entry)
DE Human neurotrophic biglycan; chondroi kW Biglycan; proteoglycan; chondroi kW learning.

OS Homo sapiens.

Key Learning.

OS Homo sapiens.

Location/Qualifi FT peptide /label= Sig_pept /label= Hypervar /label
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Human biglycan (R87952) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients with dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human neurotrophic biglycan.
Biglycan; proteoglycan; chondroitin sulphate; neuron protection; neurotrophic; central nervous system; CNS; memory loss; dementia
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Hasenoehrl R, Huston J, Junghans U,
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                            The sequence encodes a derivative of the mature C-terminal alpha-amidating enzyme from plasmid pxA/99. amidating enzyme from plasmid pxA457. The plasmid was screened from an E.coli library using plasmid pxA457 to screen a larger library. Although pxA459 is similar to pxA457 at the N-terminus, it has an arm.
                                                                                                                                                                                                          Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.
                                                                                                                                                                                                                                                                                                                                              (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka
WPI; 89-017279/03.
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Expression plasmid pUCPICI799 BglII gene product.
alpha-amidating; pAX799; alpha amide; ds.
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Although pX
hydrophobic
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17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuArgGluLeuHisLeuAspAsnAsnLysLeuSerArgValProAlaGl
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elements suggesting a
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membrane function
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                                   it has an area
                                       of.
seq_documentation_block:
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Sequence 693 AA;
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seq_name: A_Geneseq_36:P94854
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US-09-323-427-1 x P94856
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                                                                                   GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA
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                                                                                                                                                                     AATGCTGATGGATGTGCTCTTGATAAATATTTG.....CTAAATAATTT
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                                                                                                                             TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA
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                                            eGluMetProHisAspIleAlaAlaGlyAspAspGlyThrValTyr 655
                                                                                                                                                                                                                                                                                                   rGly......AspSerThrProValGlnGlyPhe.....
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alignment_block:
US-09-323-427-1 x P94854
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Ratio:
Percent Similarity:
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18-JAN-1989.
15-JUL-1988; 306508.
17-JUL-987; JP-177184.
05-DEC-1987; JP-306867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.

Disclosure; 7pp; English.

Plasmid pXA799 contains a sequence derived from Xenopus laevis.

The plasmid was screened from an E.coli library using plasmid pXA457 to screen a larger library.

Although the gene product is similar to that of pXA457 at the N-terminus, it has an area of hydrophobic elements suggesting a membrane function. See also N93060.

Sequence 875 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-1990 (first entry)
27-JUN-1990 (first entry)
C-terminal prepro-C-terminal alpha-amidating enzyme of pXA799.
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Ohsuye K, Kitano K, Tanaka
WPI; 89-017279/03.
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                                  AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT
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   laValSerTyrAlaPro
                                                                   uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA
                                                                                                  AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
                                                                                                                                    AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                                                                                                       AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
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SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
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Percent Identity:
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alignment_block:
US-09-323-427-1 x R73053
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                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP-649900-A.
26-APR-1995.
07-SEP-1994;
08-SEP-1993;
                                                                                                                                                                                                                                                                                 Jmu-IS cells (i.e. CHO cells expressing a peptidyl C-terminal alpha-
amidase enzyme (AE)) were suspended in F-12 medium to which aliquots
of trichostatin were added. Cells were cultured for 3 days at 37 dec
and then assayed for AE. Without trichostatin, AE productivity was
708 U/ml. At 10, 50, 100 and 200 nM trichostatin, AE productivities
were respectively 866, 1897, 1894 and 3359 U/ml.
                                                                                                                                                                                                                                                                                                                                                                                                     wp1; 95-156754/21.

N-PSDB; Q87970.

Increasing protein prodn. from cultured animal cells - by a trichostatin to the medium, effective at low concn. and injurious to host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-1995 (first entry)
Peptidyl C-terminal alpha-amidating enzyme.
Peptidyl C-terminal alpha-amidating enzyme;
trichostatin; CHO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R73053 standard;
                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 10-15; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Furukawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
lAlaAspGlyTyr....
                               AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                          TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 312
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                                                         CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
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JP-257881.
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0.945
43.103
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1. .39
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Percent Identity:
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ACC CCC
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                                                                                                                        06-MAR-1997.
28-AUG-1996; U14192.
31-AUG-1995; US-521872.
11-OCT-1995; US-540804.
26-JAN-1996; US-590399.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
(WHED ) WHOME AND THOMPSON CM, Young
                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
Purified RNA polymerase II holo:enzyme - comprises RNA polymerase II and one or more regulatory proteins, pref. suppressor of RNA polymerase B proteins or SNI/SNF proteins Claim 11; Fig 10a-b; 154pp; English.

Novel yeast SRB (suppressor of RNA polymerase B) proteins SRB4, SRB5.
                                                                                                                                                                                                                                                         04-JUN-1997 (first entry)
04-JUN-1997 (first entry)
Yeast transcription regulatory factor SRB8.
Transcription regulatory factor; suppressor c
SRB8; RNA polymerase II; holoenzyme; SWI/SNF.
Saccharomyces cerevisiae.
W09708301-A1.
                                                                                              N-PSDB; T59908
                                                                                                             Chao DM, Koleske AJ,
WPI; 97-179258/16.
                                                                                                                                                                                                                                                                                                                                                                                     W13825 standard;
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US-09-323-427-1
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Percent Similarity:
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luIlePheAsnPheAspGlnValValGluIleThrGluGlnIleLysMet
                                                                                             nTyrAsnMetValLeuArgAsnValMetGluTyrAspValLysPheTyrG
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1032 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG

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seq_name: A_Geneseq_36:R99462
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seq_documentation_block:
ID R99462;
AC R99462;
DT 30-JAN-1997 (first entry)
DE Biosynthetic enzyme of icosapentaenoi
KW Icosapentaenoic acid synthase; EPA; of
KW foodstuffs; animal feed; lipid balanc
antiinflammatory; anticancer agent.
Shewanella putrefaciens.
PN W9621735-Al.
18-JUL-1996; J00030.
PR 13-JAN-1995; JP-004299.
PR 13-JAN-1995; JP-004299.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PI KRAto S, Kondo K, Yamada A, Yazawa
MPI; 96-342288/34.
DR N-PSDB; T34137
DR N-PSDB; T34137
Production of icosapentaenoic acid us
PT DNA coding for icosapentaenoic acid us
PT DNA coding for icosapentaenoic acid serial
CC The DNA sequence (T34137) which encod
CC icosapentaenoic acid (EPA) can be use
CC The DNA sequence allows efficient mid
CC is a raw material for drugs, agroched
CC feedstuffs. EPA is also useful for li
CC an antihypertensive, antiinflammatory
SQ Sequence 2756 AA;
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US-09-323-427-1 x R99462
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The DNA sequence (T34137) which encodes the biosynthetic enzymes of icosapentaenoic acid (EPA) can be used to transform Escherichia coli. The DNA sequence allows efficient microbial production of EPA, which is a raw material for drugs, agrochemicals, foods and animal feedstuffs. EPA is also useful for lipid balance correction and as
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Blosynthetic enzyme of icosapentaenoic acid synthase.
Icosapentaenoic acid synthase; EPA; drugs; agrochemicals; foodstuffs; animal feed; lipid balance correction; antihypertensive; antiinflammatory; anticancer agent.
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KRATO S, KONDO K, Yamada A, Yazawa K;
WPI; 96-342288/34.
N-PSDB; T34137.
Production of icosapentaenoic acid using transformed E. co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             638 TTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416
                                                oThrGlnAlaProAlaProLysAlaGlnPro.....AlaProValT 1211
                                                                                                                                                                                                              GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA.. 1066
                                                                                                                                                                                                                                                                       CACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCC 1018
                                                                                                                                                                                                                                                                                                                                                                                   aProAlaIle......HisAsnGluAlaIleGlnS 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lnAlaGlnThrLeuGlnSerHisThrGlnPheLeuGluMetGlnAlaGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hrGlyIleValThrSerGlnIleGluHisValIleGluCluLysIleVal 1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGAC 968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrPheThrThrLeuMetThrGluGlnAlaLysLeuAlaSerSerGlyVa 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGCGGTTGTCCATTCCTGCTTT.....GTCGATGATGGTAACGGTGAT 781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uValGluLysValValGluValGluAlaProValAsnSerValGlnAlaA
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                                                                                                        .....TCTGCAGAACCGGAGAATATCATTGATGTAC 1097
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seq_documentation_block:
ID R05159 standard; prot
AC R05159;
DT 09-OCT-1990 (first e
DE Sequence of human bon
KW Osteoporosis; rheumat
KW Osteoporosis; peri
OS Homo sapiens
PN US7432044-A.
PR 3-NOV-1989; US-432044
PR 3-NOV-1989; US-432044
PR 3-NOV-1989; US-432044
PR 3-NOV-1989; US-432044
PR N-PSDB; OS-432044
PR (USSH) Nat Inst of He
PI Termine J;
DR WPI; 90-178641/23.
DR N-PSDB; Q04490.
PT used in detection, di
PT and/or connective tis
PS Disclosure; p: Engils
CC probes and Abs raised
CC diseases states such
CC diseases states such
CC Proteins may also be
Sequence 368 AA;
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                                                                                                                                                                                                                                                                                                                                       1055 CTCA.....AGAAAAGAT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1005 AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1198 ACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAA 1247
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1163 CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 1212
                                                                                                                                                                                                                            1068 ....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; p; English.

Disclosure; p; English.

Probes and Abs raised to the proteins can be used to determine their levels useful in diagnosis of associated conective tissue diseases states such as osteoporosis, osteo/rheumatoid arthritis, Paget's disease, artherosclerosis and periodontal disease.

Paget's disease, artherosclerosis and periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1249 laGluThrAlaLeuSerAlaThrLysValGlnAlaThrMetLeuGluVal 1265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of human bone proteoglycan I (biglycan).
Osteoporosis; rheumatoid arthritis; Paget's disease;
atherosclerosis; periodontal; human bone matrix; proteoglycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone matrix DNA and proteins - used in detection, diagnosis and treatment involving skeletal and/or connective tissue disease states.
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3-NOV-1989; US-432044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH) Nat Inst of Health.
                                                                                                                                                                                                                                                                                                                                                                                                 86 LysGluIleSerProAspThrThrLeuLeuAspLeuGlnAsnAsnAspIl 102
                                                                                                                                                                     euValLeuValAsnAsnLysIleSerLysIleHisGluLysAlaPheSer 135
                                                                                                                                                                                                                                                                                   eSerGluLeuArgLysAspAspPheLysGlyLeuGlnHisLeuTyrAlaL 119
                                                                                                              CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC 1162
                                                       TGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATT 1297
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41.472
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Gaps: 14
Percent Identity: 19.732
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seq_name: A_Geneseq_36:R88469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1423 ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC
                                                                                                                                                                                                                            Feline infectious peritonitis 1 virus spike protein. Feline infectious peritonitis 1 virus; FIPV-I; spike vaccine; prevention; treatment. Feline infectious peritonitis 1 virus.
DNA encoding feline infectious peritonitis I virus spike protein used in a vaccine for prevention and treatment of FIPV-I infection Claim 1; Page 14-17; 23pp; Japanese.
                                                                                        10-JUN-1994; 129300.
10-JUN-1994; JP-129300.
(KITA ) KITASAFO KENKYUSHO SH.
WPI; 96-072341/08.
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                                                                                                                                                                                       J07327683-A
19-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 GluAsnSerGlyPheGluProGlyAlaPheAspGlyLeuLysLeuAsnTy
                                                                          N-PSDB; T10166
                                                                                                                                                                                                                                                                                                                                                                   R88469 standard; Protein; 1464 AA.
                                                                                                                                                                                                                                                                                                                         14-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAATAGTTTCGTTTGTTATTATCA...TCATTATCAACTTGTCCT... 1616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lAspValArgIleHisAspAsnArgIleArgLysValProLysGlyValP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAAATCAGAAGGCATAAAAATAATGTTAGA.....ATCA 1347
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alignment_block:
US-09-323-427-1 x R88469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
r.....TyrValCysAsnGlyAsnThrHisCysLeuLysLeuL
                                                                                                                                                                                                                                                                                                TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC 794
                                                                                                                                                                                                                                                                                                                                                                                                 TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt rH1sValGluIleValAspAspSerIleGlyValIleLysProValSerT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \verb|alAsnGlnThrAspLeuPheGluPheValAsnAsnThrGlnAlaArgArg|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCACTTCCA.....TTTGATTCATGCAAT......GTTGCGCGT
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                                                GlyAlaArgLeuGluSerLeuMetLeuAsnAspMet.....
                                                                                              GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA
                                                                                                                                               euThrGlnTyrThrSerAlaCysGlnThrIleGluAsnAlaLeuAsnLeu
                                                                                                                                                                                             TA.....AATGCT.....GAT
                                                                                                                                                                                                                                                                                                                                            TyrIleGlnIleGlnValLysProValValAsp.....CysAlaTh
                                                                                                                                                                                                                                                                                                                                                                                                                                               hrGlyAsnIleSerIleProLysAsnPheThrValAlaValGlnAlaGlu 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerSerPheAlaIleCysAsnThrGlyGluIleLysTyrValAsnValTh 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oGlnPheTyr.....TyrIleThrLysTrpAsnAsnAspThrSerSerA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ... GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT
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Gaps: 16
Percent Identity: 19.895
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seq_name: A_Geneseq_36:W88310
              Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food, or faces or patient samples suscess or patient samples places or patient samples suscess fig 7; 165pp; English.

Provided the second of the protein encoded by the wbdM gene of a gene cluster (see X06748) involved in the biosynthesis of the Escherichia coli Olli O antigen. The protein shows high the biosynthesis of the Escherichia coli Olli O antigen. The use of nucleic acid be a colitose or glucose transferase. The use of nucleic acid concludes derived from particular assembly and transport genes, particularly wbd (transferase), wzx (flippase) and wzy (polymerase) genes, within O antigen gene clusters improves the specificity of methods for the detection and identification of O antigens, e.g. in testing food- or faecal-derived samples, or samples from patients.

The O antigen is a major virulence factor of enteropathogenic E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. coli colitose or glucose transferase.
O antigen; Ol11 antigen; wbdM gene; colitose transferase;
glucose transferase; diarrhoea; haemorrhagic colitis; diagnosis Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; X06748.
                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997; AU-006545.
(UNSY ) UNIV SYDNEY.
Reeves PR, Wang L;
WPI; 99-059669/05.
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22-JUL-1997; AU-008162.
01-MAY-1997; AU-006545.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleGlyGlyMetAlaLeuGlySerIleThrSerAlaValAlaVal.ProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTATGGGTTTAAGCATT...GCATTGATTGCTGCCGTCATTATTACCAT 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATG 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rAspValAlaAspLeuValCysAlaGlnTyrTyrAsnGlyIleMetValL
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  diarrhoea and
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  haemorrhagic
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alignment_block:
US-09-323-427-1 x W88310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 ATAACAATCAATTTTAATACACGTAATGCATTCGAAGGAC...... 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 277
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8
                                               ACTGTGGAA.....ATTCTAAATGCTGATGGATGTGC 813
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euLeuIleAlaGlyAspGlyAlaLeuArgAsnLysLeuLeuAsp...
                                                                                                                                                  TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGAT.....
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                                                                                                aIleAsnHisLeuIleLeuSerLysThrSerAsnCysAsnAspPheIleL
                                                                                                                                                                                                                                                                                                       spSerThrAlaValLeuLeuAlaVal........GlyArg
                                                                                                                                                                                                                                                                                                                                                                                                        pPheAspIleAsnValArgLysLysThrArgAspAlaPheAsnLeuLysA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AAATGGACATGCGATTCTGAAACCGTTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lePheSerArgPheIleArgMetLeuIleProAlaValProLeuIleCys 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGT
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863 3	TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGG	814
5	::::::: uLeuIleAspValGlyProArgGluLeuArgSerSerLeuHisGl	7
813	ATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	764
763 2575	ATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGCTTTGTC:::	714 2561
713 2560	AGTTCAATTIGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG::::::::::	664 2544
663 2544	ATGCCAGTATGCAGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACC ::	614 2537
613 2536	AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG:::::: ::: ::: LysileArgSerPheLeuProSerLeuLysLeuGlu.	564 2525
563 2524	CTGATAAAACAGTTAGTGCAC	543 2508
542 2508	GTACAATGCTTTTACATGGAAG	521 2491
520 2491	CGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGA : : : : : : : : :	477 2475
476 2474	GAATCCACGTGGTATTTTTGTAACAACAGCTGTTGTCATTT :: :: ::::: ::: spPheLysAlaValTyrMetGlnTyrValTrpLeuLeuLeuLeuAspAsp	436 2458
435 2458	TCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCT	392 2441
391 2441	GTAATGATGAAGGTGGACGTCAAGTTGCCGGAATT :: :::	357 2425
356 2424	GAAAGGTCTTTATGATCAAGAAGGTTGCC	328 2408
327 2408	ACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGT:::	281 2392
280 2391	GTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA ::: ::: heLeuGlyValIleGlyLysSerLeuAlaGluSerAsnProGluLeuThr	236 2375
235 2375	ATTCCGGTTGACAAT rHisPheHisArgSerProGluValTyrValProGluAspThrThrP	221 2358
220 2358	ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCG:::! :::::::::::::::::::::::::::::	173 2342
172 2341	TTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATG :: ::::	132 2325
131 2325	AGCAATAATAACCCCATCAAGTGGAGGAAGAAGAACAGGAAGCAATCTTAG :::::::::::::::::::::::::::::::::::	82 2316

1401 AATAACTAATTTTAGCTAACAAATATATATGTAGGAAATAATTACTG 1450	TATCAATGCCAGATCAGTATAACGAACC allels	::: ::: 2592 euLeuMetAsnValCys
alignment_scores: Quality: 88.00 Length: 500 Ratio: 0.376 Gaps: 23 Percent Similarity: 46.800 Percent Identity: 18.200 alignment_block: US-09-323-427-1 x R42452 Align seg 1/1 to: R42452 from: 1 to: 1634	1300 LIGHT CHARLAND TITLAND TO THE CALL CONTROL OF THE CONTROL OF THE CONTROL OF THE CANADA THE CONTROL OF THE CANADA THE	ysSerThralapheaspPheLeuLysMetMetPheArgAsnSerTyrPheGCTTCTGAAAAGCTTATTCATTATTCAGTAATCTTTTA [

781	GCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGAT	738 081
737 1080	GCCAGTTTATCATAAATGGACATGCGATTCTGAAAACCGTTGATACTTTCT::::::::::	8901 889
687 1068	TTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA ::: ::::::::: ::: valSerLysasnSerLysProAlavalGlnSerIleSerGlyas	638 054
637 1053	CTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATT::: ::: ::: ::::::::::	588 1037
587 1037	AGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAA ::::: :::: ::::::: :::::: uvalGluLysvalvalGluValGluAlaProValAsnSerValGlnAlaA	541 1020
540 1020	TTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGA	491 1004
490 1003	TTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTA ::: ::: ::: hrGlylleValThrSerGlnIleGluHisValIleGluGluLysIleVal	452 987
987	${\tt aAsnHisIleSerLysAlaThrArgAlaLysMetAlaLysSerLeuGluT}$	970
451		451
451 970	GTTGCGCGTACACGATCTCTGAATCCACGTGGTATT	416 954
415 953	CCGGAATTTCACTTCCATTTGATTCATGCAAT	3 84 938
383 938	TCTTTATGATCAAGAAGGTTGCCCGTAATGATGAAGGTGGACGTCAAGTTG	932
	TTTTAATACACGTAATGCATTCGAAGGACATGTTTATGT::::: ::: ::: ::: ::: ::: ::: ::: ::	284
915	 InLysLeuValGlnGlyThrLeuValAsnThrGluAsnGluValCysThr	668
283	ACA	281
280 899	TGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA : :::::: ::: ::: pGlyAlaArgValPheValGluPheGlyProLysAsnIleLeuG	235 884
234 884	GCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAA	185 873
184 872	TTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATT ::: :::	135 859
134 859	AATAATAACCCCATCAAGTGGAGGAAGAAGAAGAAGAAGCAATCTTAGTTT ::: ::::::	85 843
84 843	CCGACTGCAGCAACAACAACAACAACAACAACAACAACAACAACAA	35 827

782 1097	ACTGTGGAAATTCTAAATGCTGATGGATG 8	810 1113
811 1113	TGCTCTTGATAAATATTTGCTAAATAATTTGGAA	844 1130
845 1130	TATCCAACAGATTTAATGGCTGGC	868 1146
869 1147	CAAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCA 9 :::::: :::::::::::::::::::::::::::::	918 1163
919 1163		968 1173
969 1173	CACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCC	1018 1180
1019 1181	GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA : : : : : : : : : :	1066 1197
1067 1197		1097 1211
1098 1211	GAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCA :::::	1147 1227
1148 1228	GTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAAT 1	1197 1236
1198 1236	ACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAA :::::::::::::::::::::::::::::::	1247 1249
1248		1297

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Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-07-07-367-2 + 100.00 158.80
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Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-303-238-3 + 91.50 153.01
Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-67 + 90.00 142.94
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Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-63 + 89.00 121.31
Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-63 + 89.00 121.31
Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-63 + 89.00 121.31
Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-637-640-2 + 87.00 118.10
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Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-637-640-2 + 87.00 117.47
Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-637-640-2 + 86.50 127.71
Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-637-640-2 + 86.00 127.71
Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-305-071-65 + 86.00 127.72
Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-305-071-65 + 86.00 127.73
Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-305-071-65 + 86.00 127.73
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Database length: 13297546
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Query length: 1779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search time (sec): 99.320000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MODEL=frame+_n2p.model -DEV=xlp
-Q-/cgn2 1/USPFO_spool/US09323427/runat_14042000_170513_19887/app_query.fasta.1
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=backtrans.rai
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS-human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-MINLEN=0 -MAXXEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3
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                         alignment_block:
US-09-323-427-1/rev x US-08-415-751-6
                                                                                                                                 alignment_scores:
Quality:
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                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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COMPUTER: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                     ORGANISM:
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-415-751-6
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APPLICANT: PETERSEN, CAROLYN
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 324-16' INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING LAND. 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/071,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/01
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/88
FILING DATE: MAY 29, 1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08 FILING DATE: 03-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6, Application US/08415751
o. 5643772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
: United States of America
                                                                                                                                                                                                                                                                                                     362 amino acids
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                                                                                                                                                                                                                                                                                                                                                                       (415) 324-1678
                                                                                                                                                                                                                                                  ss: single
linear
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                                                                                                                                                  Positions coded by nonsense codons
                                                                                                                                    identified as Xaa.
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NUMBER: 07/891,301
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CRYPTOSPORIDIUM ANTIBODIES, DNA
AND RNA ENCODING THEM, HYBRID
VECTOR AND TRANSFORMED HOST AND
METHODS FOR IMMUNOTHERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/415,751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 CAATAAGACGAATCATCATTTCAGAAGATTTAGTAAATTCGATTTTTAGA 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 CGCGCAACATTGCATGAATCAAA...TGGAAGTGAAATTCCGGCAACTTG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 ACG.....ATCAACTTTGGTAAC.....AAATAATGGATGAAACGAAA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 655 GGTTGGTCCACCATCCAA.....AATTTCATAACGGCATACTGGCATCG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 ATTGTTATTGAAGTTGGTCCACATTCAATTTCTGGCTCACCTTCGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 eGlyLysProValLeuLeu***Val***ThrTrpGlu***IleAlaCysI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 TGACAACAGTTGTTGCTACAAAATACCACGTGGATTCAGAGATCGTGTA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 GCACTAACTGTTTTATCAGCTTCCATGTAAAAGCATTGTACTCGATATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      611 GGACAATTTGAGTTTGAAAAGCAGTTGTGATTTCAGATACCTCAATCTGT 562
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                                                                                                     u***CysCysCysCysCys 215
                                                                                                                                                                                                                                                   .... TGCTGCAGTCGGTGT 32
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                                                                                                                                                                                                                                                                                                            ...........ValSerLeuGlySerSerSerCysArgTrp...HisCys 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....AsnValThrAspIleArg***TrpCysArgCysCysCys..... 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrLysLeuProAspPheGlySerAsnGlyArgProThrIleGlySerIl 105
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                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-415-751-35
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alignment_scores:
Quality:
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                                                                                                                                                                            alignment_block:
                                                                                                                          Align seg 1/1 to: US-08-415-751-35 from: 1 to:
                                                                                                                                                            US-09-323-427-1/rev x US-08-415-751-35
                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35, Application US/08415751 Patent No. 5643772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 324-1678 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of A ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5
COMPUTER: PC
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATE: 08/071,880
PPLICATION NUMBER: 07/891,301
APPLICATION NUMBER: 07/891,301
                                                    135 CysCysCysLeuAsnTrpThrLeuTrpTrpTyrGlyCysCysCysCy 151
                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                     124 TGCTTCCTGTCTTCCTCCACTTGATGGGGTTATTATTGCTGTTGTTG
                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Hana Dollezalova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
LENGTH: 362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/415,751 FILING DATE: 03-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NELSON, RICHARD, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
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0
51.613
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151 sCys***LeufrpTyrAsnCysCysCysCysPheCysCys 165

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COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, Barbara G.
REGISTRATION NUMBER: 331.13
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-651-3708
TELEPHONE: 510-655-3542
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3300 mnino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    1216 ATTTTGTACTGCAGCAAGTAT......TACAGGTTGTCCATTATGTT 1176
                                                                                                                                                                                                        1125 CTAATTTCAAGGGTTGATATC.....AGTTCGTACATCAATGATATT 1082
::||||| ::: ::: |||
                                                                                                                                                                                                                                                                                              1031 CAGGTTTTGCTGCGGCACCACCTGTTTTAACAGCTCCGAATCCTTGTGGT 982
                                                                                                                                  1081 CTCCGGTTCTGCAGATCTTTTCTTGAGTAAACGAAGTTGCGCAGCTGCAG 1032
                                                                                                                                                                            774 alAsnPheLeuSerGlnPheLeuIleProLysProTyrLeuThrGluIle
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804 uProTyrAsnThrGlnThrThrCysTyr............
                                                                                   791 IleAsnPheIleMetProPhe.....GlnArgGluAlaArgCysLe
                                                                                                                                                                                                                                                                       761 sLysThrCys...........PheSerPheTyrArgLeuIleGluIleV 774
                                                                                                                                                                                                                                                                                                                                                             745 IleValPheCysArgIlePheGluLeuValTyrArgLeuLeuIleAlaLy 761
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ADDRESSEE: Chiron Corporation
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TYPE: amino acid
STRANDEDNESS: sind
TOPOLOGY: linear
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CITY: Emeryville
STATE: CA
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Ratio:
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0.537
41.501
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Helicobacter Pylori Cagi Region
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Gaps: 24
Percent Identity: 22.075
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145 103	TACAGAAAGCAATAAGACGAATCATCATTTCAGAAGATTTAGTAAATTCG ::: ::: ::: : uAlaGlu	194 1020
195 102	TTCGACACCATTGTCAACCGGAATAAGACAATGAGACAATAAGTGTAG	244 1005
245 100	AAATTGATTGTTATTGAAGTTGGTCCACATTCAATTTCTGGCTCACC ::: ::: ysValPheAsnPheAsnProPheTrpIle	291 995
292 995	CATAAAGACCTTTCACATAAACATGTCCTTCGAATGCATTACGTGTATTA: ::::: eileginSerCysilei	341 989
342 989	AATTCCGGCAACTTGACGTCCACCTTCATCATTACGGCAACCTTCTTGAT:: ::	391 982
392 981	GGATTCAGAGATCGTGTACGCGCAACATTGCATGAATCAAATGGAAGTGA::	441 969
442 969	ATAATGGATGAAACGAAATGACAACACTTGTTGTTACAAAAATACCACGT :::::: ::: ::: :::	491 957
492 956	TTCCATGTAAAAGCATTGTACTCGATATGCACGATCAACTTTGGTAACAA :::::::: fyrargLeu	541 946
542 945	GATTTCAGATACCTCAATCTGTGCACTAACTGTTTTATCAGC ::: ::: lulleGlyArgLeuLeuTyrProThrGlulleThrArgCysPheSerHis	583 929
584 929	GCATCGGGACAATTTGAGTTTGAAAAGCAGTTGT	617 917
618 916	TGGTCCACCATCAAAATTTCATAACGGCATACTG ::: ::: :::: IleTyrPheArgPhePheSerSerIleGluThrPheIlePhe	652 903
653 902	TGATAAACTGGCTGACCAATGATAGCAAATTGAACTGGTTGACCGGT ::::: ::: ysLeuArgProIleThrAspGlySerIleH1sThrIleLeuAsnGlyLeu	886
700 886	GGACAACCGCGCAGAAAGTATCAACGGTTTCAGAATCGCATGTCCATTTA :	749 873
750 873	ATCACCGTTACCATCATCGACAAAGCAGGAAT	781 857
782 856	AGCAAATATTTATCAAGAGCACATCCATCAGCATTTAGAATTTCCACAGT :: SerIleAsnGlyPheValPheGluSer	831 848
832 847	CGTGAGCTTCTTGGCCAGCCATTAAATCTGTTGGATATTCCAAATTATTT:::::: e:1leasnPhe	881 844
882 844	ACTGATCTGGCATTGATAGAAAAGCTGTGATCGATCCGCATATTTGTATA ::::::::::::::::::::::::::::	931 828
932 827	TCTGAACATTGTGGTCGAACACATTCGCTATTTGGTTCTTTAATGGTAAT ::: ::: :::: ::: ::: ::: ::: :::	981 814

us-09-323-427-1.backtrans.rai

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seq_documentation_block:
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                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1080 LeuIlePheLeuAlaValSerLeuSerPheCysPheHisPheIlePheVa 1096
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 935 amino acids
TYPE: AMINO ACID
                                                                                                                                           REGISTRATION NUMBER: 30,598
REFERENCE/DOCKET NUMBER: 4-18110/A/CGJ 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914)785-7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
MOLECULE TYPE:
                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 329911/90
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Villamizar, Johnn
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 210535/90 FILING DATE: 10-AUG-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 141678/90
FILING DATE: 01-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kangawa, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: U. FILING DATE: 19910530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                        TOPOLOGY:
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Shimoi, Hiroko
Suzuki, Kenji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kangawa, Kenji
VENTION: No. 5196316el Enzyme and DNA Coding Therefor
EQUENCES: 2
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Nishikawa, Yoshiki
Kawahara, Takashi
                                                                                                                              (919)541-8689
                      linear
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alignment_block:
US-09-323-427-1 x US-07-707-367-2
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Quality:
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692 lyAspAlaHisAlaAsnAlaValTrpLysPheSerProSerLysAlaGlu
                                                                                                                                                               841 GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAAT 890
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                                                  891 ATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGT.....
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                                                                                                             eAspMetProHisAspIleAlaAlaAlaAspAspGlyThrValTyrValG
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Percent Identity: 19.437
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16,
                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1143 TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCT 1192
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                                       FILING DATE: 24-MAY-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
STREET: 1233 20th Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING
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                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 20036-8218
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FILING DATE:
                           APPLICATION NUMBER:
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5871995
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IFUKU, Ohji
KATO, Ichiro
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                                                                                              24-MAY-1991
    15-AUG-1989
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                           JP 1-209687
                                                                                                                                                                  Version
                                                                                                                                                                       #1.25
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alignment_block:
US-09-323-427-1 x US-08-070-301-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 887-041
TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        679
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                                                                                                                                                                                                                                                                                                                                            664
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ORIGINAL SOURCE:
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APPLICATION NUMBER: JP 2
FILING DATE: 02-AUG-1990
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APPLICATION NUMBER: JP 2-106412
FILING DATE: 24-APR-1990
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                                     550 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Player, William E. REGISTRATION NUMBER: 31,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 989 amino acids
uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA
                                                                               AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                                                                                                 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                               AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lAlaAspGlyTyr......
                                                                                                                         AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
                                                                                                                                                                                                                                                   \verb|nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI|
                                                                                                                                                                                                                                                                                                                                     Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                                                                                                                                           ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 499
                                                                                                                                                                                                                                                                                             Quality:
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Patent No. 5919666
GENERAL INFORMATION:
                                                                                                                                                       APPLICATION NUMBER: US 08/521,872

PRIOR APPLICATION DATE: 21-AUG-1995

PRIOR APPLICATION DATE: S08/218,265

PRIOR APPLICATION NUMBER: US 08/218,265

APPLICATION NUMBER: US 08/218,265

APPLICATION NUMBER: US 08/218,265

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WHI94-03A2

TELEPHONE: 617-861-6240
                                                                                                                TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 5919666el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Young, Richard A. APPLICANT: Koleske, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797 AATGCTGATGGATGTGCTCTTGATAAATATTTG.....CTAAATAATTT 840
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                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01 FILING DATE: 11-OCT-1995
                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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alignment_block:
US-09-323-427-1 x US-08-540-804-12
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                                                       1132 TAATC.....AAGCTTTGCCAGTTGATTTACGTCACC 1163
                                                                                                                                                                                                                                                                                                1032 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG 108
                                                                                                                                                                                                                                     451 ArgIleLeuSerAsn.......AspIleThrAsnLeuGl 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384
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472 etValAlaGluTrpTyrLeuSerHisLeuCysSerGlyIleLeuSerSer 488
                                                                                                                                                                                                                                                                                                                                                           434 luIlePheAsnPheAspGlnLeuValGluIleThrGluGlnIleLysMet 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417 nTyrAsnMetValLeuArgAsnValMetGluTyrAspValLysPheTyrG 434
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Ratio:
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                                                                                                                  LysThrProLeuSerIleLysIleM
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                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08218265 Patent No. 5922585
                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1533
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                                                               APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5922585el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Thereof
                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       536 IleLeuLeuCysTyrGlnLysLeuPheSerGlnPheIleAsnAspHisIl 552
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTAGCTAACAAATATATAGTAT ......GTAGGAAATAATTACTG 1450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAsnGlnAlaValGlyGlnThrTrpAsnPheProGluValPheGlnVa 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gIleGluLeuGlnSerValTyrAsnAspGluLysLeuLysThrGluLysL 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAATACAATAAGTGATATTTTC.....ATCAAAACTTCTTCTA 1488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....TTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....CTGCCATATATTCGTTTCTTCTTATCATCCTTCTAATAACTAA 1409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....MetLeuLeuIleAlaThrAsnLeuLysGluTyrIleLysPheMe 693
                                 OF SEQUENCES:
                                                                                                                                                                                                           Young, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-218-265-12
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US-09-323-427-1 x US-08-218-265-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-218-265-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617-861-624
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/218
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHIS
                                                                                                                                                                                                                                                                                              677
                                                                                                                                                                                                                                                                                                                                        323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 CATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 TyrValAspGlnAsnProLeuThrMetHisLysIleIleGlnLeuIleLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 uTrpSerIleHisProSerArgGlnPheAspHisTyrGluSerAsnGlnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02173
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                                                                                TyrMetMetProSerLeuTyrArgLeuLeuAsnIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......GTGCACAGATTGAGG......TATCTGAAATCACAAC
                                     GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT
                                                                                                                                                                                                           TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG
                                                                                                                                                                                                                                                  pSerLeuValPheGlnLeuAlaLysAsn.....
                                                                                                                                                                                                                                                                                            ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT 726
                                                                                                                                                                                                                                                                                                                                                                           TGGATGGTGGACCAACCGGTCAACCAGTTCAAT.....TTGCT 676
                                                                                                                                                                                                                                                                                                                                                                                                                euValAlaLysLeuLeuLeuLeuArgIleAsn......
.....IleThrTyrGlyIleIleLysValProThrTyrIleArgLysL
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                                                                                                                                                                 ......PheSerAlaGlnLysArgValValSer
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47.444
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Gaps: 24
Percent Identity: 19.836
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1410
1573 ATGAATAGTTTCGTTTATTATCATCATTATCAACTTGTCCTATTTTA 1622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1164 GTGCAC.....TTCTGCAACATAAT 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1082 AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1032 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 gIleGluLeuGlnSerValTyrAsnAspGluLysLeuLysThrGluLysL 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 etValAlaGluTrpTyrLeuSerHisLeuCysSerGlyIleLeuSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434
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                                                                       lAsnIleArgPheLeuLeuHisAsnSerGluIleIleAspThrAsnThrS
                                                                                                                                                                                                                       SerAsnGlnAlaValGlyGlnThrTrpAsnPheProGluValPheGlnVa 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGCTTTTATAGCTTCTGAAAAGCTTATTCATTATTCAGTAATC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAC...AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA 949
                                                                                                                                                                                                                                                                                                                                                                               euLysAsnAspLysSerGluValLeuLysValTyrSerMetIleAsnAsn 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTAGCTAACAAATATAGTAT......GTAGGAAATAATTACTG 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....CTGCCATATATATTCGTTTCTTCTTATCATCCTTCTAATAACTAA 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AAAAATAATGTTAGAATCATCGAAGCAATAATAAAA.... 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IleLeuLeuCysTyrGlnLysLeuPheSerGlnPheIleAsnAspHisIl 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lnLeuLeuSerAsp......IleGluSerLeuGluAlaLeuMetAsp 535
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                                                                                                                                               ......TTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC 1572
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alignment_block:
US-09-323-427-1 x US-07-906-349A-6
                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: US-07-906-349A-6
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-07-906-349A-6
                                                                                                                                                                                       Percent Similarity:
                                                                                  Align seg 1/1 to: US-07-906-349A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5434064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,349A
FILING DATE: 30-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1673 CCCAATTTTTATGGGCATCATTTCCTATTCTGTAAACAATTCACTTATTT 1722
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573 ThrThrAlaAlaAlaThrCysAlaCysThrGlyCysThrGlyCysThrCy
                                         982 ACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Margolis, Benjamin L.
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES
TITLE OF INVENTION: TARGET PROTEINS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                709 InLeuIleSerLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              668 erLysGlnPheGlnLysAlaArgAsnAsnVal......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 419 Seven CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/07906349A
                                                                                                                                                                                                                                                                                                                                                                                                                     801 amino acids
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419 Seventh Street, N.W.
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Skolnik, Edward Y.
                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                       93.00
3.000
40.260
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                                                                                from: 1
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28.571
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seq_documentation_block:
; Sequence 35, Applicati
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FILING DATE: 03-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                         TELEFAX: (415) 324-16;
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     613 rThrThrThrCysAlaThrCysCysThrThr 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 TELEPHONE: (415) 324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: DOS
     NAME/KEY:
                                         ORGANISM:
                                                                                                 TOPOLOGY:
                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                     ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG 1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NT: GUT, JIR: INVENTION:
                                                                                                                                                                                                                                                                                                             Hana Dolezalova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: PHILLIPS, MOORE, LEMPIO & FINLEY
                                                                                                                                                     362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wordperfect 5.1
                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEECH, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETERSEN, CAROLYN
                                       Cryptosporidium parvum
Positions coded by nonsense codons
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                                                                                                               single
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                                                                                                                                                                                                               324-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND RNA ENCODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRYPTOSPORIDIUM ANTIBODIES, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYPEPTIDES BINDING ANTI-
                                                                                                                                                                                                                                                                                         30,518
                                                                                                                                                                                               35:
                                                                                                                                                                                                                                                                         480.19-2 (HHD)
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alignment_block:
US-09-323-427-1 x US-08-415-751-35
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US-08-415-751-35
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                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-303-238-3
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                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application Patent No. 5654270
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 .....TyrGly......CysCysCysCysCys***LeuTrpTyrAs 157
                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                  APPLICANT: PIERSCHBACHER, MICHAEL D. APPLICANT: BORDER, WAYNE A. TITLE OF INVENTION: INLIBITORS OF CETITLE OF INVENTION: AND METHODS FOR
                                                                                                                                                                                                 APPLICANT: WHITBY, DAVID J. APPLICANT: HARPER, JOHN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 n 157
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                                                                                                                                                                                                                                                    APPLICANT: RUOSLAHTI, ERKKI I. APPLICANT: LONGAKER, MICHAEL T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
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STREET:
                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....LeuValGlu*****LeuGlnLeuArgLeuValValLeuLeu* 97
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                                                                                                                                                                                                                                                                                                                                                         Application US/08303238
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4370 LA JOLLA VILLAGE DRIVE, SUITE 700
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                          CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.50
1.220
49.669
                                                                                               INHIBITORS OF CELL REGULATORY FACTORS AND METHODS FOR PREVENTING OR REDUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 25.828
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                                                                                                    REDUCING SCARRING
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TELEFAX: 619-535-8949

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-238-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-323-427-1 x US-08-303-238-3
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    Quality:
    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-303-238-3 from: 1 to: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY,AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION UNMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
1113 CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1068 .....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1005 AAACAGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA 1054
                                                                                                                                                 1263 GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT 1312
                                                                                                                                                                                                                                                1213 AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAA 1262
                                                                                                                                                                                                                                                                                                                                               1163 CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 1212
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                                                                                                                                                                                                                                                                                                                                                                                        136 ProLeuArgAsnVal......GlnLysLeuTyrIleSe 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 euValLeuValAsnAsnLysIleSerLysIleHisGluLysAlaPheSer 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 eSerGluLeuArgLysAspAspPheLysGlyLeuGlnHisLeuTyrAlaL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||:::::: |||::::||||:::||| 102
86 LysGluIleSerProAspThrThrLeuLeuAspLeuGlnAsnAsnAspIl 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                              .....IleProProAsnLeuProSerSerLeu.....Va 162
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0.738
41.472
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Percent Identity: 19.732
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179 h	heSerGlyLeuArgAsnMetAsnCysIleGluMetGlyGlyAsnProLeu 195
1359 .	ATAAAACTGCCATA 1372
196 G	snSerGlyPheGluProGlyAlaF
1373 T	ATATTCGTTTCTTCTTATCATCCTTCTAATAACTAATTTTTAGCTAACAA 1422
212 r	rLeuArgIleSerGluAlaLysLeuThrG 222
1423 A	TATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC 1472
222 1	:: lyIleProLysAspLeuProGluThrLeuAsnGluLeuHis 235
1473 A	ATCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA 1522
236 L	euAspHisAsnLysTleGlnAlaIleGluLeuGluAspLeuLeuArgTy 252
	TTCAGTAATCTTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC 1572
252 r	SerLysLeuTyrArgLeuGlyLeuGlyH 262
73	16
262 1:	sasnGlnIleargMetIleGluAsnGlySerLeuSerPheLeuProThr 278
1616 .	
279 L	LeuArgGluLeuHisLeuAspAsnAsnLysLeuAlaArgValProSerGl 295
1617 . 295 yi	ATTTATTCTAACAGTTTATCATTTGTGATAATA 1650 ::: ::::::::::::::::::::::::::::::
1651 TO 1 312 1	TCACAAATTATACCTTGTATTGCCCAATTTTTATGGGCATC 1691 ::: ::: ::: ::: ::: ::: ::: 1eThrLysValGlyValAsnAspPheCysProMetGlyPheGlyVal 327
seq_name: ,	/cgn2_6/ptodata/1/iaa/backfiles1.pep:5340934-2
Pa.	eq_documentation_block: Patent No. 5340934 APPLICANT: TERMINE, JOHN D.;YOUNG, MARIAN F.;FISHER, LARRY W. ROBEY, PAMELA G. TITLE DE INVENTION: CONA SECUENCES OF HUMAN ROME MATRIX PROTETUS
NUMBER OF NUMBER OF CURRENT AI APPLICAY FILING! SEQ ID NO:2: LENGTH: 5340934-2	SEQUENCES: 13 SPELICATION DATA: PPLICATION DATA: ION NUMBER: US/07/432,044 DATE: 03-NOV-1989 368
alignment_s	scores: Quality: 90.50 Length: 299 Ratio: 0.730 Gaps: 14 Similarity: 41.472 Percent Identity: 19.732
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Align seg	1/1 to: 5340934-2
1005 A <i>l</i> 	AAACAGGTGGTGCCGCAAGCAAAACCTGCTGCAGCTGCGCAACCTTCGTTTA 1054 :::::: ::: : ::: LysGluIleSerProAspThrThrLeuLeuAspLeuGlnAsnAsnAspI1 102
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seq_documentation_block:
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; Patent No. 5587311
                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-67
                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                      1651 TCACAAATTATACCTTG.....TATTGCCCAATTTTTATGGGCATC 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1263 GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT 1312
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     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212
                                                                                                                                                                                                                                                      312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATATTCGTTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAA 1422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAATCAGAAGGCATAAAAATAATGTTAGA.....ATCA 1347
                                                                                                                                                                                                                                                leThrLysValGlyValAsnAspPheCysProMetGlyPheGlyVal 327
                                                                                                                                                                                                                                                                                                                                                          yLeuProAspLeuLysLeuLeuGlnValValTyrLeuHisSerAsnAsnI 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuArgGluLeuHisLeuAspAsnAsnLysLeuAlaArgValProSerGl 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAATAGTTTCGTTTGTTATTCA...TCATTATCAACTTGTCCT... 1616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rLeuArgIleSerGluAlaLys.....LeuThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGAAGCAATA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isAsnGlnIleArgMetIleGluAsnGlySerLeuSerPheLeuProThr 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rSerLysLeuTyrArgLeu......GlyLeuGlyH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyIle.....ProLysAspLeuProGluThrLeuAsnGluLeuHis 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heSerGlyLeuArgAsnMetAsnCysIleGluMetGlyGlyAsnProLeu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....ATTTTATTCTAACAGTTTATCATTTGTGATAATA 1650
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                                                                                     // Application US/08325071
5587311
COBON, Stewart Gary MOORE, Joanna Terry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135
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alignment_scores:
Quality:
Ratio:
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                                                                                                                         Percent Similarity:
                                            Align seg 1/1 to: US-08-325-071-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION DATA:
PRIOR APPLICATION UMBER: US 08/
APPLICATION NUMBER: 17-MAY-1993
                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/111 BIAU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acid
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APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
              304 TGCATTCGAAGGACATGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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TELEFAX: 904136
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                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 06-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: AU PI2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEMP, David Harold
SRISKANTHA, Alagacone
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                                                                                                                                                                                                                               protein
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16-OCT-1987
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                                                                                                                                     90.00
0.612
                                                                                                                         40.947
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                                                                                                                                                                                                                                                                                                           67:
                                                                                                                         Percent Identity:
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22
21.727
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              326
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459 200	427 ACGATCTCTGAATCCACGTGGTATTTTTGTAAC	427 187
426 186	CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC ::::::::::::::::::::::::::::::::::	377 173
376 173	TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT ::::: ::: sGluLysAsnLeuLeuGlnArgAspSerA	327 163
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seq_documentation_block:
; Sequence 22, Application US/08477451
; Patent No. 5928865
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; TITLE OF INVENTION: Helicobacter P
NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
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Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: li
; MOLECULE TYPE:
US-08-477-451-22
                                                                                                                                                                                                                             alignment_block:
US-09-323-427-1 x US-08-477-451-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 035.002
TELECOMMUNICATION INFORMATION:
TELEPAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1129 TGATAATCAAGCTTTGCCAGTTGAT 1153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1052 .....GAACCG 1078
                                                                                                                                     333 GTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||::::|||||::::|||||| 418 etTyrProLysLeuILeuILeLysLysAsnSerAlaThrGluIleGluGlu 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 yGlnAsnLysCysValLysValAsp 459
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CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
                                                                                            10 ValIleLeuValTyrProIleLeuPheLeuPheAlaLeuIleIleLys..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Chiron Corporation STREET: 4560 Horton Street
linear
                                                                                                                                                                                                                                                                                             89.50
0.393
40.426
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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                                                                                                                                                                                                                                                                                             Length: 564
Gaps: 28
Percent Identity: 18.085
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989	981 AACCACAAG
980 292	AACCAAATAGCGAATGTGTTCGACCACAA :: :: :: AsnPheMetAlaGluValLeuLysAsnGl
7	59 tLeuMetMetGlyLeuAsnGluAlaLeuGlyLysLysPhe
٠	
911 259	870 AAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTT
869 243	0 TAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGC
226	0 ProAsnLysGlnGluLeuThrGl
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769 209	CCTGCTTT
9	79 uLeuIleAlaPheHi
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609 133	Tyrse
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545 105	GAGTACAATGCTTTTACATGGAAG ::: ::: :PheLeuSerAlaTyrThr
92	
495	ACAACTGTTGTCATTTCATCCATTAT
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446 88	426
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	: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-61	seq_name:
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465		449
1599	Н	1550
449	SerSerAspAsnProTyrProThrPheIleTyrLeuTyrPheMetProVa	433
1549		1500
432	erSerThrSerPheAspAlaLeuIleSerValMetSerValIle	418
1499		1450
418	eArgGlyS	415
1449	AACTAATTTTAGCTAACAAATATATAGTATGTAGGAAATAATTACT	1400
415		400
1399		1350
399	rgLeuGlyPhePheLeuLeuHisArg	391
1349	AAAATAATGTTAGAATCATC	1300
391		386
1299		1250
385		385
1249		1200
385	lePheThrThrAspLeuAlaPheCysGlu	376
1199		1153
376	eThrAspSerPheLeuLysMetSerTyrLeuAspProLeuPheLeuArgI	359
1152		1106
359		343
1105		1068
342	rpCysIleAsnTyrLeuLysValLysPhePheHisLeuSerArgArgAla	326

Seq_documentation_block:
 Sequence 61, Application US/08325071
 Patent No. 5587311
 GENERAL INFORMATION:
 APPLICANT: COBON, Stewart Gary
 APPLICANT: MOORE, Joanna Terry
 APPLICANT: JOHNSON, Law Anthony York
 APPLICANT: WILLADSEN, Peter
 APPLICANT: KEMP, David Harold
 APPLICANT: RIDING, George Alfred
 APPLICANT: RIDING, George Alfred
 APPLICANT: RAND, Keith No. 5587311man
 TITLE OF INVENTION: DNA Encoding A Cell Membrane
 TITLE OF INVENTION: Glycoprotein Of A Tick Gut
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:

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alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
us-09-323-427-1 x us-08-325-071-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-325-071-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-325-071-61 from: 1 to: 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-CCT-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
19-PLICATION D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/111 BIAU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5399
TELEPAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
                                                                                         377 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 426
                                                                                                                                                                                                                           327 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                            304 TGCATTCGAAGGACATGT.....TTATG
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92 rgCysCysGlnGlyTrpAsnThr.....AlaAsnCysSerAlaAla 105
                                                                                                                                                                          82 sGluLysAsnLeuLeuGlnArgAsp
                                                                                                                                                                                                                                                                                                                                           66 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Gaps: 22
Percent Identity: 22.284
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	TGATAATCAAGCTTTGCCAGTTGAT 1153	1129
1 370		354
A 1128	AGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAG	1079
ս 353	rProLysLeuIleLysLysAsnSerAlaThrGl	337
3 1078	TTACTCAAGAAAAGATCTGCAGA	1052
м 337	$_{y}$ sLeuGlnAlaCysGluHisProIleGlyGluTrpCy	320
. 1051	GT	1045
a 320	IleLysAlaArgLeuIleAlaG	306
A 1044	TTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTG	995
. 305	As	294
C 994	AGCGAATGTGTTCGACCACAAT	945
V 294	USASPARGValLeuGluAlaILeArgThrSerILeGlyLysGluV	279
2/9	pSerAsp	,
œ	TAATGGCTGGCCAAGAAGCTCACGTATACAAATATG	4
r 269	LeuLeuAsnGluTyrTyrTyrThrValSer	253
A 844	AATTTGGA	810
C 253	LysSerArgLysProGlyProAsnValAsnl	239
T 809	AACGGTGATACTGTGGAAATTCTAAATGCTGATG	773
r 239	etAsnArgGlnSerCysTyrCysPr	223
. 772	TTGTCGATGATGGT	758
K) .	:::	0 0
c 757	TGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCC	708
A 707	CAATTIGCTATCATTGGTCAGCCAGTTTATCATA :::::: :::H1sLeuValGlyAsp	658 202
s 202	alHisLysGly	186
G 657	GAAATTTTGGATGGTGGACCAAC	617
r 185	and the Clohant Cachacte CITITCAAACTCAAATTGIC Coorte :: ::	169
		J
G 569 S 169	CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	529 152
, 15	::: ::::: ::: sGluHisGlyCys.ArgSerThrAlaLysAlaTyr	w
G 528	TCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTAC	479
7 13	::: ProAspGlyGlnCysIleAsnAlaCysLysMetLysGl	-
3 47		O)
. 462	ACGATCTCTGAATCCACGTGGTATTTTTGTAACAACACGATCTCTGAATCCACGTGGTATTTTTTTAACAAC	106

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Seq_name: /cgn2_6/ptodata/1/laa/5A_COMB.pep:US-08-325-071-63

seq_documentation_block:
    Sequence 63, Application US/08325071
    Patent No. 5587311
    GENERAL INFORMATION:
    APPLICANT: MILLADSEN, Law Anthony York
    APPLICANT: MILLADSEN, David Haroid
    APPLICANTION MILLADSEN, David Haroid
    APPLICANTION MILLADSEN, DAVID
    APPLICANTION MILLADSEN, DAVID
    APPLICANTION MILLADSEN, DAVID
    APPLICANTION MILLADSEN, DAVID
    APPLICATION MILLADSEN, DAVID
    APPLICATION MILLADSEN, DAVID
    APPLICANTION MILLADSEN, DAVID
    APPLICATION M
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alignment_scores:

895 360	845 351	810 334	773 320	758 304	708 290	658 283	617 267	570 250	529 233	479 217	463 200	427 187	377 173	327 163	304 147	Align s	alignmen US-09-3	Percent
GGATCGATCACAG	TATCCAACAGATT	GTGCTCTTGATAAAT ::::: ysLeuLeuAsnGluT	pLysSerArgLys	TTTGTCGATGATG	CATGCGATTCTGAA	TCAACCAGTTCAA	CCAGTATGCCGTT GluAspCysArgV	AGGTATCTGAAATC::::::::::::::::::::::::::	CTTTT	TTTCATCCATTAT	yProAspGlyGln	ACGATCTCTGAATC ::::: ProProAlaAspSe	CAAGTTGCCGGAA ::::: rgCysCysGlnGl	TGAAAGGTCTTTA ::::: sGluLysAsnLeu	TGCATTCGAAGGA ::: CysValProThrT	eg 1/1 to: US	t_block: 23-427-1 x US-	Quality: Ratio: Similarity:
CTTTTCTATCAATG :::::: ValLeuGluAlaIl	TAATGGCTGGCCA	ATTTGCTAAAT 	AACGGTGATACTG	GT 	ACCGTTGATA(CysValAspL)	TTTGCTATCATTG	ATGAA ::: alHisLysG	ACAACTGCT: CysThrAla	ACATGGAAGCTG ;;; hrValAlaGluA	TTTGTTACCAAAGTT 	AACTGTT	CCACGTGGTATTTTG	ATTTCACTTCCATT	TGATCAAGAAGGT ::: LeuGlnArgAsp.	CATGT hrCysLeuArgPro	-08-325-071-6	08-325-071-63	89.00 0.614 40.390 Perc
GCCAGATCAGTATTACCA ::: leargThrSerIleGlyI	AAGAAGCTCACGTATAC	ValSerPheThrPro	TTCTAAATG AsnI	nArgGlnSerCysTy	CTTTCTGCGCGGTTGTC sLysCys	TGGTCAGCCAGTTTATC	ATTTTGGATGGTGGA ::: lyThrValLeuCysGluCys	TTTCAAACTCAAATTGTC 3luGlnLysGlnThrCys	TAAAACAGTTAGTG ::: pGlyIleThrCysL	GATCGTGCATATC ::: : AlaLysAlaTyrG	TGTCAT	TTGTAACAAC : ::: rCysSerProGlySe	TTCATGCAATGT::: 	GCCGTAATGATG	oAspLeuThrCysLy	3 from: 1 to:	:	Length: Gaps: ent Identity: 2
CCATTAAAG 944 ::: lyLysGluV 375	CAAATATGC 894	AATTTGGAA 844 :::::: AsnIleSer 350	CTGATGGAT 809 ::: leAsnGlyC 334		TCCATTCCTGC 757	ATAAATGGA 707 290	GACCAACCGG 657 :: YsProTrpAs 283	ArgProThr 266	CACAGATTG 569 ::: : ysSerIleS 250	GAGTACAATG 528 :: LuCysThrCy 233	TTCG 478		TGCGCGTAC 426 SerAlaAla 186	AAGGTGGACGT 376 ::: SerA 173	TATG 326	650		359 22 2.284

GATTC GCGCA GCGCA HisVa GCGCA GAGCG GAGCGA GAGCA GAGCGA GAGCA GAG	1079 GAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGA 1128 ::: 435 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 451 1129 TGATAATCAAGCTTTGCCAGTTGAT 1153 :: :::::: 451 yGlnAsnLysCysValLysValLsp 459	401 ILEUAIGLYSLEUGINAIACYSGLUHISFIGIIEGIYGLUIIPGYSMEUM 410 1052TACTCAAGAAAGATCTGCAGAACCG 1078 ::: ::: 418 etTyrProLysLeuLeuIleLysLysAsnSerAlaThrGluIleGluGlu 434	387IleLysAlaArgLeuIleAlaGluLysProLeuSerAsnHisVa 401 1045 ACTTCGT	945 AACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTC 994 ::: ::: ::: :::::: 375 alPheLysValGluIleLeuAsnCysThrGlnAsp 386 995 GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 1044
	CAACACCCTTGAAATTAGCGA ::: :nGlnGluAlaAlaTyrLySGl 53	YCOTTEGIYGIUTIPCYSMECM WTCTGCAGAACCG SeralaThrGluIleGluGlu	 uLysProLeuSerAsnHisVa	.TGTTCAGAACCACAAGGATTC ::::: CysThrGlnAsp AAAACCTGCTGCAGCTGCGCA

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pir2:T15789
pir1:A35269
pir2:A36054
pir2:S05356
pir2:S17855
pir1:VGBE11
pir2:E71615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pir2:A40970
pir2:C71607
pir2:G71613
pir2:S55098
pir2:C71618
pir2:E71604
pir2:S57242
pir2:T03099
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pir2:B26696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search information
Query: US-09-323-4:
Query length: 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database sequences: 142080 Database length: 47169319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database: PIR_62:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pirl:RNZQBF
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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOD=6.000 -FGAPEXT=7.000 -START=1 -MATKIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN-0
-MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
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2:H71616
2:B71612
2:C70126
        2:H71606
2:B42239
2:S20811
2:S32793
2:I51703
                                                                                                                                           2:S32559
2:S23344
2:C71608
                                                                                                                                                                                                                                                       2:T14594
2:F71613
2:A05037
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2:S72278
2:D71606
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+ 897.
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ESCOTE Len
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R:Sebastiano, M.; Lassandro, F.; Bazzicalupo, P. Dev. Biol. 146, 519-530, 1991
A;Title: cut-1 a Caenorhabditis elegans gene coding A;Reference number: A49772; MUID:91323673
A;Accession: A49772
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cuticle protein cut-1 - Caenorhabditis
C:Species: Caenorhabditis elegans
C:Date: 07-Apr-1994 #sequence_revision
C:Accession: A49772
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US-09-323-427-1 x A49772
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                      TTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA 687
                                                     GlnPheValThrLysValAspArgAlaTyrArgIleGlnCysPheTyrMe
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R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P. submitted to the EMBL Data Library, July 1991 A;Description: CUT-1a Caenorhabditis elegans ge A;Reference number: S27799 A;Accession: S27799 A;Molecule type: DNA
                                                                                                   seq_documentation_block:
cuticlin 1 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
C;Accession: S27799
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A;Cross·references: EMBL:M55997; NID:g156271; PID:g156272 C;Genetics: A;Gene: CUT-1 A;Introns: 245/3
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                                                                                                                                                                                                                          aHisAlaAlaAlaAlaProGlnAlaGlyValGluGluValGlnAlaAlaP
                                                                                                                                                                                                                                                                                                           TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAA 1026
                                                                                                                                                                                                                                                                                                                                                                             TCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTTCGACCACAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                               aHisValTyrLysTyrAlaAspArgSerGlnLeuPheTyrGlnCysGlnI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGA 926
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                                                                                     ProAlaValProArgAlaThrLeuAlaGlnLeuArgLeuLeuArgLysLy
                                                                                                                                                        roValGlyAlaAlaProValAlaAlaProValAlaAlaAlaAlaAlaAla
                                                                                                                                                                                      ACCTGCTGCAGCT.....
                                                                                                                                                                                                                                                                                             SerGluProGlnGlyPheGlyAlaValLysGlnAlaGlyAlaGlyGlyAl 172
                                                                                                                                                                                                                                                                                                                                                               leSerIleThrIleLysAspProGlySerGluCysAlaArgProThrCys
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A;Genome: plastid A;Note: this apparently degenerate plastid is referred to as the apicoplast C;Keywords: nucleotidyltransferase; plastid; transcription
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C;Accession: S72284

C;Accession: S72284

C;Accession: R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyte, Wol. Biol. 26, 155-172, 1996

J. Mol. Biol. 26, 155-172, 1996

A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium factorial parasite Plasmodium 
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A;Gene: rpoC2
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A;Note: blosynthesis of this protein involves a -1 frameshift in the codon for residue
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
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530 TTTTACATGGAAGCTG.....ATAAAACAGTTAGTGCACAGAT 567
                                                                                                                                                                                                                                                                                                                                                                           483 ATCCATTATTTG...TTACCAAAGTTGATCGTGCATATCGAGTACAATGC 529
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                                                                                                                                                                  58 IleTyrLeuLeuIleLeuTyrLysAsnLysIleAsnAsnIleTyrAsnAs 74
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Gaps: 34
Percent Identity: 21.078
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1083 347	1039 330	989 316	960 300	925 283	885 266	. 852 . 250	802 241	755 224	705 208	672 191	174	. 158	660	630	597 124	582 108	568 91	74
ATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGAT : : : : : : : :	TGCGCAACTTCGTTACTCAAGAAAAGATCTGCAGAACCGGAGA ::: 	GGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGC ::: :::: eSerSerGluAlaIleSerGluProSerThrGlnMetValL	GTGTTCGACCACAATGTTCAGAAACCACAA ::::::::::::::::::::::::	GATCAGTATTACCATTAAAGAACCAAATAGCGAAT:	ACAAATATGCGGATCACAGGCTTTTCTATCAATGCCA ::: ::: :::	CAGATTTAATGGCTGGCCAAGAAGCTCACGTAT	TGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAA ::::: 	TGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGC ::::::::::::::::::::::::::::::::::::	GGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCC ::: ::: ::: :::: :::: ::::	TTGCTATCATTGGTCAGCCAGTTTATCATAAAT	rGlySerLysLysGlyIleIleAspThrAlaLeuLysThrAlaAspSerG	TyrGluTyrIl	ysalylyttesetasmittebysalymettteiyfaluhysetavattie		AAACTCAAATTGTCCCGATGCCAGTATGCCGTT ::: ::: ::: ::: :::	TCACAACTGCTTTTC ::: ::: LeuTyrAsnLysIleAsnProIleTyrSerAsnLeuPheLeuPhePheAs	TGAGGTATCTGAAA	nLysTyrTyrGluIleLysAsnAsnTyrIleAsnValPheLeuAsnAsnT
1132	1082 346	1038 330	988 316	959 299	924 283	884 266	851 249	801 241	754 224	704 207	191	174	671	659	629 141	596 124	581 107	91

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seq_documentation_block:

probable multiple transmembrane domain protein PFB0770c - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999 C;Accession: F71606
C;Accession: F71606
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: F71606
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1456 CAATAAGTGATATTTTCATCAAAACTTCTTCTATCGCTTT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1206 CAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATG 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  556 ysLysLeuPheIleTyrLeuAsnIleIle.....AsnAsn... 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheTyrValAsnAsnIlePheIle.....TyrTyrLys.TyrGluL 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \verb"nTyrAsnPheIleAsnSerAsnTyrTyrPheLysLysMetAsnPheIleL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAATAAACTGCCATATATTCGTTTCTTCTTATCATCCTTCTAATAA 1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTATTGCCCAATTTTATGGGCATCATTTCCTATTCTGTAAACAATTCA 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \verb"euLys......AsnPheAsnAsnIleGlnIleLeuAsnLysLeu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAGGCCATGAATAGTTTCGTTTGTTATTATCATCATTATCAACTTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAATTTTAGCTAACAAATATATAGTATGTAGGAAATAATTACTGTAATA 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTCGTCCAAATCAGAAGGCATAAAAATAATGTTAGAATCATCGAAGCA 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sCysAsnPheIleTyrAsnSerIleSerLysAsnPheLysTyrAsnLeuA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluTyrLys.....TyrIleLeuGlnAsnGlnTyrIleLy 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e {\tt PheLysLeuIleIleAsnPheLysLysTyrIleAsnIleLysPheAsnL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......IleIleIleLysLysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rTyrLeuTyrTyrTyrHisIleLysPheTyrAsnLeuTyrAsnLysGlyI 480
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A;Cross-references: GB.AE001417; GB:AE001362; NID:g3845271; PID:g3845273; TIGR:PFB077
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0770c
                                                                                                                                                                                                                                                                                              631
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alignment_block:
US-09-323-427-1 x F71606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: F71606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                         615 snAsnLeuPheGlyAla.SerAsnLysLeuThrSerHisHisGluAsnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676 TATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGAT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 CysAsnAsnHisThrSer...AspAsnAsnThrCysAsn......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514 sThrCysAsnAsnHisThr.....CysAsnAsnHisThrCysAsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 AsnThrCysAsnAsnHisThr......CysAsnAsnHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 TCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTA 425
                                                                                                                                                                                                                                                                                                                                                                                                            sAspGly.....LeuTyrLeuAsnThrLysSerTyrAspA
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                                                                                                                                                                                                                                                                                                                                         CAGATTTAATG...GCTGGCCAAGAAGCTCACGTATACAAATATGCGGAT 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAA
                                                  CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGC 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AsnHisThrCysAsnAsnHisThr 535
  LeuAsnGluTyrPhe....
                                                                                                       sn.....SerLeuLeuAspIleAsnGluTyrAsnAsnAsnSerAsnAsp
                                                                                                                                                       AAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAG 998
                                                                                                                                                                                                          eLysLysIleIleGluLeuAsnThrThrLysLeuValGluGluArgAsnA
                                                                                                                                                                                                                                                          CGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....SerHisAsnAspThrGlnGluAsnAsnIleMetLysAsnLy 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCGATGATGGTAACGGTGATACTGTGGAA....ATTCTAAATGC 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....TCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTT 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......AsnAsnHisThrLeuGlyAsnPro 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGC 675
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Gaps: 31
Percent Identity: 21.654
..AspAsnLeuIleGluAsnAsnIleLe
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hypothetical protein 1 (CYb-COII intergenic region) - Leishmania tarentolae mitochondrioc; Species: mitochondrion Leishmania tarentolae
                                                            seq_documentation_block:
                                                                                                                      seq_name: pir2:B26696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1242 TCTCAATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATT 129:
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                                                                                                                                                                                                                                                  1699 ATTCTGTAAACAATTCA 1715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        843 ysTyrAlaProTyrPhePheLeuThrPheAlaValIleProSerPheLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           761 rAspTyrLysMetTyrPhe...LysLeuPheGluHisLysAsnIleIleP 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          710 TyrTyrLeuAspAspAsnLeuLysValSerTyrIleAsnGlnLeuArgLe 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             693 leMetAsnLysLeuMetTyrThrAsnValSerAsnAsnGluArgTyrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATATAGTATGTAGG.......AAATAATTACTGTA 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerPheIle.,PheLeuSerSerPhePheGluValValLeuSerThrLeu
                                                                                                                                                                                  yrAsnAsnAsnAsnAsn 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCATTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATAA 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheIlePheIleLysCysIleSerGluPheLeuPheLeuLeuLeuLeuVa 826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCT 1241
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                                                                                                                                                                                                                                                                                                         .....LysAsnIleSerLysLeuProAsnPhePhe.AsnIleLysGluT
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alignment_scores:
Quality:
Ratio:
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A;Genetic code: SGC6
C;Superfamily: hypothetical protein 1 (CYb-COII intergenic region)
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Simpson, L.; Neckelmann, N.; de la Cruz, V.F.; Simpson, A.M.; Feagin, J.E.; Jasmer, J. Biol. Chem. 262, 6182-6196, 1987
A;Title: Comparison of the maxicircle (mitochondrial) genomes of Leishmania tarentola A;Reference number: A92643; MUID:87194837
A;Accession: B26696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-323-427-1 x B26696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-443 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: B26696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474
                                                                                                                                                                                                                                                                                                                                                                                524 CAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGT 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT
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AACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTC.....
                                       nLeuIleAsnPheIleLeuLeuPheValLeuLeuTyrTyrMetIleLeu.
                                                                                           TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA 720
                                                                                                                                                                                    TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eIleIleLeuCysAspTyrThrSerLeuPheTyrLeuSerPheAspLeuI
                                                                                                                                     TyrLysIleLeuIleLeuTrpTyr.....TyrTyrMetIleAs
                                                                                                                                                                                                                                                                                ATCTGAAATCACAACTGCTTTTCAAACTCAAATTG...TCCCGATGCCAG
                                                                                                                                                                                                                                                                                                                               eIleSerIleLeuPheGluLeuPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                           TTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heAspThrArgPheValPheMetIleIleIleMetGlnTyrIleIleIle 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leTrpLeuIleIleIleAsnIleIleIleLeuThrIleLeuAspSerTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuPheLeuTyrLeuIleHisIleIleLeuPheLeuLeuTyrSerPh
                                                                                                                                                                                                                                   ....SerLeuLeuLeuPheLeuIleLeuIleSerSerArgPheGly 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....LeuPheLeuPheCysPhePhePheLeuPheCysPheLeuAsnP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity:
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29
19.853
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C for resid
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1585	1547 340	1497 329	. 316	1397 300	1350 288	1300 274	1250 265	1200 248	1162 232	1112 219	1062 210	206	204 1012	962	203	912	199	862	183	812	764 167	153
GTTTGTTATTATCATCATTATCAACTTGTCCTAT	TATTGTAAATGTTTCATCATTAGGCCATGAATAGTTTC ::::::::::::::	ATAGCTTCTGAAAAGCTTATTCATTATATCAGTAATCTTTTATATGCATAC ::: ::: :: ::: PheSerPhePheAsnAsnLeuLleuIleSerIle	ACTGTAATACAATAAGTGATATTTTCATCAAAACTTCTTCTATCGCTTTT :::::	TTCTAATAACTAATTTTAGCTAACAAATATAGTATGTAGGAAATAATT ::: ::: ::: ::: ::: eulleileLeuTyrTyrPhePheIleValTyrAsnMetPheAspIle.Ly	GAAGCAATAATAAAACTGCCATATATATTCGTTTCTTATCATCC	GTTTAAATTTCGTCCAAATCAGAAGGCATAAAAATAATGTTAGAATCATC ::: ::: ::: :: IlePheIleSerThrLysAsnTyrIlePheTyrMetTyrLeu	TTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATTTC	TTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTTGGCTTCTCAATG :::::::::::::::::::::::::::::::::::	CCGTGCACTTCTGCAACATAATGGACAACCTGTAATAC ::: :::::::: yrIleIlePheIleLysLeuIle.IleIleGlnSerIleThrCysValLe	ACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCA ::: :: !:: ::	AAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAAC ::: ::: ::: ::: ::: ::: ::: ::: :::		TPheTP	GTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGG	GlyVa	TCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGT	TyrileArgLeu	GGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGATC	<pre>:::: :::: :::: ::: uPheLysLeuTyrIleAlaIleLeuIleLeuPheLeuGluGlnLeu</pre>	GCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAAT	GATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	
1618	1584 356	1546 339	1496 328 ,	316	300 ′	287	1299	265 .	1199	232	218		205	_	204	961	202	911		861	811 .	. 167

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A;Cross-references: EMBL:x95275; NID:g1171583; PIDN:CAA64572.1; PID:e220243; PID:g117 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996 R;Gardner, M.J.; Williamson, D.H.; Wilson, R.J.M. submitted to the EMBL Data Library, March 1990 A;Reference number: $10438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-323-427-1 x RNZQBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: this apparently degenerate plastid is referred to as C;Superfamily: DNA-directed RNA polymerase beta chain C;Keywords: nucleotidyltransferase; plastid; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; J. Mol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite A;Reference number: S72277; MUID:96346169
A;Accession: S72282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Plasmodium falciparum plastid C;Species: plastid Plasmodium falciparum C;Date: 31-Dec-1990 #sequence_revision 15-May-1998 #text_change 11-Jun-1999 C;Accession: S72282; S10438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 328-1024 <GAR>
A;Cross-references: EMBL:X52177; NID:g9879; PIDN:CAA36427.1; PID:g9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: pir1:RNZQBF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: S10438
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A; Residues: 1-1024 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                          119
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                                                                                                                                                                                                                                                                                                                                                       197 ACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 AATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 yPhePheLeuLysValPheCysLeuLeuLeuHisLeuSerTyrLeuGlyI 373
                                                                                                                                                                                                                                                                                                                                                                                                                  70 AsnIleAsnAsnLeuLeuLysIleIleLeuThrLeuLysLeuAsnPheIl
                                                                                                                                                                             roPheIleTyrAsnAsnIleIleIleLeuAsnGlyLeuTyrLysThrCys 118
                                                                                                                                                                                                                                                                                               eAsn...IleAsnLysIleIleLysPheAsnIleLeuIlePheIleLeuP 102
                                                       IleGlnLeuPheLysLysAsnAsnLysIlePheIleIleLysPheLysAs 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....TyrPheArgLeuIleIleAsnIle......
                                                                                                               .....GTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA 280
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Ratio:
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0.373
45.113
.ATTTTAATACACGTAATGCATTCGAAGGACATGT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 665
Gaps: 28
Percent Identity: 17.594
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A.; W

1052		1052
390	nGluGlyLeuThrCysGlyLeuValAsnTyrLeuTh	374
1052	AGCTGCGCAACTTCC	1035
373	AspLeuArgGluLeuProArgAsnIleLeuGly	357
357	tIleThrThrGlyLeuAsnSerLysPheIleI aGCTGTTAAAAACAGGTGGTGGCGCAGCAAAAA	985
· &		975
340	TyrSerAspGlnValAsnAsnLeuSerGluIleAsnGlnLysF	324
974	ACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAAT	933
323	AIRCAMAIRIBUSONAIUSELANCANSCLITITULANGARISCHAARISCH	310
310	AsnI	3 9
882	AATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTC	i iii
295	ePheLysTyrGlnLeuLeuAsnIleAs	281
832	GGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAAI	783
00		277
782	STTGTCCATTCCTGCTTTGTCGATGATGGTA	733
732 277	AAATGGACATGCGATTCTGAAACCGTTGATAC	701 260
260	ا LysLeuAsnPhes	244
700	GCTATCATTGGTCAGCC	672
. 4	leTyr	ũ
671	GACCAACCGGTCAA	622
621 236	GTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGT : ::: :::	572 219
219	LysPheIleTyrSerLysTyrAsnAsnIle	205
571	ATGGAAGCTGATAAAACAGTTAGTGCACAGA	522
204	eIleAsnLysLysIleLeuIle	191
521	TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGT	472
191	:	179
471	ACACGATCTCTGAATCCACGTGGTATTTTTTGTAACAA	422
179	TyrPheAsnAsnPheLysPheAsnPheLeuIleLeuLeu	163
421	CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTG	372
371 162	GGTCTTTATGATCAAGAAGGTTGC ::: ::: .IlePheLysIleSerLys	322 152
152	::::::: /alTyrIleTyr	135

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	: pir2:S78177	seq_name
	AsnAsnIleProGluIleCysSerIleAsnLeuSerLysMetTyr 661	647
		1710
1709 646	TGTATTGCCCAATTTTATGGGCATCATTTCCTATTCTGTAAAC	1666
٠	reinilienwsbyraiieiieiseryldhlaiterentlikanysun	٠ +
, 0	:	1635
613	euValGlyTy	597
1634	TTATCAACTTGTCCTATTTTATTCTAACAGTTT	1602
596	alAsnIleGlyGlnIleLeuAlaIleAsnSerAsnLeuLeuAsnSerGlu	580
1601	TAAATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCATCA	1552
580	nGlnAsnIleLeuLeuIleTyrLysProIleValTrpValGlyGluLysV	563
1551		1551
563	LeuPheAsnArgGlnIleIleTyrTyrLeuAsnAsnTyrLysLysIleAs	547
1550	CTTATTCATTATTCAGTAATCTTTTATATGCATACTATT	1512
546	luGlyIleVallleTyrValSerCysIleLysIleIleIleArgAsp	531
1511	GCTTCTGA	1462
531	eIleSer	514
1461		1427
514	SSILEUSERASNILE	506
1426	TTCGTTTCTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAAATAT	1377
505	snLeuMetSerIleLysMetHisThrGlnIleValProIleIleTyrPro	489
1376	ATAAAAATAATGTTAGAATCATCGAAGCAATAATAAAACTGCCATATATA	1327
489	e:::: ::: ::: :::::::: ::: : e::eGluAsnLeuIleProPheIleHisTyrAsnAspSerIleArgA	473
1326	ATTATTACCATTTCGTTTAAATTTCGTCCAAATCA	1277
473	PheAsnTyrLeuLeuSerPh	467
1276	TGGCT	1227
466	snIleThrGlnAsnIleIleTyrIlePro	457
1226	ACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCA	1177
457	eAsnLysThrThrIleLeuThrIleAsnLysAsnThrPheLysIleCysA	440
1176	TTGCCAGTTGATTTACGTCACCGTGCACTTCTGCA	1142
440	PheTyrAsnIleSerPheAsnAsnIleTyrLeuLysLysAsnIleAsnPh	424
1141	ATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCT	1092
423	::: eTyrAsnArgTyrAsnPheLysLeuLeuLeuAsnIlePheAsnLysA	407
1091	TACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTG	1053
407	$\verb nilePheLeuAsnLeuLysTyrLeuPheValIleTyrTyrLysHisIleP \\$	390

seq_documentation_block:

632 GAAATTTTGGATGGACCAACCAGTCAACCAGTTCAAT	509 CG/GCATA/CGAT/ACAA/GCT/GAT/AAAC/AGTTAG 558 :::	409 ATGCAATGTTGCGCGTACACGATCCTCTGAATCCACGTGGTATTTTTGTAA 458 1157	Align seg 1/1 to: S/BL// Irom: 1 to: /1/ 309 TCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGT 358 ::: ::: 126 ThrLysaspLeuIlePheLeuLeuMetPheLeuAsnAspProIleLysTy 142 359 AATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTC 408 :::::: ::::::::::::: 142 rAsnLysasnLeuIleAsnAsnGlnAsnGlnAsnGlnLeuTyrPheHis 156	ent_scores: Quality: 108.00 Ratio: 0.414 Ratio: 46.359 Percent Ident_block: -323-427-1 x S78177	A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-717 < CLAN> A;Cross-references: EMBL:AF007261; NID:g2258325; PID:g2258376 A;Experimental source: ATCC 50394 A;Rote: the nucleotide sequence was submitted to the EMBL Data Library, June 1997 C;Genetics: A;Genome: mitochondrion C;Keywords: mitochondrion	nas americana (ATCC s americana on 06-Feb-1998 #tex J.; Cedergren, R.; DNA resembling a eu 11393
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seq_documentation_block:
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Aug-1999
C;Accession: A40970
R;Just, M.; Herbst, H.; Hummel, M.; Duerkop, H.; Tripier, D.; Stein, H.; Schuppan, D.
J, Biol. Chem. 266, 17326-17332, 1991
A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular management in the sequence of the fibronectin-tenascin family of extracellular materials. A; Reference number: A40970; MUID:91373351
A; Recession: A40970
A; Molecule type: mRNA
A; Residues: 1-843 < JUS>
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US-09-323-427-1 x A40970
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: A40970 from: 1 to: 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1552 TA...AATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCA 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1699 ATTCTGTA.....AACAATTCACTTATTTGCATTATTGCAATTAAA 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1649 TATCACAAATTATACCTTGTATTGCCCCAATTTTTATGGGCATCATTTCCT 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563 TyrLeuLys..... 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            596 GluIlePhe.....LysLysLysIleTyrLysLys 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     579 yrLysIleLysLysAsnAsnTyrPheLeuTrpGlnSerLeuIleGlu 595
270 AsnSer...MetArgValLysTrpAspAlaValProGlyAlaSerGlyTy 285
                                                                                                                                                                                                                     108 GAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAAATCGAATTTACTAAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 LeuThrGluTyrGlnIleAlaValPheAlaIleTyrAlaHisThrAlaSe
                                                                            158 TCTTCTGAAATGATGATTCGTCTTATTGCTTCTGTACTACACTTATTGC 207
                                                                                                                                                                                                                                                                                                     244 rGluGlyLeuArgGlyThrGluThrThrLeuAlaLeuProMetAlaSerA 261
                                                                                                                                                                                                                                                                                                                                                                             58 CAACAAACAACAACAACAACAACAACAATAATAACCCCCATCAAGTGGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 TTACCCAAGTTTGAGGTGTCTATAACACCGACTGCAGCAACAACAACAAA
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0.527
51.768
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Gaps: 21
Percent Identity: 21.212
                                                                                                                                                        LeuLeuTyrAspValThrGlu
                                                                                                                                                    269
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1012	962	912	871	842	795	773	725	675	631	590	540	490	440	390	340	293	255	208
	546	531	514	498	483	466	450	433	417	401	384	371	364	348	331	319	302	285
TGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCA	GTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGG 1	TCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGT 9 ::: :::::::: thrGluProAlaThrThrIleValProThrThrSerValThrSerVa	AGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTT 9 :! ::::: ::: rGluSerGluVal.ValThrAlaValGlyThrThrLeuAspSerPheTrp 5		TAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG 8 ::	AACGGTGATACTGTGGAAATTC 7 :::	GTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTCTCGATGATGGT:	CTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACC::::::::::	TGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTG (::::	GCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTA (::::::::::::::::::::::::::::::::::::	AAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACT::: :: snalaaspGlyThrGluIleAsnGluValGluValAspProIleThrThr	ATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGG	CCACGTGGTATTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATT (TTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAAT (:: ::: :: :: ::	TGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAA: ::: ::: eGlyGluGluAlaSerAspProValThrGlyGlnGluThrThrLeuAlaL:	AATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTA 3	AAATTGAATGTGGACCAACTTCAATAACAATCTTT	ATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAG:
1058	1011	961	911	870	841	794	772	724	674	630	589	539	489	439	389	339	292	254
	555	546	530	514	497	183	466	449	433	417	400	384	370	363	348	331	318	302

mentation_block: ical protein F80745w - malaria parasite (Plasmodium falciparum) s: Plasmodium falciparum si plasmodium falciparum protein C1160ttesin, H.; Carucci. D.J.; Cummings, L.M.; Aravind, L.; Kooain, E.V.; M.J. Sloberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. 282, 1126-1122, 1998 chromosome J sequence of the human malaria parasite Plasmodium falciparum. Ince number: A71500; MVID:99021743 references: GB:AE001415; GB:AE001362; NID:93845264; PID:93845265; TIGR:PF80745w mental source: clone 307 PF80745w Quality: 107.00 Quality: 107.00 Quality: 107.00 Quality: 43.832 Percent Identity: 19.303 Similarity:	ypotheti;;Species ;Species ;Accessi ;Accessi ;Accessi ;Accessi ;Accessi ;Accessi ;Cross-r ;Accessi ;Accessi ;Cross-r ;Accessi ;Ac
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116 654	GATAATCAAGCTTTGCCAGTTGATT:::::::::::::::	1113 641
640	AGAATATCATTG	636
· w	::: AsnAsnPheLeuPheValTyrValProAspLeuLeuTyrSerGln	61
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836 566	GGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATA :::	787 553
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661 503	TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAA	621 487
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520 458	CATTATTTGTTACCAAAGTTC	483 442
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hypothetical prote-in PFB0470w - malaria parasite (Plasmodium falciparum)
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R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
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                                                                                                                                                                                                                                                                                                                                               seq_name: pir2:G71613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             862 uValLeuLysThrValGluGluGluLysGluGluGluGluLysG
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luLysGluLys 882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euPhe.......TyrPheValAsnLys.....ValCysGly 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eIleAsnAlaLeuSerLysMetCysTyrThrTyrGluMetTyrValValL
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C;Genetics:
A;Genetics:
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alignment_block:
US-09-323-427-1 x G71613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 TCG...TCTTATTGCTTTCTGTAC.....TACACTTATTGCATTGT
                                                                                                                                                                                                                                                                                                                                           460 AACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                410 TGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 CTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             665 uHisAsnAsnLeuAspAsnLysAsnAsnAsnMetAspPheAsnAsnMetM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 AAGCAATCTTAGTTTTCTAAAAATCGA............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        etThrSerProLeuTyrTyrTyrTyrTyrTyrTyrTyrAspAsnAspPro
... TATGCCGTTATGAAATTT......TGGATGGTGGA
                                     yrLeuTyrLeuGluIleLeuHisArgMetLysIleTyrAsnHisAspIle
                                                                             {\tt ATCTGARATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAG...}
                                                                                                                          sPhePheIleLeuLysGluAsnTyrTyrTyrLeuSerIleAspAsnLeuT
                                                                                                                                                                ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGG.....T
                                                                                                                                                                                                                                                                                                 luGlnAsnLeuAsnHisGluAsnMetLysTyrIleIleHisAsnLeuMet
                                                                                                                                                                                                                                                                                                                                                                                 n..........IleSerAspLysIleLeuLysIleIle........G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAAGGTGGACGTCAAGTTGCCG...GAATTTCACTTCCATTTGATTCA 409
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                                                                                                                                                                                                            IleSerLeuSerLeuCysAspIleLysTyrLeuAsnLeuTyrAlaLeuCy
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Ratio:
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0.319
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48
21.280
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1332	GTCATTATTACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGCATAAAA	1283
1282 1101	TATGGGTTTA <i>l</i> ::::: LePheValAsr	1251 1085
1250 1084	GTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAA :::::::: ::: .PheAsnIleGluSerSerLeuIleGlnLeuPheSer	1201 1073
1200 1072	ACGTCACCGTGCACTTCTGCAACATAATGGACA	0 14
1150 1067	CGATGATAATCAAC :: :: allysasnLysGlnTyrMetLeuaspLys	1116 1051
1115 1050	ATCATTGATGTAC	1075 1038
1074 1038	GCGCAACTTCGTTTACTCAAGAAAAGAT	1040 1023
1039	GTTAAAACAGGTGGTGCCGCAGC ::: ::: sileLysGluCysAspGluLysI	990
989	AC yrīle	955 992
954 992	heLysLysIleGluLysThrGluThrLe	950 975
949 975	GATCAGTATTACCA	918 959
917 958	GATCA 	877 942
876 942	snAspAsn	845 926
844 925	CT. LysLeuProThrAspIleGluIleLysGlnAsnLe	830 909
829 909	AATTCTAAATGCTGAT LeuMetLeuGly	781 896
780 896	<pre>3TCCATTCCTGCTTTGTCGATGATGGTAA ::::: ssail ssailysileGluLysGluAsnGlyAs</pre>	731 880
730 879	CTGAAAC	683 868
682 868	rAsnIlePheG	650 851
851	cHisValHisAla	835

	C;Keywords: transmembrane protein F;241-257/Domain: transmembrane #status predicted <tmm></tmm>
	A;Gene: SGD:SKY1 A;Cross-references: SGD:S0004829; MIPS:YMR216c A;Map position: 13R
IPS:YMR216c	A;Molecule type: DNA A;Residues: 1-742 <ded> A;Residues: 1-742 <ded> A;Cross-references: EMBL:Z49809; NID:g854459; PID:g854468; M: A;Experimental source: strain AB972 C;Genetics:</ded></ded>
	R;Dedman, K.; Brown, D.; Bowman, S. submitted to the EMBL Data Library, June 1995 A;Reference number: S55089 A;Accession: S55088
nge 06-Feb-1998	e sion 01-Sep-1995 #text_cha
evisiae)	- yeast (Saccharomyces cer otein YM8261.10c
	seq_name: pir2:S55098
	1295 r 1295
	1726 T 1726
1295	10/9 IIIIMIGGGAICAIIICCIMIICIGIAAACAAIICACIIMIIIGCA : ::: ::: :: ::
1	
1678 1278	1629 CAGTTTATCATTTGTGATAATATCACAAAATTATACCTTGTATTGCCCAAT 1
1628 1266	1604 .ATCAACTTGTCCTATTTTATTCTA
4	233 AspAsnPheLeuIleSerAspIleLeuLeuIleLeuGluLysGlnAsnLy
1603	TCGTTTGTTATTATCATCATT
23	::: ::: 216 yrLysAsnAsnLysTyrIleIleLysAspIleLysThrPheTyrLysLeu
1573	TTCATCATTAGGCCA
1558 1216	1525 CAGTAATCTTTTATATGCATACTATTGTAAATGT
1199	
1524	1478AACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTATT :
1182	1166 snAsnLysLysLysAsnThrTyrAsnAspPhePheAsnGluAsnAsn :
1477	GTGATATTTCATCAA
1437 1166	1406 CTAATTTTAGCTAACAAATATATAGTATGTAG: : ::: 1149 sTyrPheGlnLeuLysLysIleAspLeuGluTyrIleAsnSerAsnIleA:
1405 1149	1359ATAAAACTGCCATATATATTCGTTTCTTATCATCATCCTTCTAATAA :
1134	118 alTyrileAsnIleMetLysIleValLysLysMetLysAsnTyrAspGlu
ω υ	333 ATAATGTTAGAATCATCGAAGCAATA
1118	1101 lAsnGlnIleMetPheIleLeuAspPheIleLysIleIleAsnGluLysV :

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alignment_block:
US-09-323-427-1 x S55098
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Quality:
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736 CTGCGCGGTTGTC......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 CCCCATCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAA 142
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|AsnSerAsnAsnAsnAsnAsnGluAspIleMetAsnThrProLeuHisGl 497
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                              CAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTT 735
                                                                                                                                      TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT 685
                                                                                                                                                                                                         AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 635
                                                                                                                                                                                                                                          IleLysIleAlaAspLeuGlyAsnAlaCysTrpTyrAspGluHisTyrTh
                                                                                                                                                                                                                                                                                                               erAsnSerAsnValSerThrAspIleAsnSerProGluAsnLeuIleGln
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0.816
42.244
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13
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US-09-323-427-1 x C71618
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                             439
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0.477
44.422
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hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13:Nov-1998 #sequence_revision 13:Nov-1998 #text_change 07:May-1999
C;Accession: C71618
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, I.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: C71618
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-1712 <GAR>
A;Cossidues: 1-1712 <GAR>
A;Cross-references: GB:AE001386; GB:AE001362; NID:g3845148; PID:g3845151; TIGR:PFB031
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0315w
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1150 LysTyrSerPheHisLysLeuArgIlePheTyrGluTyrLysIleGluMe 1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 ATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAA 438
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                                                                       TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT
                                                                                                                                              ysLeuGluPheLeuIleLysLysLysMetGlnHisTyr.....
                                                                                                                                                                                                                  AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA
                                                                                                                                                                                                                                                                                         tGluLysLeuLysLysAsnTyrIleHisCysIleTyrAspIleSerAspL 1183
                                                                                                                                                                                                                                                                                                                                                 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC
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Percent Identity:
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` E:

1307	TTCGTTTAAAT ::: snAsnLysAsnArgLeuThrHisAlaIl	1468
, 4	Svatelintstterieeriieetiirie	1 0
27	ATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATTGCATTGA	22
1224 1459	TGTAATACTTGCTGCAGTACAAAATGGAATCTG ::::: ::: :PheValLeuAsnLysIleIleGlnLysL	1175 1445
1174 1445	TGCCAGTTGATTTACGTCACCGTGCACTTCTG ::::::: !::!!#! !nileAsnThrGluArgPheTyrTyrCysIleArgTyrCy	1143 1429
1142 1428	LysArgLysGluCysLeuMetLysTyrPheTyrThrLeu	1132 1412
1131 1412	TAGCGATGA :: ::: !eAlaIleGluLysGlyIleAsnGlnIleAspCysL	1109 1395
1108 1395	GAATATCATTGATGTACGAACTGATATC :: :::	1074 1379
1073 1378	CTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAG ::::::: :::::::::::::::::::::	1024 1367
1023 1366	.CAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGC .:: raspasnHisLysTyrasnalaPheLeuLys	978 1355
977 1355	CACAATGTT	957 1339
956 1338	CCATTAAAGAACCAAATAGCG ::: :: eGlyTyrLeuArgIleArgAspAsnArgIleAsnIleLys	928 1322
927 1322	AGCTTTTCTATCAATGCCAGAT :::::: SerTyrPheCysPheThrMetTyrLysIleTyrLeuArgA	906 1305
1305	yrGluArgArgIleLysSerPheIlePheSerLysLeuLysPheAsnTy	1289
905		905
905 1288	eLeuValLeu	868 1272
867 1272	CAACAGATTTAATGGCTGG :::::: IleLysValSerLysLysL	818 1255
817 1255	<pre>!GCTGATGGATGTGCTCTT :: ! !USerMetTyrLysLysLysMetAl</pre>	774 1239
773 1238	GTTGTCCATTCCTGCTTTGTCGATGATGGTA :: :: :: /SSerAlaTyrGlnAsnHisLeuGlyLysAsnTyr	727 1222
726 1222	ATAAATGGACATGCGATTCTGAAACCGT ::: ::: TleLysThrAsnAspMetLeuTyrAsnL	1205

TRATTITCTAAAAATGAAATGTACTAAATCTTCTGAAATGATGCTTCT ::::: ::::: ysAsnLysLysLysAsnLysLeu	AACACCGACTGCAGCAACAACAACAACAACAACAACAACAACAACAACAA	Alignment_Scores: Quality: 104.50 Ratio: 0.415 Percent Similarity: 47.727 Percent Identity: 19.886 alignment_block: US-09-323-427-1 x E71604 Align seg 1/1 to: E71604 from: 1 to: 2380	seq_documentation_block: hypothetical protein PFB0870w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999 C;Accession: E71604 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E ; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743 A;Accession: E71604 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-2380 GGAR> A;Cross-references: GB.AE001421; GB:AE001362; NID:93845293; PID:93845297; TIGR:PFB08 A;Experimental source: clone 3D7 C;Gene: PFB0870w	1471 TCATCAAAACTTCTTCTATCGCTTTTA 1497 ::: ::::: 1536 AsnArgLysLeuLeuAsnPheLeu 1544 seg_name: pir2:E71604	1421 AAATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTT 1470	GAATCATCGAAGCAATAATAAAAACTGCCATATATTC	TTCGTCCAPATCAGAAGGCATAAAAATAATGTTA ::: ::::: eLysLeuLeuGlnValleuValGlnLysLysGluLysLysSerValllea
	TRATTTTCTAAAAATCGAAATTACTAAATCTTCTGAAATGATTCT::::::::::	AACACCGACTGCAGCAACAACAACAACAACAACAACAACAACAACAACAA	Length: 528 Quality: 104.50 Caps: 24 Percent Similarity: 47.727 Percent Identity: 19.886 Lignment_block: US-09-323-427-1 x E71604 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Solvent Similarity: 19.886 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 from: 1 to: 2380 Align seg 1/1 to: E71604 Align seg 1/1 to: E71604	seq_documentation_block: hypothetical protein PFB0870w - malaria parasite (Plasmodium falciparum) C;Species: plasmodium falciparum C;Species: plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999 C;Accession: E71604 C;Chate: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999 C;Accession: E71604 R;Gardner, M.J.; Tettelin, H., Garucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, Science 282, 1126-1132, 1999 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum A;Reference number: A71600; MDID:99021743 A,Accession: E71604 A;Status: preliminary nucleic acid sequence not shown; translation not shown A;Residues; 12380 GGAR- A;Cacoss references: GB:AE001421; GB:AE001362; NID:g3845293; PID:g3845297; TIGR:PFB A;Cacoss references: GB:AE001421; GB:AE001362; NID:g3845293; PID:g38452	1471 TCRICARABACTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1421 AAATATATATATATATATATATATATATACTATAATACATAAGGEARATT 1470 1533	1342 GANCONCORACCANANARAACCACCATATATATC 179 1301 pysileuGinleuTyrasplysTyrTigsheGintyrLysasp 1317 1302 pysileuGinleuTyrasplysTyrTroTyrTleheGintyrLysasp 1317 1303

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1132	83 ATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA
85	:::::::: ::: ::: 774 euAsnIleAsnAsnPheTyrAspAspAsnAspLeu
0	3 TGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG
1032 774	983 CCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCGCAGCAAAACCTGC ::: ::::: 764
763	751 IleTyrLeuAsnAsnArgIleGlyAsnValPheValGly
982	TACCATTAAAGAACCAAATAGCGAATGTGTT
5	LeuAsnIleGluLeuAsnLysTyrLeuTyrGluAspSerTy
932	euGLuAsı ATCGATC
- 00	33 AATAATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAA
N	14 TyrPheLeuIleGluAsnIleIleSerAsnValTyrLysHisGlyCys.
832	95 TAAATGCTGATGGATGTGCTCTTGATAAATATTTGCT
794 713	745 TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAATTC
697	nIleLeuAsnMetHisThrSerIleAlaGly
744	TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC
683	70ProTyrHisLeuGlyValSerSerLeuLeuIleGluLysA
٥	45 GTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGT
644 669	595 TCAAACTCAAATTCTCCCGATGCCAGTATGCCGTTATGAAATTTTTGGATG :::::::::::
658	43 lValLeuLeuAspAspThrLysGluLysAlaAspProMetAsn
594	ATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACT
. 4	:::
4	95 TTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC
494 626	445 TGGTATTTTTGTAACAACTATGTTGTCATTTTTG : :::::: ::::::::::::::::::
444 610	416 GTTGCGCGTACACGATCTCTGAATCCACG ::::::::::::::::::::::::::::::::::
415 593	CTTCCATTTGATTCATGCAAT :::
374 584	GATGAAGGTGGAC ::: :::: LysAspGlyAsnL
567	54IleAsnAspGluIleArgGluLysLysAsnAsnLysGl

twitchin - Caenorhabditis elegans N;Alternate names: myosin-regulating protein N;Contains: protein kinase (EC 2.7.1.*) C;Species: Caenorhabditis elegans C;Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 #text_change 18-Jun-1999 C;Accession: S57242; S07571; S60797; S57218 R;Benian, G.M.; L'Hernault, S.W.; Morris, M.E. submitted to the EMBL Data Library, Rebruary 1993 A;Description: Additional sequence complexity within twitching of Caenorhabditis elegans A;Reference number: S57242 A;Accession: S57571 A;Accession: S57572 A;Accession: S57572 A;Accession: S57571 A;Accession: S57571 A;Accession: S57571 A;Accession: S57571 A;Accession: S57572 A;Accession: S5757 A	801SerAsnIlePheValAsnPheArgAsnLysCysI 813 1183 TGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGCA
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A; Map position: IV

A; Map po
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A;Accession: $57218
A;Accession: $57218
A;Molecule type: DNA
A;Residues: 2-99:108-194,'Q',196-206;374-468;658-753 <BEN4>
A;Experimental source: var. Bristol
C;Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
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US-09-323-427-1 x S57242
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                                                                                                           3415 .AsnArgGlnGlyThrSerAlaProLeuThrSerAspHisAlaIleValA 3431
                                                                                                                                                                                                                                                                                                                                             3409 PheArgValLysAlaVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393 spThr...SerLeuLysValAsnLysLeuSerGluGlyHisGluTyrLys 3408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3376 lGluLysGlnGluAspGlyGlyArgTrpValProCysGlyGluThrSerA 3393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3360 TrpAspGluProLeuAspAspGlyGlySerProIleThrAsnTyrValVa 3376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3339 oGlyAlaProGluGlyProLeuArgHisLysAspIleThrLysGluSer. 3355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3306 ysSerThrAlaArgAlaAspSerGlyLysTyrLysIleValAlaThrAsn 3322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3290 AsnThrHisIleAspAsnAsn.ThrAspAsnAsnThrLysLeuThrThrL 3306
420 CGCGTACACGATCTCTGAATCCACGTGGTATTTTGTAACAACAACTGTT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 TAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTAT... 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 CGAAGGTGAGCCAGAA.....ATTGAATGTGGACCAACTTCAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 TATTCGATTCCGGTTGACAATGGT......GT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 AAATGATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 TCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAAATC.. 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 CAGCA.....ATAATAACCCCA 97
                                                                                                                                                                                                                                  TGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....GTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....ValValLeuLys 3359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....GAATTTACTAAATCTTCTG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.485
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0.479
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Percent Identity: 19.403
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1039	GATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCCTGCTGCAGCT	990
3712	uValProGlyLysGluTyrAlaPheArgValLysAlaValAsnLeuGlnG	3695
989	CAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAG	943
3695	GlyThrPheProAspCysThrAlaLysValAsnLysLe	3679
942	TCTATCAATGCCAGATCAGTATTACCATTAA	908
3678	CCAMBARAGE LCACGIAIRCAGARIGE GORDE CACAGO CONTROL C	3662
2	**************************************	0 0
866 3662	TAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTG	817 3651
3651	uIleHisLysGluGlyCys	3635
816	GGAAATTCTAAATGCTGATGGATGTGCT	785
3634		3618
784	TGATAC	777
3618	::::: ::: :::::: ArgGlyAspThrGlyValTyrLysIleIleValGluAsnGluHis	3601
776	GGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG	742
3601		3585
741	TGC	734
3584	OValAlaLySTrpLysAlaAsnAspAlaThrIleAspThrGlyAl	3568
733	TGGACATGCGATTCTGAAACCGTTGATAC	695
3568	leL	3551
694	AATTTGCTATCATTGGTCAGCCA	668
3551	ArgMetAlaProLysLeuAsnLeuAlaGlyLeuLeuAspLeuArgIleLy	3535
667		667
3534	lyProGlyLysProSerAspProThrGlyAsnValValAlaLysProArg	3518
667	GTGGACCAACCGGTCAAC	638
3518	uThrProGlyGluThrTyrGlnPheArgValLysAlaValAsnLysAlaG	3501
637	TCCCGATGCCAGTATGCCGTTATGAAAT	607
3501	CysAlaArgValAspGlyLysThrThrLysAlaThrAlaAspAsnLe	3486
606	ACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAA	557
3485	leAspAlaTyrIleValGluLysLysAspLysPheGlyAspTrpValGlu	3469
556	TTCGAGTACAATGCTTTTACATGGAAGCTGATAAAAC	509
3469	pHisValAspLeuGluTrpLysProProAlaAsnAspGlyGlyAlaProI	3452
508		508
3452	ίο	3441
508	TTTCATCCATTATTTGTTACCAAAGTT	470
3440	:::::: aLysAsnProPheAspGluProAspAla	3431

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Michands hamaxilary - Pig

Whilerante names: apomucin
C:Species: Sus scrofa domestic pig)
C:Date: 24 Mar-1999 #sequence_revision 24 Mar-1999 #text_change 20-Sep-1999
C:Accession: T03099; A40009; A28528; B39789
R:Eckhardt, A.E.; Timpte, C.S.; DeLuca, A.W.; Hill, R.L.
J. Biol. Chem. 272, 33204-33210, 1997
A:Title: The complete cDMA sequence and structural polymorphism of the polypeptide chain
A:Reference number: Z14839; MJD:98070526
A:Accession: T03099
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Accession: T03099
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Cross: references: EMBL:AF005273; NID:92581863; PID:92581864
A:Reference number: A40009; MUID:91236743
A:Accession: A40009
A:MOlecule type: mRNA
A:Reference number: A0009; MUID:91236743
A:Accession: A40009
A:MOlecule type: mRNA
A:Cross: references: GB:MG183; NID:945837; PID:9154374
A:Title: Porcine submaxillary gland apomucin contains tandemly repeated, identical seque
A:Reference number: A38528; MUID:88087170
A:Accession: A28528
A:MOLEcule type: mRNA
A:Residues: 12139-12167, T., 12169-12641 <TIM>A:Accession: A28528
A:ACcession: B29789
A:ACcession:
                                                                          alignment_block:
US-09-323-427-1 x T03099
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Quality:
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Percent Similarity:
Align seg 1/1 to: T03099
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0.654
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from: 1 to: 13288
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Gaps: 20
Percent Identity: 21,975
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	12907	GTGTCTATAACACCGACTGCACCAACAACAACAACAACAACAACAACAACAACAACAA
	73 12923	AACAACAACAGCAATAATAACCCCATCAAGTGGAGGAAGAAGACAGGAAG
	123	CAATCTTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATG
	12935	
	173 12936	ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGAT
	223 12945	TCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTG ::::::::
	261 12962	AATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCA
	308 12979	TTCGAAGGACATGTTTATGTGAAAAGGTCTTTATGATCAAGAAGGTTGCCG
ain.	358 12982	TAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTC
	. 399 12995	CATTTGATTCATGCAATGTTGCGCGGTACACGATCTCTGAATCCACGTGGT
	449 13011	ATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTAC
1).	499 13017	CAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTG
que	546 13029	ATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCT:: ::::: :::
	593 13046	TTTCAAACTCAA
	605 13062	.ATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAA ::::
	654 13073	CCGGTCAACCAGTTCAATTTGCTATCAGTCAGCCAGTTTATCATAAA
	704 13090	TGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGC
	742 13106	GGTTGTCCATTCCTGCTTTGTCGATGATGGTA ::: ::: ::: oSerProProThrCysLysThrGlyGluArgLeuIleLysPheLysAlaA
	774 13123	ACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAA
_	824	TATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC

	TyrAsnGlyCysThr 13215	13211
	TATCATTGATGTACG 1098	1084
13210	13194 yrThrCysLysSerSerCysLysProSerProValAsnValThrValArg 13210	13194
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13194	13177 nThrTrpCysAlaGluGluAspArgValTyrAspSerLysGlnCysCysT	13177
1035	GCAGCAAAACCTGCTGC.	1008
13177	13162 CysGlnAsnThrGlyPheThrAlaValValGlnAsnCysProLysGl 13177	13162
1007	974 TGTTCAGAACCACAAGGATTCGGAGCTGTTAAAA	974
13161	IUValGlySerSerPheAspAspProAsnAsnProCysValThrTyrSer 13161	13145
973	AGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAA 973	924
13145		13145
923	874 AGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCC	874
13144	::: ::: 13137 CysLeuPheAsnAsnThrAspTyr	13137

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       SWISSPROT, 38: AACA_DICDI + SWISSPROT, 38: VALH_SVSA + SWISSPROT, 38: VALH_SVSA + SWISSPROT, 38: GALU_PSEAE + SWISSPROT, 38: GALU_PSEAE + SWISSPROT, 38: GALU_PSEAE + SWISSPROT, 38: PGSL_RAT + 9: SWISSPROT, 38: PGSL_HUMAN + SWISSPROT, 38: YALG_ECOLI + SWISSPROT, 38: YALG_CAEEL + SWISSPROT, 38: YALG_CAEET + SWISSPROT, 38: YALG_YEAST + SWI
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SwissProt_38:RMAR_CANGA +
SwissProt_38:UL52_HSV7J +
SwissProt_38:AMD_HUMAN +
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01-FEB-1994 (Rel. 28, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                      EMBL; M55997; AAA27995.1;
EMBL; Z49125; CAA88934.1;
PIR; A49772; A49772.
                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "cut-1 a Caenorhabditis elegans gene coding for noncollagenous component of the cuticle."; Dev. Biol. 146:519-530(1991).
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MEDLINE; 91323673.
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                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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! P19021 homo sapiens (human
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alignment_block:
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ATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACA
                                                                                                                                   TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA
                                                                                                                                                            GlnIleLeuAsnGluGluGlyCysAlaLeuAspLysPheLeuLeuAsnAs
                                                                                                                                                                                                                ysAlaValValHisSerCysThrValAspAspGlyAsnGlyAspThrVal
                                                                                                                                                                                                                                                                   nGlnValTyrHisLysTrpThrCysAspSerGluThrThrAspThrPheC
                                                                                                                                                                                                                                                                                                                      LeuAspGlyGlyProSerGlyGlnProIleGlnPheAlaThrIleGlyGl
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Percent Identity:
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seq_name: SwissProt_38:RPOB_PLAFA
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                                                                                                        GCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCA 1315
                                                                                                                                                                  GAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATT 1267
                                                                                                                                                                                                 aLeuValSerGlu.....GluSerValArgArgArgAlaThrSerThrG
                                                                                                                                                                                                                                                                                                                     AspIleMetGluGly.....AlaSerProSerAlaProGluAlaAlaAl
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                                                                           IleValAlaThrAlaLeuSerAlaThrIlePheTyrValAlaArgPro
                                                                                                                                       lyIleCysLeuThrProIleGlyPheAlaSerPheLeuGlyIleGlyThr 403
                                                                                                                                                                                                                               ACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATG 1217
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STANDARD;
PRT;
1024
AA
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Seq_documentation_block:
ID. RPOB_PLAFA STANDA
AC 01-MAY-1991 (Rel. 18,
DT 01-NAY-1997 (Rel. 34,
DT 01-NOY-1997 (Rel. 34,
PD 1ASMODIUM falciparum
OC EMARTH M., MHYTE A.,
RC STRATH M., MHYTE A.,
RFT Phylogenetic analysi
RT Phylogenetic analysi
RN STRAIN-BWO N.A.
RA STRAIN-BWO N.
                                                                                                                                                                                                                                                                                                            "A circular DNA in malaria parasites encodes an RNA polymerase like that of prokaryotes and chloroplasts.";
Mol. Biochem. Parasitol. 44:115-124(1991).
-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Phylogenetic analysis of the rpoB gene from the Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GARDNER M.J., GOLDMAN N., BARNETT P., MOORE P.W., RANGACHARI STRATH M., WHYTE A., WILLIAMSON D.H., WILSON R.J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
Eukaryota; Alveolata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 328-1024 FROM N.A. MEDLINE; 91187055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biochem. Parasitol. 66:221-231(1994).
                                                        MISCELLANEOUS: THIS RNA POLYMERASE IS ENCODED ON A CIRCULAR DNA. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 18, Created)
(Rel. 34, Last sequence update)
(Rel. 35, Last annotation update)
RNA POLYMERASE BETA CHAIN (EC 2.7.7.
                                                                                                                                                                                                                      ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
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alignment_scores:
Quality:
Ratio:
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US-09-323-427-1 x RPOB_PLAFA
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EMBL; X52177; CAA36427.1; -.
EMBL; X95275; CAA64572.1; -.
PIR; S10438; RNZQBF.
PROSITE; PS01166; RNA_POL_BETA; 1.
PROM; PF005562; RNA_POL_BETA; 1.
PFAM; PF005562; RNA_POL_B; 1.
Transferase; Transcription; DNA-directed RNA polymerase.
SEQUENCE 1024 AA; 122185 MW; 59EAF3E1 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                           522 TACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 rgIle.....LeuAsnIle
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                                                                                              nAsnIleIleSerLeuLysLeuPheIleIleLysLeuAsnLysPheAsnA
                                                                                                                                                                                                   GTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGT 621
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45.113
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Gaps: 28
Percent Identity: 17.594
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1376	ATAAAAATAATGTTAGAATCATCGAAGCAATAAAAAACTGCCATATATA	1327
489	heIleHisTy	473
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1276	CCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATTGCATTGAT	1227
466	::: ::: ::: snlleThrGlnAsnlleIleTyrlle	457
1226	ATAATGGACAACCTGTAATACTTGCTGCAGTACAAAAT	1177
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1176	TTGCCAGTTGATTTACGTCACCGTGCACTTCTG	1142
440	<pre>::: :::::::::::::::::::::::::::::::</pre>	424
1141	TGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAG	1092
423	heTyrAsnArgTyrAsnPheLysLeu	407
1091	CTCAAGAAAAGATCTGCAGAACCGGAGAATATC	1053
407	$\verb nIlePheLeuAsnLeuLysTyrLeuPheValIleTyrTyrLysHisIleP \\$	390
1052		1052
390	snThrAsnGluGlyLeuThrCysGlyLeuValAsnTyrLe	374
1052	GCTGCGCAACTTC	1035
373	<pre>LeuProArgAsnIleLeuGlyTyrIleSerLe</pre>	357
1034	CAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCT	985
357	eLysIleAsnMetIleThrThrGlyLeuAsnSerLysPheIleLeuAsnA	340
984	TTCAGAAC	975
340	lnValAsnAsnLeuSerGluIleAsn	324
974	TACCATTAAAGAACCAAATAGCGAATGTGTTCC	933
323	uGluAsnIleAsnIleA	310
932	TACAAATATGCGGATCGATCACAGCTTTTCTATC	883
310	ThrLeuI	295
882	TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAA	833
295	:::::: LeuLysIlePheLysTyrG	281
832	TTCTAAATGCTGATGGATGTGCTCTTGATAAATAT	783
280	leLysSerLys	277
782	TTCTGCGCG	733
277	eAsnAsnIleTyrAsnLysLysPheTyrSerIleIleAspAsnLeuLeuI	260
732	TGGACATGCGATTCTGAAACCGTTGATA	701
260		244
700	TGCTATCATTGGTCAGCCAGTTTATC	672
243	snIleTyrIleAsnLeuLeuAsn	236

AsnLeuSerAsnIle.....

snLeuMetSerIleLysMetHisThrGlnIleValProIleIleTyrPro

505

TTCGTTTCTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAAATAT 1426

ATAGTATGTAGGAAATAATTACTGTAATACAATA.....A

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seq_name: SwissProt_38:YQH3_CAEEL
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                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 55.1 KD PROTEIN C43C3.3 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
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Hypothetical protein; 'TRANSMEM 11 31
                                         WORMPEP; C43C3.3; CE01525
                                                              EMBL; Z47067; CAA87330.1; -.
                                                                                                                                                                                                                                                                                         Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     SULSTON J.;
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                  Transmembrane; ATP-binding.
POTENTIAL
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                                      .LysValGluMetLeuPheArgSerThrAspSerGlyLysThrLeuGlnA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammarra,
Eukaryota; Metartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
MEDLINE: 89255324.

MEAME P.J., CHOI H.U., ROSENBERG L.C.;

"The primary structure of the core protein of the small, leucine-rich proteoglycan (PG I) from bovine articular cartilage.";

J. Biol. Chem. 264:8653-8661(1989).
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (LEUCINE-RICH PG
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PFAM; PF01462; LRRNT; 1.
Glycoprotein; Connective tissue; Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I- TISSUE SPECIFICITY: FOUND IN THE EXTRACELLULAR MATRICES OF SEVE CONNECTIVE TISSUES, SPECIALLY IN ARTICULAR CARTILAGES.
-I- PTM: THE TWO GLYCOSAMINOGLYCAN CHAINS ATTACHED TO BIGLYCAN CAN EITHER CHONDROITIN SULFATE OR DERMATAN SULFATE.
-I- SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of the dermatan sulfate DS-PGII, from bovine articular cartilage a sepharose chromatography.";
J. Biol. Chem. 264:2876-2884(1989).
                                                                                                                                                                                                                                                                                          REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEAME P.J.;
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MEDLINE; 89123388
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE SERINE/THREONINE-PROTEIN KINASE YMR216C (EC
YMR216C OR YM8261.10C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z49809; CAA89931.1; -.
HSSP; P24941; 1AQ1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00059; pkinase; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. SIMILAR TO S.POMBE DSK1.
293 AATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGA
                                                                                                                                                                                                                                                                                                          419 SerGlyAsnArgAsnIleProSerSerIleAsnAsnAsnSerIleAsnAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Transferase; Serine/threonine-protein kinase; ATP-binding.
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                                                                                                                                                                                                                                                                        93 CCCCATCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAA 142
                                                                                                                                   TACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCG
                                                                                                                                                                                                                                        nGlyIleGlyIleLysAsnSerAsnAsnSerPheLeuAsnSerValProH
                              .....AsnAsnAspAsnSerLysAsnLysAsnAsnAsn.AsnAsn
                                                               .....AspAsnAsn......
                                                                                                                                                                   isSerValThrArgMetPheIleAsnGluAspSerAsn......
                                                                                                                                                                                                        ATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTG
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42.244
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172
187
294
83237
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Percent Identity:
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ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
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20.462
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seq_name: SwissProt_38:APMU_PIG
                                                                                                                                                                                                                                                                     documentation_block:
MEDLINE; 91236743.
ECKHARDT A.E., TIMPTE C.S.,
"Porcine submaxillary mucin
"Porcine submaxillary mucin
                                                                                                                                                                  01-OCT-1989 (Rel. 12, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
APOMUCIN (MUCIN CORE PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           591
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                                                                                    SEQUENCE FROM N.A.
                                                                                                                     Eutheria;
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                                                                     SSUE=SUBMAXILLARY
                                                                                                             י scrofa (Pig).
יאריסta; Metazoa; Chordata; Cran
יאריסta; Metazoa; Chordata; Suina;
                                                                                                                                                                                                                                                                                                                                     yLysTyr 639
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                                                                                                                                                                                                                                                      STANDARD;
                                                                     GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .TrpGlyCysGlyAlaAspIleTrpSerThrAl
                                                                                                                                                                                                                                                                                                                                                                                                      .GluLeuProSerTyrLeuLeuArgAsnGl
 ABERNETHY J.L., ZHAO Y., HILL R.L.; contains a cystine-rich, addition to a highly repetitive,
                                                                                                                    Craniata; Vertebrata;
ina; Suidae; Sus.
                                                                                                                                                                    (FRAGMENT).
                                                                                                                                                                                                                                                      PRT;
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a cystine-rich,
to a highly rep
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 GERKEN T.A., OWENS C.L., PASUMARTHY M.;

"Determination of the site-specific O-glycosylation pattern of the porcine submaxillary much tandem repeat glycopeptide. Model proposed for the polypeptide:galnac transferase peptide binding site.";

J. Biol. Chem. 272:9709-9719(1997).

-i- FUNCTION: APOMUCIN IS PART OF MUCIN, THE MAJOR GLYCOPROTEIN

SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE THE ORAL CAVITY AND TO PROTECT IT FROM THE EXTERNAL
REPEAT
REPEAT
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIMPTE C.S., ECKHARDT A.E., ABERNETHY J.L., HILL R.L.; "Porcine submaxiliary gland apomucin contains tandemly identical sequences of 81 residues."; J. Biol. Chem. 263:1081-1088(1988).
                                                                                                                                                                                  PROSITE; PS01208; VWFC; PFAM; PF00007; Cys_knot
                                                                                                                                                                                                   PROSITE; PS01185; CTCK_1; PROSITE; PS01225; CTCK_2; PROSITE; PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                  EMBL; M61883; AAA30998.1; -. EMBL; M21174; AAA30990.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 87280230
ECKHARDT A.E., TII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 45-80.
TISSUE-SUBMAXILLARY GLAND:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-503 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                       between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: EXTENSIVELY O-LINKED GLYCOSYLATED ON SER AND THR RESIDUES OF THE REPEAT UNITS. HIGHEST GLYCOSYLATION APPEARS TO OCCUR ON SER RESIDUES WHICH HAVE GLY AT POSITIONS AT +2 OR -2 FROM THE GLYCOSYLATION SITE OR, WHERE GLY IS THE PENULTIMATE RESIDUE. THE PRESENCE OF PROLINE (USUALLY AT POSITION +3 OR -3) APPEARS TO ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MULTIMERIC MUCIN STRUCTURE.
SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.
DOMAIN: CONTAINS TANDEMLY REPEATED, IDENTICAL SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 CHERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENHANCE GLYCOSYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESIDUES.
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                                                                                                                                                                                    Cys_knot;
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CTCK_2; 1.
44
125
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287
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391
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 CTCK
                   VWEC
                                  6 (INCOMPLETE).
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ATAACA ValGly AACAGC OThrGl TAGTTI CTTATI CTTATI	: x }	lity: lity: Ratio: arity:	500 500 500 500 500 500 500 500 500 500	1062 1076 1085 1089
GACTGC	APMU_PIG	104.00 0.654 39.259	145 550 550 551 551 661 666 666 667 667 677 777 777 777 77	1109 1123 1139 1141
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1035 1056	CAGGTGGTGCCGCAGCAAAACCTGCTGC.:	1008
1007 1039	TGTTCAGAACCACAAGGATTCGGAGCTGTTAAAA	974 1024
973 1023	AGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAA ::::::::::::::::::::::::::::::	924 1007
1007		1007
923	AGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCC	874
873 1006	TATTTGCTAAATTAGTTTGGAATATCCAACAGATTTAATGGCTGGC	999
9	snAspThrCysCysGlulleGlyHisCysGluLysArgThr	æ
823	ACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAA	774
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7	GGTTGTCCATTCCTGCTTTGTCGATGAT	74:
741 968	TGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGC	704 952
703 951	CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA	935
653 935	.ATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAA ::: :::	924
924	: : : GlyAlaThrGluAspGlnGluAsnGluAsnLySThrGlyCysProAlaPr	908
604	CTCAA	59:
592 907	6 ATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCT :: :::::! ::: :::! !:::	54 89
891	:::::::::::::::::::::::::::::::	87
545	TCGAGTACAATGCTTTTACATGGAAGCTG	49
878		87
498	ATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTAC	449
448 872	CATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGT	399 857
5	ValGlyThrThrGluAlaGlyIleSerSerGlyAsnSerP	844
398	TAATGATGAAGGTGGACGTCAAGTTGCCGGGAATTTCACTTC	358
4-		841
<u>ت</u>	TTCGAAGGACATGTTTATGTGAAAAGGTCTTTTATGATCAAGAAGGTTGCCG	
307	ARTGTGGACCAACTTCAATAACAATCAATTTAATACAGGTAATGCA	261 824
N	$r extsf{GlyIleSerThrGlyProGluAsnSerThrProGlyThrThrGluThr}$	0

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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US-09-323-427-1 x NU5M_APILI
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PFAM; PF00361; oxidored_q1; 1.
PFAM; PF00662; oxidored_q1_N; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 554 AA; 65590 MW; 9E256E2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 93114603.
CROZIER R.H., CROZIER Y.C.;
"The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization.";
Genetics 133:97-117(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-1999 (Rel. 39, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac
Apoldea; Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apis mellifera ligustica (Common honeybee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NU5M_APILI P34855;
                                                                                                                                                         515 TATC.....GAGTACAATGCTTTTACATGGAAGCTGA 546
                                                                                                                                                                                                                                          465 CTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCA 514
                                                                            547 TAAAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                  11 LeuPheGluPheSerPheLeuMetMetLeuMetSerLeuTyrLeuLeuTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..AGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAA 1083
                                       etLysPheAsnPheLeuLeuLeuIleAspTyrLysSerLeuMetPheIle 60
                                                                                                                    rLeuAsnLysGluPhePhePheGluTrpAsnIleTyrThrPheAsnSerM 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 103.00
0.396
46.931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endopterygota; Hymenoptera; Apocrita; Aculeata;
.....CAGTTAGTGCACAGATTGAGGTA 574
                                                                                                                                                                                                                                                                                                                                                                            Length: 554
Gaps: 34
Percent Identity: 21.480
                                                                                                                                                                                                                                                                                 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                 ۲
                                                                                                                                                                                                                                                                                 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 AA.
                                                                              551
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348	CTICHANG LANCATITION	332
، د	ECHOCOPACIONOS CONTRACTOR CONTRAC	
122	ACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA	315
315	GATGATIATICAAGCTTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCA ::: ::: uMetPheMetCysValGlySerTyrMetHisTyrMetTyrSerA	300
300	ThrGluLeuValPheLeuHisLeuPheIleHisAlaMetPheLysSerLe	0
112	CGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGC	1077
283		268
0	A TARAKA	100
0	AAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAA	987
251	TyrLysAsnTyrIleMetLeuIleAlaSerLeuThrMetLeuPheAlaGl	235
986	GTTCAGAACCAC	975
234	On tenting the contract tention to the contract tention tentio	220
J	の 4 で 7 で 7 で 7 で 7 で 7 で 7 で 7 で 7 で 7 で	
924 220	ACGTATACAAATATGCGGATCACAGCTTTTCTATCAATGCCA :::::: aProThrProValSerSerLeuValHisSerSerThrLeuValThrAlaG	879 203
203	LysSerAlaGlnIleProPheSerThrTrpLeuProMetAlaMetMetAl	187
878	CAGATTTAATGGCTGGCCAAGAAGCTC	852
186	$yr Lys {\tt MetAsnGluPheMetMetIleTyrIleLeuLeuMetAlaPheThr}$	170
851		851
170	<pre>! </pre>	153
851	AAATATTTGCTAAATAATTTGGAATATCCAA	821
U t		140
o	TA SOUTH CALCALLA TO THE SOUTH OF THE SOUTH CALCALLA THE SOUTH CALCALL	771
770 139	ATG ATG VrCysLeuValIleTyrTyrMetLysMetLysSerPheThrSerGlyMet	768 123
1	oAsnMetLeuSerIleIleLeuGlyTrpAspGlyLeuGlyLeuIleSerT	106
767	GTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATG	725
106	LeuIleSerMetTyrMetLeuIleLeuSerPr	96
724	CTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACC	675
95	euMetIleLeuPhe	91
674	CCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTG	625
\vdash		
624	TCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG	575
77	. PheLeuValSerMetIlePheSerMetIleIleIleTyrSerIleSerTy	61

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Sequence of the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: SwissProt_38:IF2_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1734 ATTAAA 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1596 TCATCATTATCAAC.....TTGTCCTATTTTATTCTAACAGTTTATCAT 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1514 TATTCATTATTCAGTAATCTTTATATGCATACTATTGTAAATGTTTCAT 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p17889; 031757;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last seq
15-DEC-1998 (Rel. 37, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1268 GCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCAAA 1317
                                                            subtilis gene (infB)
2.":
                                                                                                                                   "Isolation and molecular genetic characterization of the Bacillus
                                                                                                                                                                                                                            SPERLING-PETERSEN H.U.,
                                                                                                                                                                                                                                                                           SHAZAND K.,
                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TRANSLATION INITIATION FACTOR IF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 LysGluAspLysIleMetCysIleSerMetMetMetMetTlePheSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371
         Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCATTTCCTATTCTGTA.....AACAATTCACTTATTTGCATTATTGCA 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATTAGGCCATGAATAGTTTCGTTTGTTATT.....A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerLys 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etPheThrTyrGluValTyrIleGluLysSerIleIleGluIleLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGTGATAATATCACAAATTATACCTTGTATTGCCCCAATTTTTATGGGCA 1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euIleLeuLeuAsnAsnLysIleGlyTyrPheLysMetSer.PheLeuPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lPheLysMetIleMetValGlyLeuIleMetGlyPheAsnPheTyrLysL 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnLeuLeuGlyIleAsnLeuLeuMetIleTyr.....LysLeuMetVa 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.....TCAAAACTTCTTCTATCGCTTTATAGCTTCTGAAAAGCT 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGTAGGAA.....ATAATTACTGTAATACAATAAGTGATATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etIleLeuValLeuThrSerLysPheLeuMetMetAsnValIleTyrSer 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATCATCCTTCTAATAACTAATTTTAGCTAACAA....ATATATAGT 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tIleAsnLeuIleIleGlyThrIlePheThrValSerTyrSerPheArgM 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGAAGGCATAAAAATAATGTTAGAATCATCGAAG......CAATA 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euValGly......TyrTyr......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eMet...AsnLeuIleTyrLysIleIleTyrLysLysIleIleMetMetM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rLeuIleTyrSerLysLeuIlePheAsnLeuMet.AsnPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspLeuIleIleGluMetPhePhePheSerLysMetIleTyrPheSerMe 371
                                                                                                                                                                                                                                                                                                                     90236932.
                                                                                                                                                                                                                   TUCKER J., CHIANG R., STANSMORE K.,
TERSEN H.U., GRUNBERG-MANAGO M., RABINOWITZ J.C.,
172:2675-2687(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                    encoding
                                                                                    protein synthesis initiation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      716 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .SerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1472
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alignment_block:
US-09-323-427-1
                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                Align seg 1/1 to: IF2_BACSU
                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M34836; AAA22673.1; -. EMBL; Z18631; CAA79234.1; -. EMBL; Z99112; CAB13536.1; -. PIR; A35269; A35269. PIR; B35269; B35269. PIR; B35269; B35269. PIR; S31994.
                                                                                                                                                                                                                                                                                                                      NP_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
Submitted (NOV-1997) to the EMBL/GenBank/DIBJ databases.

-i- FUNCTION: IF-2, ONE OF THE ESSENTIAL COMPONEBYS FOR THE INITIATION
OF PROTEIN SYNTHESIS IN VITRO, PROTECTS FORMYLLMETHIONYL-TRNA FROM
SPONTANEOUS HYDROLYSIS AND PROMOTES ITS BINDING TO THE 30S
RIBOSOMAL SUBUNITS. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP
DURING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- ALTERNATIVE PRODUCTS: IT IS PROBABLE THAT BY USING ALTERNATIVE
INITIATION CODONS IN THE SAME READING FRAME, THE GENE TRANSLATES
INTO TWO ISOZYMES: ALPHA AND BETA.
                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01176; IF2; 1. PFAM; PF00009; GTP_EFTU; 1. Initiation factor; Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93259931.
SHAZAND K., TUCKER J., GRUNBERG-MANAGO M., RABINOWITZ J.C.
                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P02990; 1ETU.
SUBTILIST; BG10268; INFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 175:2880-2887(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Similar organization of the nusA-infB operon in Bacillus subtilis and Escherichia coll.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEIGHTON T.;
nAsnAsnAsnLysAsnGlnHisGlnGlnLysProValLysProLysLysG
                             CAACAGCAATAATAAC..................CCCATCAAGTGGAGGAAGA
                                                                PheAsnLysAsnLysLysAsnAsnAsnLysLysAsnLysArgAsnAs
                                                                                                 TATAACACCGACTGCAGCAACAACAACAACAACAACAACAACAACAA
                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                         716
                                                                                                                                                                x IF2_BACSU
                                                                                                                                                                                                                                                                                                                       AA:
                                                                                                                                                                                                                    102.50
0.418
47.115
                                                                                                                                                                                                                                                                                                                    716
368
233
276
276
329
56
329
78621 MW;
                                                                                                                                    from: 1
                                                                                                                                                                                                                    Gaps:
Percent Identity: 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                    G-DOMAIN.
GTP (BY S
GTP (BY S
GTP (BY S
R -> A []
                                                                                                                                                                                                                                                                                                                    GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
R -> A (IN REF. 3).
ACB9B730 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                       INITIATION FACTOR IF-2-ALPHA.
INITIATION FACTOR IF-2-BETA (PROBABLE).
                                                                                                                                    t
0:
                                                                  115
                                                                                                   77
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818	GGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTG	776
	aspLysGlyArgGlySerValAlaThrLeuLeuValGlnThrGlyThrLe	
775	TCCATTCCTGCTTTGTCGATGATGGTAAC	747
402	ysAlaAsnProAsnArgGlnAlaLysGlyThryalIleGluAlaGluLeu	386
746	TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG	697
386	GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA : ::: ::::::: ::: ::::::	647 369
6	lyGlyGluThrIlePheValProLeu.SerAlaLeuThrGlyLysGlyIl	Ú
646	AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT	597
596 353	TAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTC ::::::::::: ::: :::	547 336
336	ProIleIleValAlaValAsnLysIleAspLysGluSerAlaAsnProAs	320
546	TTTTACATGGAAGCTGA	530
319	alMetProGlnThrValGluAlaIleAsnHisAlaLysAlaAlaGluVal	303
529	TTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGC	480
479 303	TATTTTTGTAACAACTGTTGTCATTTCGT	448 286
286	ProGlyHisAlaAlaPheThrThrMetArgAlaArgGl	7
447	CCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGG	398
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347 262	CATGITTATGIGAAAGGICTITTATGATCAAG	317 248
248	LysThrThrLeuLeuAspSerIleArgLysThrLysValValGluGlyGl	232
316	AATTTTAATACACGTAATGCATTCGAAGGA	287
286 231	TTGAATGTGGACCAACTTCAATAACAATC	215
	uGluGluThrGluLeuGluLysTyrGluGluProAspAsnGluGluAspL	9
G	GAAGGTGAGCCAGAAA	4.
198	GluLeuIleAlaSerGluTyrGlyValGluThrGluGluValIleValLe	182
241	CTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTC	200
181	euLeuGlyValMetAlaThrIleAsnGlnGluLeuAspLysAspThrIle	165
199	TTATTGCTTTCTGTACTACA	180
6 ,	alaGlu.GluLeuGlyLysGluProSerGluLeuIleLysLysLeuMetL	4 (
7	AAAAATCGAATTTACTAAATCTTCTGAAATGATGATGATTCT	س
138 148	AGACAGGAAGCAATCTTAGTTTTTCT	113 132

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BHARGAVA A.K., WOITACH J.T., DAVIDSON E.A., BHAVANANDAN V.P.;
"Cloning and cDNA sequence of a bovine submaxillary gland mucin-like protein containing two distinct domains.";
Proc. Natl. Acad. Sci. U.S.A. 87:6798-6802(1990).
-:- SUBCELLULAR LOCATION: SECRETED.
-:- TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.
-:- SIMILARITY: TO PORCINE APOMUCIN.
-:- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
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                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SUBMAXILLARY MUCIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561 leIleLeuAlaSerAlaSerAsnAlaIleValIle.......GlyPhe
                                                                                                                                                                           TISSUE-SUBMAXILLARY GLAND;
MEDLINE; 90370871.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                           Bovinae; Bos.
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alignment_scores:
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DOMAIN 61 155
REPEAT 61 71
REPEAT 112 122
REPEAT 148 155
DOMAIN 338 400
DOMAIN 471 555
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PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
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TTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCAT
                            ThrAla.....ValValSerGly......
                                                                                            {\tt roGluSerSerAsnThrGlyThrSerThrGlyValGlyArgGlnThrSer}
                                                                                                                          CAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGT
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Percent Identity: 21.594
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ID AAC4_DICDI STANI
AC P14198;
DT 01-JAN-1990 'D~1 '.
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01-JAN-1990 (Rel. 13, Created)
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alignment_scores:
    Quality:
    Ratio:
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US-09-323-427-1 x AAC4_DICDI
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DICTYDB;
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"Nucleotide sequences of Dictyostelium discoideum developmentally regulated cDNAs rich in (AAC) imply proteins that contain clusters of asparagine, glutamine, or threonine.";

MOL. Gen. Genet. 218:453-459(1989).

-!- DEVELOPMENTAL STAGE: THE CONCENTRATION OF AAC-RICH MRNAS IS LOW IN DORMANT SPORES AND GROWING CELLS, BUT INCREASES DURING SPORE-GERMINATION AND MULTICELLULAR DEVELOPMENT.

-!- MISCELLANEOUS: SEVERAL PROTEINS DERIVE FROM AAC-RICH MRNA, WHICH, DUE TO A FRAMESHIFT ALSO HAVE ACA AND CAA CODONS AND THUS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
AAC-FICH MRNA CLONE PLX330 PROTEIN (FRAGMENT).
Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                            143 ATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                             193 TACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 CCCCATCAAGTGGAAGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAA 142
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ACATGTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATG
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                                                                .AsnCysPheGluThrCysAspPheLysAlaThrGluArgGl 108
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seq_documentation_block:
ID VGLH_HSVSA STANDA
AC P16492;
DT 01-AUG-1990 (Rel. 15,
DT 01-AUG-1990 (Rel. 15,
DT 01-OCT-1996 (Rel. 34,
DE GLYCOPROTEIN H PRECUR
GN GH OR 22.
OS Herpesvirus saimiri (
OC Viruses; dsDNA viruse
OC Gammaherpesvirinae.
RN [1]
                                                                                                                                                                                                                                                               seq_name:
                                                                                            01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
GLYCOPROTEIN H PRECURSOR.
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                                         Herpesvirus saimiri (strain
Viruses; dsDNA viruses, no F
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                                                                                                                                                                                                        STANDARD;
                                           RNA stage; Herpesviridae;
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alignment_block:
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    Quality:
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CARBOHYD
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CARBOHYD
CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HONESS R.W., CRAXTON M.A., WILLIAMS L., GOMPELS U.A.;
"A comparative analysis of the sequence of the thymidine kinase gene
of a gammaherpesvirus, herpesvirus saimiri.";
J. Gen. Virol. 70:3003-3013(1989).
-i- FUNCTION: GH AND GL FORM A COMPLEX THAT INDUCES NEUTRALIZING AND
SYNCYTIA INHIBITING ANTIBODIES (BY SIMILARITY).
-i- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN H.
                              174
                                                          191
                                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE; 89036162.

GOMPELS U.A., CRAXTON M.A., HONESS R.W.;

GOMPELS U.A., CRAXTON M.A., HONESS R.W.;

"Conservation of glycoprotein H (gH) in herpesviruses: nucleotide sequence of the gH gene from herpesvirus salmiri.";

J. Gen. Virol. 69:2819-2829(1988).
                                                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
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MEDLLINE; 9233688.
ALBRECHT J.-C., NICHOLAS J., BILLER D., CAMERON K.R., BIESINGER B.
NEWMAN C., WITTMANN S., CRAXTON M.A., COLEMAN H., FLECKENSTEIN B.,
HONESS R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-60 FROM N.A. MEDLINE; 90063548.
                                                                                                                                             74 ACAACAACAGCAATAATAACCCCATCAAGTGGAGGAAGAAGAAGACAGGAAGC 123
                            TTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATT 223
                                                                     AATCTTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGA 173
                                                                                                               ThrIleSerCysHisIleThrProAsn...........
                                                         ....TyrLeuPheValSerValGluPheThrLysPheAspSerLeu
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Gaps: 39
Percent Identity: 20.000
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 yrValLeuSerSerMetCysThrSerLeuGluIleGlyAsnLeuLeu	455	
	885	
	438	
09TAAA 834 	. 809 422	
71 GTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGA	771 406	
21 AACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATG 770	721	
71 TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA 720 ::: 	6 71 383	
660 AACCAGTTCAA 670 	367	
618CAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTC 659	618 350	
84 ACAACTGCTTTTCAAACTCAAATTGTCCCGATGC	584 335	
34 ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATC 583	534 330	'
490 ATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTT 533 : ::::::::::::::::::::::::::::::::	31 40	V 1-4 (
443 CGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATT 489 :::	29	w + ± +
393 CACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCA 442 ::::: ::::::::::::::::::::::::::::		
343 TCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTT 392	27	
323TATGTGAAAGGTCTTTATGA 342 261 ArgGluIleIleGluThrProProLeuThrPheIleLysAsnLeuGlnAs 277	21	
306 CATTCGAAGGACATGTT	3(2,	
256 AATTGAATGTGGACCAACTTCAATAACAATCTTAATACACGTAATG 305	2: 2:	
224 CCGGTTGACAATGGTGTCGAAGGTGAGCCAGA 255	2:	

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1111 CACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTC 1160 :: || || || || || || :::
                           1648 ATATCACAAATTATACCTTGTATTG
                                                                                                                                                                                                                                                                                      1552 TAAATGTTTCATCATT....AGGCCATGAATAGTTTCGTTTGTTATTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1261 AAGCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTC 1310
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                                                                                                                                                            ATCATTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATA 1647
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                                                                                           IleMetVal.....
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seq_documentation_block:
ID YAY3_SCHPO STANDA
AC Q10211;
DT 01-OCT-1996 (Rel. 34,
DT 01-OCT-1996 (Rel. 34,
DT 01-OCT-1996 (Rel. 34,
DT 01-OCT-1996 (Rel. 34,
DE HYPOTHETICAL 74.5 KD
GN SPACAH3.03C.
OS Schizosaccharomyces p
OC Eukaryota; Fungi; Asc
OC Schizosaccharomyces.
RN [1]
CS SCHIZOSACCHAROMYCES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 97.50
Ratio: 0.554
Percent Similarity: 43.672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-323-427-1 x YAY3_SCHPO
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318
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TRANSMEM 564 584 POTENTI
TRANSMEM 626 646 POTENTI
SEQUENCE 649 AA; 74488 MW; F04F8
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01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHROMOSOME
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euLeuAspPhePheHisArgProTrpGluAspTyrGluProLeuTyrPro 115
                                                                                                                                                              eLeuHisThrLysPheTyrSerGluArgGlyValLeu.....ArgL
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690 CAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC
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                                                                                                      CTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTT 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGATCTGCAGAACCGGAG...AATATCATTGATGTACGAACTGATATC 1108
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erLeuProGluAspLeuGlyGlyValArgAsnTrpAspTyrArgPheThr 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uGluCysPheProAlaLeuAspTyrAlaArgGlnSerHisGluThrArgV
                                                                     .....Gly.AsnAlaAlaValHisHisLeuGln.LeuAspIleT
                                                                                                                                                                                                                                                                                   ACGTCAC...CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTG
                                                                                                                                                                                                                                                                                                                                                         .....TyrSerIleHisGlyAspSerGlnAsnLeuGluGluValGluLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysLysAsnLysAspGlyGlyIleAsnIleVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TrpIleArgAspSerAlaPheThrIleTyrAlaLeuAlaGlnLeuGlyPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....GGTGGTGCCGCAGCAAAAACCTGCTGCAGCTGCGCAACTT..... 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGCGGATCGATCACAGCTTTTCTATCAA.....TGCCAGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pTyrValThrProAsn.........LeuValAspLysL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ......llePheArgGlnGluGlyLeuGlyProAsnValAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAspProLysTyrIleLeuAspCysValProSerGlyAspGlnLeuLy 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGG 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TrpLeuIleArgArgValSerCysIleArgGlyThrSerArgIleLysLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......CCAGTTCAATTTGCTATCATTGGTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID YCFZ_MARPO STANDARD;
AC P09975;
DT 01-MAR-1989 (Rel. 10, Created Procedure of the Company of the C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-323-427-1 x YCF2_MARPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: YCF2_MARPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast:
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiopsida;
Marchantiales; Marchantiaceae; Marchantia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Chloroplast gene organization deduced from complete sequence of liverwort Marchantia polymorpha chloroplast DNA."; Nature 322:572-574(1986).
-!- SIMILARITY: TO A SIMILAR ORF IN OTHER PLANTS CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-JUL-193 (Rel. 26, Last annotation updat
HYPOTHETICAL 259 KD PROTEIN (ORF 2136).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 yrGly 389
                                                                  178 TCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGG 227
                                                                                                                                                                                                             128 TTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCG
                                                                                                                                                                                                                                                                                725 rAsnSerGluTyrAsnLysIleIleTrpAsnLysLysAsnMetLysPheP
                                                                                                                                                                                                                                                                                                                                                                                                                               709 AsnAsnLysLeuIleThrTrpLysLysIleSerAsnLysLeuValIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MENDEL; 5295; MARpo;ycf2;1.
PFAM; F100004; AAA; 1.
Chloroplast; Hypothetical protein.
SEQUENCE 2136 AA; 259911 MW; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OHYAMA K., FUKUZAWA H., KOHCHI T., SHIRAI H., SANO T., SANO S., UNESONO K., SHIKI Y., TAKEUCHI M., CHANG Z., AOTA S., INOKUCHI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marchantia polymorpha (Liverwort).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X04465; CAA28078.1; -.
                                                                                                                                                                                                                                                                                                                                                         78 CAACAGCAATAATAACCCCATCAAGTGGAGGAAGAAGAAGACAGGAAGCAATC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 AACAACAAA.....AA
                                                                                                                                        heSerPheSerLysAsnSerValLeuAspThrPhePhePheAsnLysLys
SerPheAsnIleIle.....ThrValIlePheAspLys.L 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.00
0.316
46.375
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Percent Identity: 18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A2FB8B07 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 2136
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177 742 978

890

840 226 740

149

132

497

1040 1002	ATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTG :::::::::::::::::::::::::::::::::::	991 988
988	sGlnLysGluLysAsnIleGluIleIleLeuAsnAsnGlnAsnTyrPheG	971
990	GTTCAGAACCACAAGG	972
971	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::::	955
971	ATAGCGAATGTGTTCGAC	942
954	ysSerGlnLeuSerAsnValLeuLeuVal	942
941	TCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTA	892
942	LysSerPheIleGluLysLysAsnAsnL	931
891	ATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATA	842
930	Fe -	925
841	ATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG	792
924		924
791	GGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAA	742
924	snAsnLeuLeuTyrLeuArgLeuLeuLysIlePheLeuLysAspLysA	907
741	TGCGATTCTGAAACCGTTGATACTTTCTGCGC	704
907	gPheIlePheHisLeuGluLysLysThrIleLysAs	891
703	ACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATA	660
068	::: ProGluLeu	874
659	GATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGT	610
874	uIleLeuPheAsnProIleGluAsnArgGlnLeuLeuGlnAsnPhePheG	857
609	TGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGT	560
857	LysLysTyrLeuTyr.TyrArgIleTyrLysAspLysGl	841
559	ACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGT	522
841	nAspPheLeuM	827
521	CAAAGTTGATCGTGCATATCGAG	472
826	oIlePhe	816
471	CTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGT	428
815	:::::: AsnLeuThrThr	811
427	TGCGCGTACA	378
810		803
377	AGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTC	328
803	:::::: PhePheAsnSerLysAsnIleLysLysThrLysIlePheLy	787
327	TAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGT	278
786	euLysLysIleGlnLeuAsnPheGlnGluIleGlnLysIleLeuAsnCys	770
277	AATTGAATGTGGACCAACTTCA	228

	TCATTTGTGAAAAAAAAAAAAAAAAAAAAA 1776 ::: 	1747 1232
1746 1231	CTATTCTGTAAACAATTCACTTATTTGCATTATTGCAATTAAAAAGTATT ::: ::: ::: lullelle	1697 1219
1696 1219	TTATGGGCATCATTTC	1681 1202
1680 1202	TTTGTGATAATATCACAAATTATACCTTGTATTGCCCAATTT ::: ::: ::: ::: TrpValIlePheSerLeuValIlePheIlePheLeuTyrTyrGlnLysIl	1639 1186
1638 1185	TCCTATTTTATTCTAACAGTTTATCA::::::::::::::::::::::::::::	1613 1169
1612 1169	GTTTGTTATTATCATTATCAACTTG ::: ::: pAsnLeuArgPhePheAsnGluIleAsnTyrLysLysAsnTyrLeuLeuA	1585 1152
1584 1152	ATTGTAAATGTTTCATCATTAGGCCATGAATAGTTTC	1548 1136
1547 1136	AGCTTCTGAAAAGCTTATTCATTATTCAGTAATCTTTTATATGCATACT. :::::: ::: ::: ::: ::::	1499 1119
1498 1119	AATACAATAAGTGATATTTTCATCAAAACTTCTTCTATTCTA	1452 1103
1451 1102	AATTTTAGCTAACAAATATATAGTATGTAGGAAATAATTACTGT ::: ::: ::: erTrpPhePheThrLeuGluTrpTrpGluTyrAsnThrTyrIleLeuLeu	1408 1086
1407 1086	AATAAAACTGCCATATATATTCGTTTCTTATCATCCTTCTAATAACT :	1358 1075
1357 1075	TTCGTCCAAATCAGAAGGCATAAAAATAATGTTAGAATCATCGAAGCAAT ::: ::::::::::::::::::::::::::	1308 1060
1059		1059
1307	ATT?	1258
1257 1059	AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGG ::: ::: sileGluLysAsnAsnTyrCysTyrAsn	1214 1050
1213 1050	GTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAA 	1164 1041
1163 1040	CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACC	1114 1035
1113	AGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACAC :::::: ::::::	1064 1019
1063	CGCAACTTCGTTTACTCAAGAAA :::	1041 1003

seq_name: SwissProt_38:GALU_PSEAE

TTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACAT

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alignment_block:
US-09-323-427-1 x GALU_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Nice 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
UTP--GLUCOSE-1-PHOSPHATE URIDYLYLITRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE
PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHOTE
URIDYLYLITRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE).
                                                                                               397
                                                                                                                                                             350
                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALU_PSEAE
Q59633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U03751; AAB01486.1; -. PFAM; PF00483; NTP_transfera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.
                                                               90
                                                                                                                               74
                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                            GTATT.....TTTGTAACAACAACTGTTGTCATTTCGTTTCATCCA 487
                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS
lyLeuGlyHisAlaIleLeuThrGlyArgProLeuIleGlyAspGluPro
                                                             sLeuLeuAspGluCysSerPheSerTyrThrArgGlnThrGlnMetLysG
                                                                                           TCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTG 446
                                                                                                                                                             GGT...TGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACT
                                                                                                                                                                                         ysArgAlaLeuGluAspHisPheAspIleSer....TyrGluLeuGlu
                                                                                                                                                                                                                         GTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAA
                                                                                                                                                                                                                                                         uAlaLeuAspAlaGlyLeuAsnGluIleSerIleValThrGlyArgGlyL
                                                                                                                                                                                                                                                                                        AGAAATTGAATGTGGACCAACTTCAATAACAATC...AATTTTAATACAC
                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: UTP + ALPHA-D-GLUCOSE 1-PHOSPHATE
                                                                                                                           AsnGlnIleLysGlyThrAspLysGluLysTyrLeuValGlyIleArgLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYROPHOSPHATE + UDP
                                                                                                                                                                                                                                                                                                                                                                                    to: GALU_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria; gamma subdivision; Pseudomonas group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; NTP_transferase; 1.
Kinase; Nucleotidyltransferase.
79 AA; 30939 MW; D967F501 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.00
0.807
50.424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GLUCOSE.
TO THE PROKARYOTIC UDPGP FAMILY.
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                               "Structurally distinct and the first folds in Dictyostelium development.";

Cell 69:305-315(1992).

Cell 69:305-315(1992)

-!- FUNCTION: COORDINATES CELL AGGREGATION BY SYNTHESIZING THE
                                                                                                                                                                                                                                                                                                                                                         MEDIINE; 92233467.

MEDIINE; 92233467.

PITT G.S., MILONA N., BORLEIS J., LIN K.C., REED R.R., DEVR
"Structurally distinct and stage-specific adenylyl cyclase
"Structurally - in mintunetallim development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ADENYLATE CYCLASE, AGGREGATION SPECIFIC (EC 4
PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYAA_DICDI
                                                                                                                                                                                                 ENZYME REGULATION: REGULATED BY A SURFACE RECEPTOR THROUGH A GUANINE NUCLEOTIDE BINDING PROTEIN. BOTH POSITIVELY AND NEGATIVELY REGULATED BY EXTRACELLULAR CAMP; THIS REGULATION
                                                                                                                                                                                                                                                           THAT INFLUENCES DIFFERENTIATION AND MORPHOGENESIS OF CELLS WITHIN A DEVELOPING MULTICELLULAR STRUCTURE.

CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE
                                                                                                 DEVELOPMENTAL STAGE: CELL AGGREGATION AND LATER DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
                                                                               SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                            DURING AGGREGATION
                                                                                                                                                                                PART OF THE MECHANISM THAT ESTABLISHES THE
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EMBL; L05496; AAA33163.1; JOINED.
EMBL; L05497; AAA33163.1; JOINED.
EMBL; L05498; AAA33163.1; JOINED.
PIR; B42239; B42239.
HSSP; P26769; 1ABB.
DICTYDB; DD02024; ACAA.
PROSITE; PS00452; GUANYLATE_CYCLASES; 1.
PFAM; PF00211; guanylate_Cyc; 2.
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                                                                                                                             874 luAspPheLysIleLysSerLysSerAsnSerSer.Phe...GluIleGl 889
                                 903 rgValMetGlyIleLeuHisHisValLysIleSerAsnAspLysIleAsp 919
                                                                                                                                                                                                                           841 IleLeuAspThrThrValAsnAsnAsnAsnAsnAsnAsnAsnThrAsnAs
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                                                                                                                                              TCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAAATCGA 147
                                                         CACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGT
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1160	**************************************	1167
1104	CTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGA	1055
1166	GlnS	1154
1054	AGGTGGTGCCGCAGCAAAACCTGCTGC	1005
1153	CGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTA :::::: ::: GluLysAspLysPheAsnPheLeuLeu	955 1145
1144	ThrIleSerValAsnLys	سا ا
G	AGCTTTTCTATCAATGCCAGATCAGTATTA	0
1138	CysLysIleA	1122
904	AGAAGCTCACGTATACAAATATGCGGATCG	858
1121	:::: LeuIleGlnIleC	1110
857	TGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGAT	808
1109	rIleGlyPheValIle	1104
807	TGTCGATGATGGT	758
1104	SerIleLeuIleSerProThrLeuThrAsnHisLeuTyrGluThrAspTy	1088
757	CTGAAACCGTTGATACTTTCTGCGCGGTTGTC	708
1087	_	1071
707	AATTTGCTATCATTGGTCAGCCAGTTTATCAT	667
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999	AGT ATGCCGTT ATGAAATTTTGGATGGTGGACCAACCGTGATCAACC	617
616 1056	TATCTGAAATCACAACTGCTTTTCAAACTTCAAATTGTCCCGATG ::::::: ::: ::: ::: eu.IlaArgPheGlnAsnProLeuAlaArgSerSerLeuThrArgValCy	573 1040
1040	errendencysaraphecryvarcystnrvarbengru	I N
7	ACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGG	523
1023	LeuSerPheThrArgIlePheArgThrProLeuValTyrGlnIl	1009
522	TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAG	473
1008	yrLeuValmetGlyIleAlaPheLeuValTyrIleGly	996
472	STATTTTGTAACAACA	423
996	 is:TleMetAspSerAlaP	979
422	ACTTCCATTTGATTCATG	392
979	H	967
391	TTGCCG	365
966	ysTyrValIleIleAsnAsnValValGluThrLysPhePhe	953
364	ATGTTTATGTGAAAGGTCTTTATG	315
953	<pre>gLysTyrPheTyrPhePheGluAsnLeuThrThrGluLysPhePheHisL</pre>	936
314	GTAA	287
936	$ Lys {\tt GluIleIleGlnIleAspGluAspPheValLysValThrLysLeuAr} \\$	920

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sp_invertebrate:096776
sp_invertebrate:019304
sp_invertebrate:061816
sp_invertebrate:022627
sp_invertebrate:045890
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-Q=/Cgn2_1/USPTO_spool/US09323427/runat_14042000_170514_19920/app_query.fasta.1
-Q=/Cgn2_1/USPTO_spool/US09323427/runat_14042000_170514_19920/app_query.fasta.1
-DB=SPTREMBL_12 -QFMT=fastan SUFFIX=backtrans.rspt
-QBAPQP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPQP=4.500 -QGAPEXT=0.050 -XGAPQP=10.000
-XGAPEXT=0.500 -FGAPQP=6.000 -FGAPQXT=7.000 -YGAPQP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-MINLEN=0 -MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3
                                                                                                 invertebrate: Q22724
_invertebrate: Q18298
_invertebrate: Q20167
_invertebrate: O96668
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invertebrate: 018117
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invertebrate:097298
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3 8.6e-123
3 .1e-116
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 out_format :
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.2e-49
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  ! Documentation
                                                   Q25802 plasmodium falciparum.
O97236 plasmodium falciparum.
O97288 plasmodium falciparum.
O96247 plasmodium falciparum.
  94648
045618 c
7 plasmodium falciparum
8 plasmodium falciparum
caenorhabditis elegans
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sp_invertebrate:077372
sp_invertebrate:097230
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SEQUENCE
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seq_name: sp_invertebrate:Q93115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ascaris lumbricoides (common roundworm).
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia;
Ascaridoidea; Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "cut-1-like genes of Ascaris lumbricoides.";
Gene 193:81-87(1997).
                                                                                                                                                                                                                                                                                                   270 CAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACAT
                                                                                                                                                                                                                                                                                                                                                            220 GATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                170 ATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTC
                                                                                                                                                                                                                                           GTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGG
                                                                                                                                                                                                                                                                                                                                             alleProValAspAsnGlyValGluGlyGluProGluIleGluCysGlyP
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gValGlnCysPheTyrMetGluAlaAspLysThrValSerThrGlnIleG
                                                                                                            GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
                                                                                                                                                                   AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG
                                                                                                                                                                                                                             AlaTyrValLysGlyLeuTyrAspGlnGluGlyCysArgSerAspGluGl
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Ratio: 4.593
milarity: 92.784
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CUT-1-LIKE
BDEB1169
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seq_documentation_block:
ID Q19707 PRELIMINARY;
AC Q19707;
DT 01-NOV-1996 (TrEMBLrel. 01
DT 01-NOV-1996 (TrEMBLrel. 01
DT 01-JAN-1999 (TrEMBLrel. 09
DE F22B5.3 PROTEIN.
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                                                                                                                 sp_invertebrate:Q19707
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Last annotation update)
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alignment_block:
US-09-323-427-1 x Q19707
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Ratio: 4.177
Percent Similarity: 85.974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SWALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
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EMBL; 250044; CAA90355.1;
SEQUENCE 389 AA; 42983
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CTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGA
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                                                                                                                                                                                             TTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 499
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                                                                                                                                                                                                                                                   ATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTA 449
                                                            sThrValSerThrGlnIleGluValSerAspLeuThrThrAlaPheGlnT
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Gaps: 8
Percent Identity: 69.610
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seq_documentation_block:
ID 018479;
AC 018479;
DT 01-JAN-1998 (TrEMBLre
DT 01-JAN-1998 (TrEMBLre
DT 01-NOV-1998 (TrEMBLre
DT 01-NOV-1998 (TrEMBLre
CUTICLIN-1.
GN MTCUT-1.
OS Meloidogyne artiellia
OC Eukaryota; Metazoa; N
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                                                                                                                                                                                                                                                                                                                                                      luAsp.....SerPheArgGlnGluLeuCysIleSerSerPhe
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   e artiellia.
Metazoa; Nematoda;
                                                            3 (TrEMBLrel.
3 (TrEMBLrel.
3 (TrEMBLrel.
                                                                                                                         PRELIMINARY;
                                                              05,
                                                         Created)
Last sequence update)
Last annotation update)
 Secernentea; Diplogasteria;
                                                                                                                           PRT;
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 Tylenchida;
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alignment_block:
US-09-323-427-1 x O18479
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MEDLINE; 97218031.

DE GIORGI C., DE LUCA F., DI VITO M., LAMBERTI F.;

BE GIORGI C., DE LUCA F., DI VITO M., LAMBERTI F.;

"Modulation of expression at the level of splicing of cut-1 RNA infective second-stage juvenile of the plant parasitic nematode Meloidogyne artiellia.";

Mol. Genet. 253:589-598(1997).

EMBL; X96677; CAA65452.1; -.
                                                                                    166
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[1]
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                                                                                                                                                       ATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTTGGATGGTCGACCAAC:::||||||||||:::||
                                                                                                                                                                                                               TTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAA
                                                                                                                                                                                                                                                                                                              ValSerThrThrValValIleSerPheHisProGlnPheValThrLysVa
                                                                                                                                                                                                                                                                                                                             GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGT
                                                                                                                                                                                                                                                                                                                                                                     AAATTGAATGTGGACCAACTTCAATAACAATCAATTTAATACACGTAAT
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                                                                                                               CGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAAT
                                                                                                                                        ValValProMetProValCysLysTyrGluIleLeuGluGlyAlaAlaLe
                                                                                                                                                                                                alSerAlaGlnLeuGluValSerGluIleThrThrGlnPheGlnThrGln
                                                                                                                                                                                                                                                       lAspArgAlaTyrArgValGlnCysPheTyrMetGluAlaAspLysThrV
                                                                                                                                                                                                                                                                                     TGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTG
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TGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           luIleGluCysGlyProThrSerIleThrValAsnPheAsnThrArgAsn
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4.042
77.751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 63.636
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Gaps:
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Seq.
AC DT DT DT DT DE GN OC OC OC OC RN RN RR RR RR RR RR
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                                                                                                                                                                            _documentation_block:
    Q9XVM7 PRELIMI
                                                                                                                                                                                                                                                                 1293 CCAT 1296
SEQUENCE FROM N.A. MEDLINE; 94150718.
BURTON J.;
"2.2 Mb of contiguous
                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                         350
                                                                                                   F53F1.1.
                                                                                                                                                                 Q9XVM7;
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                                                               Rhabditina; Rhabditoidea;
                                                                                                               F53F1.1 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                        eArgHisHisHisLeuMetGluAsnLeuSerAlaGluProGlnArgA
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                                                                                                                                                                                                                                                                                                                                       {\tt rgPheIleTyrGlnGlyGlyGlnGlnValCysMetSerSerPheArgAla}
                                                                                                                                                                                                                                                                                                                                                              TTGCTGCAGTACAAAATGGA.....ATCTGCATGTCACCATTTGGCTTC
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                                                                                                                                                                             PRELIMINARY;
  nucleotide
                                                              oda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                             PRT;
 sequence
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  from
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  chromosome
                                                              Caenorhabditis.
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US-09-323-427-1 x Q9XVM7
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                            132
                                                                                                                                                                                                                                                    471
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EMBL; Z81088; CABO3124.1;
SEQUENCE 364 AA; 40843
                                                                                                                                                                                                                                                                                                                                                    371
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3.455
77.491
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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GRADNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMER B., O'CALLAGHAN M.,
PARSONS J., PECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATENSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elegans.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 ATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTG
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rValAspGluIleSerThrIleSerTyrAsnValAsnLeuThrMetProT
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PheGlyLeuTleGlyGlnGlnValTyrHisGlnTrpLysCysAspAsnAs
                                                TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA
                                                                                                                                                                                                                                                                                                                             GGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAG
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LeuLeuCysLeuTyrArgGluSerGlnValThrValAlaAsnAsnIleSe
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alignment_block:
US-09-323-427-1 x Q9XYU9
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Percent Similarity:
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O1-NOV-1999 (TrEMBLrel. 12,
O1-NOV-1999 (TrEMBLrel. 12,
O1-NOV-1999 (TrEMBLrel. 12,
CUTICULLW-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAMZY R., HELMY H., ADELY M., CURTIS K., WEIL G.; "Wuchereria bancrofti L3 cuticulin-1 cDNA partial sequence."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wuchereria bancrofti.
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Filarioidea; Onchocercidae; Wuchereria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF125580; AAD28743.1; -. NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. RAMZY R., HELMY H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249
                   872
                                                                                                                                    772 TAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9XYU9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 aProvalValGly 319
                                                                                                                      17
                                                                                                                                                                                   1 ThrValAspThrPheCysAlaValValHisSerCysPheValAspAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCC
::::::||||||::::|||||||
SerAsnGlyCysSerIleAspLysPheLeuLeuSerAsnLeuGluTyrPr
                                                                   ACCGTTGATACTTTCTGCGCGCGTTGTCCATTCCTGCTTTTGTCGATGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAGCGAATGTGTGCGACCACAATGTTCAGAACCACAAGGATTCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTAAAACAGGT 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspGlnGluCysValArgProIleCysGluAspValGluGlyGlyGlyAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isThrCysSerValAspAspGlyArgGlyGluThrSerPheLeuIleAsp
                   GAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATG
                                                   ysPheLeuLeuAsnAsnLeuGluTyrProThrAspLeuMetAlaGlyGln
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                              206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        695.00
4.064
86.364
                                                                                                                                                                                                                                                                                                                                                                                                                                              22602 MW;
                                                                                                                                                                                                                                                                                                                                  Length: 198
Gaps: 4
Percent Identity: 69.192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4DEE20D0 CRC32;
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                                                                                                                                                                                                                       771
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                 921
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alignment_scores:
Quality:
Ratio:
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US-09-323-427-1 x 096775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_invertebrate:096775
                                        Align seg 1/1 to: 096775
                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1213
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 CUT-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   096775;
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470 GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
                                                                                                                                                                                                                                                         "cut-1-like genes are present in the filarial nematodes Brugia pahangi and Brugia malayi and, as in other nematodes, code for components of the cuticle.";
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda;
Filarioidea; Onchocercidae; Br
                                                                                                                                                                                                                                                                                                                                                                                 Brugia malayi.
                                                                                                                                                                                                                                 EMBL; AJ012617; CAA10074.1;
                                                                                                                                                                                                                                          Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                    DEVANEY
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
LEWIS E.K., HUNTER S.J., TETLEY L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTG 1118
:::::::
pValArgAspGluAsnIleValAspValArgThrAspLeuAsnAlaLeuA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lePheValIleValSerValAlaThrIleValAlaIleThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACTTCTGCAACAT...AATGGACAACCTGTAATACTTGCTGCAGTACA 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaAlaAlaSerArgGlnAlaAlaAlaPheArgValLeuLysLysArgAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATC 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluAlaHisValTyrLysTyrAlaAspArgSerGlnLeuPheTyrGlnCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..TTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rGlnGlyIleCysMetSerIleThrGlyPheThrLeuAlaGlyMetLeuI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerLeuLeuAlaHisGluAsnGlyHisProValIleValAlaThrMetTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sGlnIleSerIleThrIleLysGluProAsnSerLysCysGlnArgProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spIleAsnGluGluPheThrSerLeuProAsnAlaLeuArgHisArgSer
                                                                                                                                                                                          127
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                          AΑ;
                                                                                                         662.00
5.296
98.425
                                                                                                                                                                                          \frac{127}{14119}
                                        from:
                                                                                                                                                                                          MW;
                                                                                                           Percent
                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                       a; Secernentea; Spiruria; Spirurida; Brugia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                          3F738071 CRC32;
                                        ţo:
                                                                                                         Identity:
                                        127
                                                                                                                                                                                                                                                                                                               PAVIA NUNES C.,
                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
                                                                                                            96
                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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520

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VallleSerPheHisProLeuSerValThrLysValAspArgAlaTyrAr AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG

17

US-09-323-427-1 x Q21808

17

gValGlnCysPheTyrMetGluAlaAspLysThrValSerThrGlnIleG

34

569

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alignment_block:
                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_invertebrate:Q21808
                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _documentation_block:
Q21808 PRELIMINARY;
                                                                                                                                                    WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VANGHAN K., WAPTERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q21808;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
                                                                                                             Nature 368:32-38(1994).
EMBL; Z49207; CAA89068.1;
SEQUENCE 290 AA; 33215
                                                                                                                                                                                                                                                                                                                                MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R07E3.3 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValCysArgTyrGluIleLeuAspGlyGlyProThrGlyGlnProIleGl
                                      Quality:
Ratio:
                         654.50
3.306
69.965
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                                                                                                             MW;
                      Length: 283
Gaps: 8
Percent Identity: 45.230
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Rhabditidae; Pelc
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                                                                                                               441587FE CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                               tea; Rhabditia; Rhabditida;
Peloderinae; Caenorhabditi
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Align seg 1/1
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                                                                                               GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 1143
                                                                                                                                                                                                                                                                                                                                                                                                                     CATTAAAGAACCAAATAGCGAA...TGTGTTCGACCACAATGTTCAGAAC 983
                                                                                                                                                                                                                                                           ThrAlaIleAlaAlaHisIleGluTyrGlu.AspSerGluIleIleSerA
snAlaPheLeuPheIleIleSerLeuValSerIleValHisValCys
                              GCCAGTTGATTTACGTC.....ACCGTGCACTTCTGC 1175
                                                                                                                                                           AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnPhe.....AspMetArgIleSer....
                                                                                                                                                                                           {\tt spTyrIleIleProAsnAspAspIleIleSerLeuAsnTrpLeuGlnArg}
                                                                                                                                                                                                                           AGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProThrMetHisSerLysGlnLeuAsnMetProValCysLysTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCC
                                                               ....GluLeuCysMetThrAlaIleGlyThrThrLeuLeuValPheLeuA 259
                                                                                                                                                                                                                                                                                                                           roProArgArgArgSerAsnThrLeuProAlaProAspAspAsnIle
                                                                                                                                                                                                                                                                                                                                                                                          rValLysGluProGlyLeuAspTyrCysAspValProSerCysProAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysTyrAlaAspArgAspAsnMetTyrPheAspCysGlnIleSerIleTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lnMetValTyrHisLysTrpThrCysAspThrGluHisGluAsnThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lLeuAspGlySerProThrGlyProProValTyrPheAlaThrValGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \verb|etGluMetGluArgArgIleGlnLysValIleGlnIleSerMetProPro|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerProArgGlyLeuPheLeuSerThrAsnValValValAlaPheAsnPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: Q21808
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6
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                                                                                                                               243
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seq_name: sp_invertebrate:Q21540

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I Sequence of the control of the con
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US-09-323-427-1 x Q21540
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01-NOV-1996 (TrEMBLrel. 01, La
01-NOV-1999 (TrEMBLrel. 12, La
M142.2 PROTEIN.
M142.2.
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Q21540 PRELIMIN
Q21540;
Q1-NOV-1996 (TrEMBLr
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BONFIELD J., BURTON J., CONNELL M., COPERY J., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea;
Eukaryota; Metazoa; Nematoda; Pelv
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EMBL; Z73428; CAA97806.1; -.
PFAM; PF00092; vwa; 1.
PRINTS; PR00453; VWFADOMAIN.
SEQUENCE 550 AA; 61445 MW;
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                                                                                                                         GTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGT
                                                                                                                                                                                         {\tt sTyrHisAspGluGluCysArgAlaGlyProGluLysPheProAspSerA}
                                                                                                                                                                                                                                                            TTATGATCAAGAAGGTTGCCGT.....AATGATGAAGGTGGAC
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ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT
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Last annotation updat
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seq_documentation_block:
ID Q19053 PRELIMINARY;
AC Q19053;
DT 01-NOV-1996 (TrEMBLrel. 01
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JAN-1999 (TrEMBLrel. 09
DE E04D5.3 PROTEIN.
GN E04D5.3 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemato
OC Rhabditina; Rhabditoidea;
RN [1]
                                                                                                                                                                                                                                              seq_name: sp_invertebrate:Q19053
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                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441
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                                                                                                                                                                                                                                                                                    520 alThrValLeuGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euAspAlaValLeuLeuSerThrProAspTyrAspThrSerLeuArgLeu
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                                                                                                                                                                                                                                                                                                                      TCAACACCCTTGAA 1120
                                                                                                                                                                                                                                                                                                                                                       lArgArgLeuAlaAspGlyValGlyThrIleAspValPheThrAspSerV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyAlaAspLysAspThrPheGlyMetLeuValHisSerCysTyrValAs
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                        Rhabditoidea;
                                                                                                                                                                                                                                                                                    524
                       Nematoda; Secernen
oidea; Rhabditidae;
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Last sequence update)
Last annotation updat
                                        Secernentea; Rhabditia; Rhabditida;
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                        Peloderinae;
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                          Caenorhabditis.
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alignment_scores:
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Percent Similarity:
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BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
CARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
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SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THLERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATENSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
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EMBL; Z66496; CAA91280.1;
SEOUJENCE 484 AA; 53325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1995)
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                                                                         TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT
                                                                                                                                                       luAla...GlyGlySerProIleLysTyrAlaArgIleGlyAspGlnVal
                                                                                                                                                                                                                                                                                                               uLeuGluSerGluThrGlnLeuProValCysArgTyrGluIleLeuAsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrLysLysValHisAsnHisValAspIleSerAlaLeuThrThrGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sThrArgAsnSerPheAsnGlyLysValPheValLysGlyTyrValSerG
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                                                                                                                                                                                                                                 GTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT
                                                                                                                                                                                                                                                                                                                                                                                         TCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 4
Percent Identity: 45.020
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alignment_block:
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Quality:
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ID Q93532 PRELIMINARY;
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                                               Align seg 1/1 to: Q93532
                                                                                US-09-323-427-1 x Q93532
                                                                                                                                   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                  WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTLMORE B., O'CALLAGHAN M.,
PARSONS J., PECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VANDERAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
BLEGGRIS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                    Nature 368:32-38(1994).
EMBL; 278542; CAB01742.1;
SEQUENCE 315 AA; 35785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-JAN-1999 (TrEMBLrel. 09,
                 158 TCTTCTGAAATGATGATTCGTCTTATTGCTTTC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Last sequence update)
Last annotation updat
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                                                                                   CTCACGTATACAAATATGCGGATCGA 901
                                                                                                                                                                                                                                     GGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATA 825
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                                                                                                                           rLeuIleAsnAsnLeuGluTyrSerSerAspLeuThrGlyGlyGlnLeuS
                                                                                                                                                                     GlyLysGluValGlnIlePheAspGluAsnGlyCysAlaValAspLysTy
                                                                                                                                                                                                                                                                                                                                                                                     yGlnIleValTyrHisGluTrpSerCysGluAlaProGlyGlnAsnGlnT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eIleThrLysIleAspLysSerTyrLysValGlnCysPheTyrAlaGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hr {\tt ValSerTyrSerAlaCysAspValIleArgGlnArgSerSerAsnPro}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysThrGlnGlyAlaPheGluGlyHisValTyrValLysGlyHisTyrSe
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                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGCCAGTTTATCATAAATGGACATGCGATTCT.....GAAACCG
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sp_invertebrate:Q22164
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alignment_block:
US-09-323-427-1 x Q22164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERT T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMOR B., O'CALLAGHAN M.,
PARSONS J., PECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLRE1. 01, 01-NOV-1996 (TREMBLRE1. 01, 01-JAN-1999 (TREMBLRE1. 09,
                                                                                                                 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
EMBL; Z66565; CAA91480.1; -.
SEQUENCE 384 AA; 43964 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                              364 TGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCA 413
                                                                                                                                                                                                                                                                                                                                                     279 TAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                229 TGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LeuValGluPheThrTyrPheValLeuGlyPheSerAlaAlaIleGlnAs
                                                                                                                                                                                                                                                                       AAAGGTCTTTATGATCAAGAAGGTTGCCGT......AATGA
                                                                                                                                                                                                                                                                                                                                                                                             pAspAsnGluLeuIleGlyGlnProGluIleGlnCysAsnAlaAspThrI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTATTGCTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGT
                                                                           snMetAspArgGlnArgMetIleAlaProGluGlyMetMetPheSerThr
ValLeuIleIleSerPheHisProLeuPheLeuThrArgMetAspLysAl
                  ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGC
                                                                                                                                                      pGlnPheGlyArgProValGlyGlyIleLySLeuAsnHisGlyAlaCysA
                                                                                                                 ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA 463
                                                                                                                                                                                                                                   LysGlySerTyrAsnArgProGluCysArgValAspTyrSerThrLysAs
                                                                                                                                                                                                                                                                                                              leAspMetGlnPheArgThrArgLysGlnPheAsnGlyLysValTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546.50
2.240
61.929
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Last sequence update)
Last annotation updat
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seq_name: sp_invertebrate:Q9XVN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 laIleAspValSerAsnLeuProThrGluSerValGlnSerAspLeuPro 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||:::::::|||:::||| ||||||| :::|||||:::|||
aTyrHisIleArgCysMetTyrLysGluAlaAlaArgThrValThrAlaA 143
                                                                                                                                                                                               alValValTyrHisArgTyrCysLysAsnGlu 375
                                                                                                                                                                                                                                                      TTACCATTTCGTTTAAATTTCGTCCAAATCAG 1321
                                                                                                                                                                                                                                                                                                             aValThrPhePheThrPheIlePheValLeuPheValThrThrIleLeuV 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAATACTT 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAAC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgPheGlnCysGluIleArgLeuCysLeuLysAsp...AspGlyGlyCy 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sThrAspArgLeuLeuGlyAspProThrTyrValGluAlaLeuAsnM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG
                                                                                                                                                                                                                                                                                                                                                                 CTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTA 1289
                                                                                                                                                                                                                                                                                                                                                                                                                        ...LeuAspProGlnThrIleCysLeuAlaProLysLeuLeuValValAl 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGCAGTACAAAATGGAATCTGCATGTCACCA......TTTGG 1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etAlaTyrArgGluSerPheValPheLysPheAlaAspArgIleAlaVal
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alignment_block:
US-09-323-427-1 x Q9XVN2
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COBSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMUBRAY A., MCRUMCRE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                          304 TGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTT
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                                                                                                                                                                                                                                                                                                                                254 GAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
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448 TATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 TCTTATT.....GCTTTCTGTACTACACTTATTGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "2.2 Mb of contiguous nucleotide sequence from chromosome
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 LeuArgPheGluSerValGlnPhe...LysAsnProProIleLeuLeuLe
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                                                                                                                                                                                                                                                                                                euSerThrSerCysPheGluIleGlnAsnGlyValValGlyLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uLeuIleTyrAsnArgIlePheLeuGlnSerIleThrIleLeuIleLeuL
                                        ProIleGlyAlaCysAsnMetArgArgGlnArgThrLeuHisProArgGl
                                                                                   CCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGG 447
                                                                                                                              ysValGlnHisSerAlaAspAlaHisSerSerProGlnGluPheThrIle 132
                                                                                                                                                                         GC.....CGTAATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCTTATTCG.....ATTCCGGTTGACAATGGTGTCGAAGGTGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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2.593
66.443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 35.906
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D793181D CRC32;
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Q23097 PRELIMINARY;
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RITKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THLERRY-MIEG J., THOMAS K., VAUGIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 94150718.
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EMBL; Z71267; CAA95850.1;
SEQUENCE 387 AA; 43212
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elegans.";
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aAspSerAsnGlnLeuTyrPheThrCysGlnIleArgLeuCysGlnLysG
                                 GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG
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                                                                                                WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTING B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER.E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
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01-FEB-1997 (TrEMBLrel. 02,
01-NOV-1998 (TrEMBLrel. 08,
01-JAN-1999 (TrEMBLrel. 09,
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                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                     LENNARD N
                                          SEQUENCE FROM N.A.
                                                                                 Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alIleArgArgGlnAsnHisLysLysGluLeuAspIleMetGlnSer 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCC 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuLeuSerGluAlaSerGlyAspGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..AlaProSerProPheCysValProArgLeuLeuLeuProValLeuPro 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGCATGTCACCATTTGGCTTCTCAATGTTTATG.....GGTTTAAGC 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACT 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ysArgGluAlaAspArgSerAspTyrGluIleAspValAlaThrSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ....TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lnMetGlyMetCysGlnGluValThrProProAsnCysGlyValLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACCAAAT.....AGCGAATGTGTTCGACCACAATGT......
(JUL-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuValLeuAspProAlaAspArgGlyLe 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....AsnArgThrL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323
                                                                                                                                                                                                                                                                                                           COULSON A.,
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alignment_block:
US-09-323-427-1 x Q93967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQ DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: Q93967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 281143; CAB03520.1; -
EMBL; 275713; CAB03520.1; -
EMBL; 275713; CAB00057.1; -
EMBL; 275713; CAB00057.1; -
EMBL; 281143; CAB00057.1; -
SEQUENCE 440 AA; 49299 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464
                                                                                                                                                                                                                                                                                                                                                                                          614 ATGCCAGTATGCCGTTATGAAATT.....TTGGA 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 TCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LeuLysIleLeuIleIleAlaTrpThrGlyTrpArgValAlaAsnAlaIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pValIleAspAspLysGlyCysProIleAspProIleLeuIleThrGlyI
                                                                                                          GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyMetLysSerLeuArgSerValAspProArgGlyMetTyrTyrGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
                                           AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATT
                                                                                   ValLeuIleAsnAsnCysTyrValThrAspGlyPheGlyLysLysAlaAs
                                                                                                                                                                       rgValLeuHisGlnTrpHisCysAsnAspGln......MetTyrGly
                                                                                                                                                                                                                    CAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC
                                                                                                                                                                                                                                                               pAlaGlyArgProAlaGlyAsnValIleGlnPheAlaArgValGlyGluA
                                                                                                                                                                                                                                                                                                    TGGTGGA...CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC
                                                                                                                                                                                                                                                                                                                                                 IleProGlyCysThrTyrSerIleHisArgSerThrIleAspGluLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                       luLeuGlyValSerMetIleProThrThrGluLeuGluAlaArgHisGly 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aTyrHisValLysCysPhePheGluGluAlaAsnLysGlyLeuThrAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yAsnGlnLysThrArgLysProHisPheAspLeuGlnPheGlyAlaCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGTCAAGTTGCC......GGAATTTCACTTCCATTTGATTCATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrAlaLysGlyArgAlaGluLeuGluAspCysTyrLysAspAspPheGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spGluIleArgIleTrpValLysThrArgLysIlePheAlaGlyArgIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477.50
2.296
65.000
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MW; 3F2BBBA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 33.438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
to:
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  234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  613
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319

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407

73

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369

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alignment_block:
US-09-323-427-1 x Q22680
                                                                                                                                                                                            alignment_scores:
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                                      Align seg 1/1
                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       documentation_block:
Q22680 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1069 TGCAGAACCG 1078
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                                                                                                                                                                                                                                                     EMBL; Z49071; CAA88879.1; -. HSSP; P03000; ITIF. SEQUENCE 609 AA; 68882 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T22C8.7 PROTEIN.
T22C8.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
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                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                     elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
169 GATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATT
                                                                                                                                                                                                                                                                                                                                                 "2.2 Mb of contiguous nucleotide sequence from chromosome III of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sMetLysLys...HisGlyMetCysAspGlyIleThrProProSerCysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lySerMetSerArgValIleSerValGlyGlyGluAspAsnGlyGlyPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysPheAlaAspLysProGlyValTrpPhePheCysGlnValGlnMetCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leArgTyrSerSerAspLeuGlnArgAlaTyrAlaGluSerSerValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAATATCCAACAGATTTAATG...GCTGGCCAAGAAGCTCACGTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATC 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCC 1018
                                                                                                                                                                            Quality:
                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (APR-1995)
                                        to:
                                        022680
                                                                                                                                      453.50
2.399
65.854
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                                      from: 1
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                                                                                                                       Length: 287
Gaps: 11
Percent Identity: 37.282
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218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654 CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 rAspValThrValIleIleGlnHisHisProLeuPheValThrSerPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 CCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 CGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ysThrArgLeuThrAsnArgProIleValMetAspLeuProPheArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt sValTyrValArgGlyPhePheProGlnThrValCysHisLeuAsnTyrC}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTCAAACTCA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGT
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AspAsnSerAsnTyrAsnPhe...TyrTyrThrHis........ee
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                                               snGlyCysGluGlyIleSerProProIleCysArgProMetAspLeuGly
                                                                                         ATAGC...GAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGA
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                                                                                                                                                                                                                                   AspLeuLysSerAlaPheThrAlaValArgAlaPheArgTyrAlaAspGl
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No

Score

Query Match

Length

DB

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Description

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RESULT 1
CEF22B5/c
LOCUS
DEFINITION
ACCESSION

VERSION KEYWORDS

CEF22B5 25823 bp DNA INV 02-SEP-1999 Caenorhabditis elegans cosmid F22B5, complete sequence. 250044 250044.1 GI:899234 E750044.1 GI:890254 E750044.1 GI:890254 E750044 E75004 E75004

ALIGNMENTS

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Query Match
Best Local Sir
Matches 633;
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Wilson, R., Alnscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditina; Rhabditoidea; Rhabditidae; Pelo (bases 1 to 34831)
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IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small content of the specified clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone C47G2.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neighbouring submissions.

The true left end of clone C47G2 is at 1 in this sequence. The true right end of clone C47G2 is at 6388 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bin/display?db=wormace&class=Sequence &object=C47G2
Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence Z49912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 34831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end of this sequence (34731. .34831) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from this gene; cDNA EST EMBL:C12078 comes from this gene; cDNA EST yk262c12.3 comes from this gene; cDNA EST yk262c12.5 comes from this gene; cDNA EST yk265h3.5 comes from this gene; cDNA EST yk278g8.3 comes from this gene; cDNA EST yk278g8.5 comes from this gene; cDNA EST yk278g8.5 comes from this gene; cDNA EST yk439e8.3 comes from this gene; cDNA EST yk439e8.5 comes from this gene; cDNA EST yk380a11.3 comes from this gene; cDNA EST yk380a11.3 comes from this gene; cDNA EST yk580a11.3 comes from this gene; cDNA EST yk580a11.3 comes from this gene; cDNA EST yk580a11.5 comes from this gene; cDNA EST yk580a11.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2562. .4878
/gene="cut-1"
join(2562. .26
                                                                                                                                                                       GPSGQPIQFATIGQQVYHKWTCDSETTDTFCAVVHSCTVDDGNGDTVQILNEEGCALD
KFLLNNLEYPTDLMAGQEAHVKYADRSQLFYQCQISITIKDPGSECARPTCSEPQGF
GAVKQAGAGGAHAAAAPQAGVEEVQAAPVAAAAPVAAAAAAAPAVPRATLAQLRL
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/translation="MTWKPIICLAALVLSASAIPVDNNVEGEPEVECGPNSITVNFNT
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RNPFEGHYVVGGLYDQAGCRSDEGGROVAGIELPEDSCUTARTRELNPKGVFVSTTVLV
RSFEDSCHYVGGVVFNFVCKYEILDG
ISFHPQFVTKVDRAYRIQCFYMESDKTVSTQIEVSDTVAFAGTQVVPMVATVLKTEGCALD
                                                                      IGFASFLGIGTIVATALSATIFYVARPTSHKH" 15433. .17108
                                                                                                                                         LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGICLTP
                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA88934.1"
/db_xref="GI:3875030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Join(2562. .2679,2992. .3217,3898. .4636,4687. .4878)
∕gene="cut-1"
                                 /gene="C47G2.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to cuticulin; cDNA EST EMBL:C10444 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="C47G2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Caenorhabditis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       start=1
.15770,16205.
.16531,16772.
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for a small
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/note="similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D36149 comes from this gene; cDNA EST EMBL:D36131 comes from this gene; cDNA EST SWBL:C11361 comes from this gene; cDNA EST SWBL:C13631 comes from this gene; cDNA EST Yk358b10.3 comes from this gene; cDNA EST Yk30164.3 comes from this gene; cDNA EST Yk30164.5 comes from this gene; cDNA EST Yk30164.3 comes from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="C47G2.2"
/note="similar to fork head domain protein; cDNA EST /note="similar to fork head domain protein; cDNA EST EMBL:D70725 comes from this gene; cDNA EST EMBL:D6805 comes from this gene; cDNA EST yk288f8.3 comes from this gene; cDNA EST yk288f8.5 comes from this gene; cDNA EST yk474g11.5 comes from this gene; cDNA EST yk670a12.3 comes from this gene; cDNA EST yk670a12.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: Cl3621 comes from this gene; cDNA EST yk27d8.5 comes from this gene; cDNA EST yk25/e7.5 comes from this gene; cDNA EST yk319c4.5 comes from this gene; cDNA EST yk319c4.5 comes from this gene; cDNA EST yk35bl2.5 comes from this gene; cDNA EST yk3675.5 comes from this gene; cDNA EST yk486d7.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIEKLASEKSEAEENVKDIYKKVRVLFNSMKNDSNGQRRKVRTILSKFSDDVIDNLFF
SRQVIDNAHLDESGPCSEAKLISLHKKTIYAVQTLNNATAGNVLVDRALFLENLAFS
ESNGYNLLESRNTCVPIGVRREWYTRALOFPSGRILGIYTVFMTFEVLFSECTFFVVS'
TLSPAAFVTEYASTRFHYKYTQFVAFGIIVYLITSAVFTIFRLQIYKYYHLDPNGHTD
ENSILFSAILLCRTFPICLNFLGMIHNDSHISMAKSFGIETYKLMGHLDVIFILA
KGINYLFICIILLCAIHYYRYGGYVLHNIGFDQFVEADMININGRSLVQIERN
SIKRSNDRSQRTQNWTNSFGSSNAGNGSTTSKFKRSNKNDEERPMLEDDDEEVEESST
                                                                                               PMLLNLDDSLDHNVEARPEQEPEPDLNIVHSPNEMEQPNQEDLEHEGMKFEEQSGSRR
IAQESASEAVTDGRSSDEDSHTARRSLCYHRSRKSMPAKKLSKMFTSIFQMFWAKEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="cDNA EST CEMSB75F comes from this gene; cDNA EST EMBL:C13621 comes from this gene; cDNA EST yk227d8.5 co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(30076. .30134,30184. .30492,31050. .31274,31321. .3
31534. .31653,31701. .31835,31889. .32104,32160. .32570,
32639. .32935,32998. .33215,33263. .33651,33802. .34049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30076. .34049
/gene="C47G2.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLIIVFVLPLDVAITEFHKCENDRQRILNTTTSTPAPVVPECELPGGYVPDDVLFNLW
RVVYWSAQLLTWLILPLLQSYVTAGNETILGKIRAAVINNALYYAIYSLCELAILIYA
MFKGVSINIENLKVIVVSASNTWGLFLLVVLLGHGLVELPRSLWHHGNRHYRLRKTYF
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25668. .25907,25967. .26054,26106. .26227,26277. .26608,
26681. .26785,26846. .26914))
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MPAFFIPQNIDSQKLLSMMASRIMPMDAPVSSGQKRTSSSSSPNENGSSAVSDKLSA"
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/db_xref="GI:3875033"
/db_xref="SPTREMBL;018696"
/translation="MWAEGKRRNNRKKSRRDREGTSASSDAYSSDSDAEDDITQDDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RISMMSPTEHPSSSGFFDDM"
TDLPMKQQYRLSFIASEILTIRGTDVFQKQIVTTEETRKCLVDFLNDKTPLNHLVAGF
                                                     ENSLMRLLKTONFTLEDVLLNEFVVQESRYGKAELVQYITSRENMKALLELSLNPKIN
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FEYYKEKFPAWQNSIRHNLSLNDCFVKVARGPGNPGKGNYWALDPNCEDMFDNGSFLR
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/translation="MLFSMESILSSTKPKLEPPPKLEPEVTINEQVVDLPRSNTRLSE
PSTSASVLEHDLKFGESRKRSRSLGDEPTEDEDGVPVRKANKRNHSTSSAADSSSDDA
                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="C47G2
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/translation="MGTISLAVQLFIVFLLTSYLLNKYSTIRKQNPIVTISTFIGWYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=
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BASE CO

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SOURCE
ORGANISM
                                                                                                                                                                                               DEFINITION
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Best Local Similarity 74.2
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ttcagaaccacaaggattcggagctgttaaaaacaggtggtgccgcagcaaaacctgctgc 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcaatgccagatcagtattaccattaaagaaccaaatagcgaatgtgttcgaccacaatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAACGAAGAAGGATGTGCTCTTGACAAGTTCTTGCTCAATAACTTGGAGTACCCAACTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaatgctgatggatgtgctcttgataaatatttgctaaataatttggaatatccaacaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCATCGGACAACAAGTCTATCACAAATGGACTTGCGATTCTGAGACCACTGACACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tatcattggtcagccagtttatcataaatggacatgcgattctgaaaccgttgatacttt 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCCACAGATCGAAGTCTCGGATCTCACCACTGCCTTCCAGACCCAGGTCGTACCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tagtgcacagattgaggtatctgaaatcacaactgcttttcaaaactcaaattgtcccgat 615
                                                                                                                                                                                                                                                                                                                                  CGCTGCTCCAC 4433
                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAGAGCCACAAGGATTCGGAGCCGTCAAACAAGCTGGTGCCGGAGGAGCTCATGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAGTCTGCAAATACGAGATCCTTGACGGAGGACCATCCGGACAACCAATCCAGTTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAATGCCAAATCTCCATCACCATCAAGGACCCAGGAAGCGAATGTGCCCGTCCAACTTG
                                                                             cuticle protein; cuticlin C.elegans DNA. Caenorhabditis elegans
                                                                                                                                                                         CELCUT1 2310 b
C.elegans cuticlin
M55997
1 (bases 1 to 2310)
Sebastano, M., Lassan
                                         Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                      M55997.1 GI:156271
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MDETLIAKIADNLIVEBGCPAEELVKKSALISASAKILEAFIKTNEVSNAPAQQLEEI
ERNLIEERHYSYGLMRPCMDNDPYEHSYQPDPERIVGGILANRLPNILQTVLRDIEAN
GSVWQPLLRLIIELCNTWCMSTHEKIAVAFRSLPFINLIKAAKMLPRASVLHCLLVKV
VILLHSSFPCDELSPAAEYLTEEGGLIQNIYDTATSPNPGSSVACSGLRSFNQNLGD
AINRAKKAGIPNQKLLAILSADNTWTELEDIILYNLKHRQMQHBFNDSSVVSSIRN
DSHGFNDSEEMTDASTKFAEMDATSSAKQAFSGFSSPFEDNWQRRSDFEQDETPDE
DEFRKLCSERANSSSCAGISFETSPIKWPGEAEKTSEKASEPPSVVASTYPQQTNGNQ
AFLEQGEGDGEWWPTVPPLGFTEVVTQTGHRPENNWVDETAPDFSHLDMAPPKEDDM
WADPSSFPTISPTAAANSASSSSSDAWPGSDIHLQGEASDWPLNNSHESKASDPVMVG
LAASISHBGDSSEA*
B 6786 c 6432 g 11024 t
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  Lassandro, F.
                                                                                                                                                                                           n bp
                                                                                                                                                                                               (cut-1)
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Pred. No. 2.1e-46;
0; Mismatches 142;
  and
                                                                                                                                                                                             gene,
                                                                                                                                                                                               ń
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                                                                                                                                                                                                                                                                                                                                                                                                                    4422
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ACCESSION VERSION

KEYWORDS

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Best Local Similarity
Matches 393; Conser
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                                                                                                                                                     caatgcttttacatggaagctgataaaacagttagtgcacagattgaggtatctgaaatc 583
                                                                                         tggacatgcgattctgaaaccgttgatactttctgcgcgggttgtccattcctgctttgtc
                                                                                                                                                                                                                                                                                              99t99accaacc99tcaacca9ttcaatttgctatcattg9tcagccagtttatcataaa
                                                                                                                                                                                                                                                                                                                                                                                                       gaaccaaatagcgaatgtgttcgaccacaatgttcagaaccacaaggattcggagctgtt
                                                TGGACTTGCGATTCTGAGACCACTGACACCTTCTGCGCCGTCGTTCACTCTTGCACTGTC
                                                                                                                                                                                                                                                                              GGAGGACCATCCGGACAACCAATCCAGTTCGCCACCATCGGACAACAAGTCTATCACAAA
                                                                                                                                                                                                                                                                                                                                           ACCACTGCCTTCCAGACCCAGGTCGTACCAATGCCAGTCTGCAAATACGAGATCCTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUT-1 a Caenorhabditis elegans gene coding noncollagenous component of the cuticle Dev. Biol. 146, 519-530 (1991)
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/protein_id="AAA27995.1"
/protein_id="AAA27995.1"
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GPSGQPIQFXTIGQQVYHKMTCDSETDTFCAVVHSCTVDDGNGDTYQILNEBGCAL
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EGAVKQAGAGGAHAAAAPQAGVEEVQAAPVGAAPVAAPAVAAAAAPAVPRATLAQLLL
LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGISSTP
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567 c 433 g
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join(1186. .1920,1971.
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/product="cuticlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 315; DB 34;
Pred. No. 9.1e-45;
0; Mismatches 130
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TITLE
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    1017
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                                                                                GATCACAACTTTTTTATCAATGTCAAATTAGCATAACAATTAAGGAACCAAATAGTAAAAT 240
ccgcagcaaaacctgctgcagctgcgcaacttcgtttactcaagaaaagatctgcagaac 1076
                                                                                                                                    TAGAATATCCAACAGATTTAATGGCTGGACAAGAAGCACGCTATACAAATACGCTGATC 180
                                           gtgttcgaccacaatgttcagaaccacaaggattcggagctgttaaaaccagg---tggtg 1016
                                                                                             gatcacagcttttctatcaatgccagatcagtattaccattaaagaaccaaatagcgaat 959
                                                                                                                                                   tggaatatccaacagatttaatggctggccaagaagctcacgtatacaaatatgcggatc 899
                                                                                                                                                                                       ATAAAGTAGAGCTATTAAATGCTGATGGTTGTGCTTTGGACAAATTTCTACTTAATAATT 120
                                                                                                                                                                                                     atactgtggaaattctaaatgctgatggatgtgctcttgataaatattttgctaaataatt 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACAAGCTGGTGCCGGAGGAGCTCATGCCGCCGCTGCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (03-FEB-1999) Research & Training Center on Diseases, Ain Shams University, Abassia Square, Cairo,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Filarioidea; Onchocercidae; W
1 (bases 1 to 724)
Ramzy,R., Helmy,H., Adely,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wuchereria bancrofti
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
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Wuchereria bancrofti
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Ramzy,R., Helmy,H., Adely,M., Curtis,K. and
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AF125580.1
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                                                                                                                                                                                                                                                                                                                                                                          /product="cuticulin-1"
/proteth_id="AAD28743.1"
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ASRQAAAFRVLKKRDVRDENIVDVRTDLNALDINEEFTSLPNALRHRSSLLAHENGHP
VIVATMYGGICMSITGFTLAGKLIFVIVSVATIVAITLLRSHSTKV"

112 c 128 g 236 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Wuchereria bancrofti"
/db_xref="taxon:6293"
/dev_stage="L3 larvae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to Ascaris lumbricoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           country="Egypt: Nile Delta"
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                                                                                                                                                                                                                                                                                               Score 263.4; DB 3
Pred. No. 6.4e-36;
0; Mismatches 261
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ulin-1 cDNA partial
                                                                                                                                                                                                                                                                                               261;
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sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 5792)
Timinouni,M. and Bazzicalupo,P.
cut-1-like genes of Ascaris lumbricoides
Gene 193 (1), 81-87 (1997)
97390131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U73005
U73005.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 5792)
Timinouni, M. and Bazzicalupo, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ascaris lumbricoides
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALU73005 5792 bp DNA
Ascaris lumbricoides CUT-1-like cuticlin
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                                                                                                                                                                                                                                                                                                                                          766.
                                      /gene="ascut-1"
/note="cuticlin gene; ASCUT-1;
proteins of other nematodes"
                                                                                                                                                                                                                                         /product="CUT-1-like 766. .5081
                                                                                                                                                                                                    /gene="ascut-1"
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                      /codon_start=1
                                                                                                  )óin(882. .954,2851.
                                                                                                                    /gene="ascut-1"
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Meloidogyne artiellia.
Meloidogyne artiellia
Eukaryota; Metazoa; Nematoda; Secernentea; Diplogasteria;
Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae;
Meloidogyninae; Meloidogyne.
                                                                                      MAMTCUT1 2584 bp DNA
M.artiellia Mtcut-1 gene.
X96677
X96677.1 GI:2648040
Cuticle protein; cuticlin 1; Mtcut-1
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/gene="ascut-1"
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PFEGHAYVKGLYDQEGCRSDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTITVVIS
FHPLFITKVDRAYRVQCFYMEADKTVSTQIEVSEITPAFQTGTYMPVCRYEILDGGP
TGQPTQFATIGQQVYHKWTCDSETVDTFCAVVESTVDDGSGDTIQILNEEGGALDKY
LLNNLEYPTDLMAGQLEHVYKYADRSQLFYQCQITITIKEDNSECPROTCSEPQGFGA
VRPGGSIAPKKQRCQLRLIKKSGGDYDNTLDVRTDFSALDISDRDEALPMDLRHRAR
HARGQQVILSPANEGICMSPFGFSIFMGLAVALAAAVVVVVSKKLRPQQKA"
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4694. .5081
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/db_xref="GI:1657625"
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                 ttatgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcact 396
                                                                                             aataacaatcaattttaatacacgtaatgcattcgaaggacatgtttatgtgaaaggtct 336
                                                                                                                                                    TGCAATTCCAGTGGACAACGGTGTGGAAGGCGAGCCAGAGATTGAATGTGGCCCAACCTC 588
                                                                                                                                                                      ttcgattccggttgacaatggtgtcgaaggtgagccagaaattgaatgtggaccaacttc 276
CTTTGACCAGGCCGGATGCCGTTCGGATGAGCACGGCCGACAAGTGGCGGGAATTGAGCT
                                                                           AATCACCGTCAATTTCAACACACGCAACCCTTTCGAGGGGCACGTCTATGTGAAAGGCCT 648
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De Glorgi,C.
Direct Submission
Submitted (15-MAR-1996) C. I
Biologia Molecolare, Via Ora
2 (bases 1 to 2584)
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Modulation of expression at the level of splicing of cut-1 RNA in
the infective second-stage juvenile of the plant parasitic nematode
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/codon_start=1
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/db_xref="SPTREMBL:018479"
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/gene="Mtcut-1"
/number=3
2518. .2523
a 639 c 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Translation="MRKILFAIGVFVALNAIFTVRAIPVDNGVEGEPEIECGPTSITV
NFNTRNPFEGHVYVKGLFDQAGCRSDEHGRQVAGIELPFDSCNVARTDAEPKGVFVST
TVVISFHPQFVTKVDRAYRVQCFYMEADKTVSAQLEVSEITTOFOTQVVPMPVCXYEI
LEGAALGQPIQFATIAQQVYTSGTCDSETIDTFCAVVHSCVVDDGNGDTVQILNEGSC
ALDKFLLNNLEYPTDLTAGQEAHVXLVADRSQLFYQCQISITIKEPHSECARPKCAESC
ALDKFLLNNLEYPTDLTAGQEAHVXLVADRSQLFYQCQISITIKEPHSECARPKCAESC
ALDKFLLNNLEYPTDLTAGQEAHVXLVADRSQLFYQCQISITIKEPHSECARPKCAESC
SGFNAVKVGAGGAGAFPPAAAAATPPPAAAAPPAPIAPAIPARVQRLRTRQLRLLRK
RRAAPGEQVLDVRTEFNALDISDKPFNLPAHIRHHHLMENLSAEPQRRFIYQGGQQV
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1736. .1824
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join(<467. .943,1139.
jene="Mtcut-1"
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/clone="puc(3000)"
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/db_xref="taxon:42426"
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Pred. No. 4.1e-28;
0; Mismatches 243
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                               BMA012617 637 bp
Brugia malayi cut-1 gen
AJ012617
AJ012617.1 GI:3858954
cut-1 gene; cuticlin.
Brugia malayi.
Brugia malayi
Eukaryota; Metazoa; Nematoda; Secernentea;
Filarioidea; Onchocercidae; Brugia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-NOV-1998) University of Glasgow, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Lewis, E., Hunter, S.J.,
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/number=1
266 .484
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/number=2
136 c 1
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/db_xref="GI:388955"
/db_xref="SPTREMBL:096775"
/db_xref="SPTREMBL:096775"
/translation="VISPHPLSVTKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFQT
QIVPMPVCRYEILDGGPTGQPIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGN
QDTVEILSADGCALDKYLLNNLEYP"
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join(<2. .164,266.
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/db_xref="taxon:6279"
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/product="cuticlin"
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Pred. No. 1.6e-23;
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d, Glasgow,
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G61 1QH, UK
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pahangi and Brugia malayi, and, as in other nematodes,
components of the cuticle
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-NOV-1998) Devaney E., Veterinary Parasitology, University of Glasgow, Bearsden Road, Glasgow, G61 1QH, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cut-1 gene; cuticlin.
Brugia pahangi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brugia pahangi cut-1 go
AJ012618
AJ012618.1 GI:3858956
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1 (bases 1 to 358)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda;
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                                                                                                      /gene="cut-1"
/number=2
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350. .356
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                                                                                                                                                                                                                          /protein_id="CAA10075.1"
/db_xref="GI:3970656"
                                                                                                                                                                                                                                                                      join(<1. .191,350. .>356)
/gene="cut-1"
                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                           /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                              /gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                           organism="Brugia pahangi"/db_xref="taxon:6280"
                                                                                                                                                                                                   translation="PIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVE?"
                                                                                                                                                                                                              'db_xref="SPTREMBL:096776"
                                                                                                                                                                                                                                                                                            'gene="cut-1"
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                                               8.8%;
87.7%;
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                                              Score 156.6; DB 3 Pred. No. 1.1e-17;
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                                                          DB 34; Length 358;
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GAATATCCAACAGGT 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     actgtggaaattctaaatgctgatggatgtgctcttgataaatatttgctaaataatttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAATTCAATTTGCTACCATTGGCCAACCAGTTTATCACAAATGGACCTGTGATTCCGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Wateon, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-007-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                       sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone F53F1. The true right end of clone M04G12 is at 21759 in this sequence. The start of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bin/display?db=wormace&class=Sequence &object=F53F1
Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                sequence (1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burton, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 39478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 39478)
                                                                     uence (1..101) overlaps with the end of sequence 281103. end of this sequence (39379..39478) overlaps with the start of
                                              AL021448
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:1627965
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/db_xref="taxon:6239" /chromosome="V"

/organism="Caenorhabditis elegans"

gene

'db_xref="GI:3877457"

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gene
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                                                                               /note="predicted using Genefinder; similar to cuticlin; /note="predicted using Genefinder; similar to cuticlin; cDNA EST EMBL:D747918 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C12451 comes from this gene; cDNA EST EMBL:C10683.3 comes from this gene; cDNA EST yK306b3.3 comes from this gene; cDNA EST yK311h10.3 comes from this gene; cDNA EST yK311h10.3 comes from this gene; cDNA EST yK311h10.3 comes from this gene; cDNA EST yK311h10.5 comes from this gene; cDNA EST yK341f6.5 comes from this gene; cDNA EST yK300g2.3 comes from this gene; cDNA EST yK300g2.3 comes from this gene; cDNA EST yK30193.3 comes from this gene; cDNA EST yK30193.3 comes from this gene; cDNA EST yK30193.3 comes from this gene; cDNA EST yK19109.3 comes from this gene; cDNA EST yK19109.5 comes from
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ANNISVDEISTISYNVNLTMPTCTYQILSGGPFGEPVEFGLIGQQVYHQWKCDNDKGM
IILIKEDSFCMYVHTCSYDDGROETSFLIDSNGCSIDKFLLSNLEYPGNLLAGQEAHV
YKFADRDALFFQCQISITVKEPDQGECVRPICEDVEGGGAPVVGPPPYGMISKNLVNIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVYNNEKEIGDALEILLPKHNLKREDIFITTKMHPNTVENVKKLVDESLSLLKTSYID
MYLIHYPKSFDYGDQDPMNKTLRIATWNDLWECKNAGKIRSVGVSSFEIRHLEELKDL
GKNFPPCCNQVEYHPHFTREELKNYCKSEGIFFQAFSSLARHNETLLSSEIITRLAEK
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19919. .20008,20072. .20251)
/gene="F53F1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(14923. .15347,15663.
16033. .16271,16318. .16486))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB03128.1"
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QSLTALDRGQHYIRCTGWLVK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKNSFLTFFKSPYMYVVGITNYHNKAIQKL"
/protein_id="CAB03125.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(21582..21670,21781..22009)
/gene="F53F1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F53F1.4"
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/gene="F53F1.2"
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                                                     codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F53F1.1
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MEDLINE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGCTCTTTTCTTCCAGTGTCAGATATCAATTACCGTCAAAGAGCCAGGACCAGGAATGCG 15111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson, R., Alscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Sultane, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulton, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P.
                                               IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small
                                                                                                                       bin/display?db=wormace&class=Sequence &object=E04D5
Current sequence finishing criteria for the C. elegans genome
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-OCT-1995) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
                                                                                                                                                                                                                                                                                                                                                                         predictions from Genefinder (P. Green, U. Washington), and other available information.
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                                                                                                                                                                                                                                                                                                                                             graphical representation of this sequence and its analysis
between neighbouring submissions. NT: This sequence is not the entir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:1041307
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0; Mismatches 106;
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  the entire insert of
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clone E04D5
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sequence Z48585.

The true left end of clone ZK673 is at 31437 in this sequence. The true right end of clone T09F3 is at 11412 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence
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The true left end of clone E04D5 is right end of clone E04D5 is at 2110
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                                                                                               / OCCUPATION OF THE CAMPIZTY OF THE CONTROL OF THE CONTROL OF THE CAMPIZTY OF 
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complement(8619. .11718)
/gene="E04D5.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone="E04D5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at 1 in
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complement(join(8619: .8761,8813. .8988,9895. .10028,
10089. .10283,10330. .10614,10730. .10935,11582. .11629,
11691. .11718))

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       646 tggaccaaccggtcaaccagttcaatttgctatcattggtcagccagtttatcataaatg 705
                                                                                                                                                                                                                                                                                              | tgatggtaacggtgatactgtggaaattctaa---atgctgatggatgtgctcttgataa 822
agaaccaaatagcgaatgt 961
                                                      CTTCAAATTTGCTGACAAAGCTGGGCTTTATTTCAATTGTCAAATTCAATTAACAATCAA
                                                                                                    atacaaatatgcggatcgatcacagcttttctatcaatgccagatcagtattaccattaa 942
                                                                                                                                                                                       GACTTGCGTTGCTGAACTTGAGAATGTGTACTGTATGAAAGTTCACTCATGTACGGTTTA 27902
                                                                                                                                                                                                                                                                                                                                                                                                                   gacatgcgattctgaaaccgttgatactttctgcgcggttgtccattcctgctttgtcga 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAAGCCGGTGGATCACCTATTAAGTACGCTCGAATCGGAGATCAAGTCTATCACAAATG 27842
                                                                                                                                                                                                                                                                 TGATGGACAAGGTGGACCACCAGTAACTGTCATTGATGCCAATGGATGTTCTGTAGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mpsrlamkelkgggepevvcetasisllfktrnsfngkvfvkgy vsepscmtvgdoktghrevrhdscgvrqprelngvvlsatvlisfhsifitkldray rvscfscmtvgdoktghrevrhdscgvrqprelngvvlsatvlisfhsifitkldray rvscffvegtkkvhnhvdisalttqllesetghpvcrteilneagsplikkarigdqv yhkwtcyhkchysctvpdgogppvtvidangcsvdgvlchokctspldta gklapvfkfadkaglyfncqiqltikdvnygcsntqpqcptsqyvvepaqkttetaep fydshesgyptradaypvsskappppgadldngveppppp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:Q19054"
/translation="MMSINLTVHIILLVTFSVSHVVTTAVTKATGETTVRGAGQDLGD
/translation="MMSINLTVHIILLVTFSVSHVVTTAVTKATGETTVRGAGQDLGD
VSSSFFYETTTASTCADDPNTDCTQYTFLCSNAKYTPLLQQFCAKTCGFCGSGSTAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VACVDTSTQ"
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VTVGD I DLPERG I LVFGLEEMEDGET I NAGDHGAT RALREARNSQEKTCFSTSRMYFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="Wegenleyadihstipfkceklkirvflsenackhlegeflkyp
Infollmavperslpssiflatlatchmliclfytllegvdag (myrknytleflyhr
Yivpyefiakvvopaipfillitterkydmitcherkregitfcyvltlslsefkapsa
Energrivtviffvcffsvairipvlyamkvktffplcddyfrsesldgtpfaateayei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA91281.1"
/db_xref="GI:3875453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LILLCLLFATTVVVFIVIVQKQRQILAQTAFFKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA91280.1"
/db_xref="GI:3875452"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="E0D5.3"
join(25834. .28873,27277. .27512,27582. .27721,27768. .28110,
28158. .28410,28491. .28811,29092. .29213)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDFHVITAIQMMFPFVVLLLLNLTIIKRLVAEKRENMYPILRGAGTTTEVKKASFVQG
NLPENYVLLQVAADVIKESLIHRSSRSKRSQLRNAIYTMLAIVTSYLVCNGVHLFLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA91282.1"
/db_xref="GI:3875454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="E04D5.4".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="E04D5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKREKSIETNSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="SPTREMBL:Q19053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="similar to cuticlin like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="E04D5.4"
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Pred. No. 1
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MEDLINE
REFERENCE
                                                                                                                                                          FEATURES
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AUTHORS
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
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BASE COUNT ORIGIN

Matches

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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small content of the specific or some content of the sequence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactor Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Eukaryota; Metazoa; Nematoda; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F53B6.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu computer analysis, Coding sequences below are predicted from computer analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A., Fulton,L., Gardner,A., Green,P., Hawkins,T., Hiller,L., Jier,M., Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N., Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B., O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A., Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        start of this sequence (1. .105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence Z81523.

The true left end of clone F32H2 is at 32306 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neighbouring submissions.
The true left end of clone F53B6 is right end of clone F53B6 is at 5116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chron
                                                                                                                                                                                                                                                                                                                                                                         sequence Z81523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368 (6466), 32-38 (1994)
94150718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; Cuticulin; Human platelet tetraspan antigen like; Initiation factor associated protein; Thrombospondin like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans cosmid F53B6, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z81086.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                 end of this sequence (32306. .32412) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 32412)
/chromosome="I"
/clone="F53B6"
                                                                                                                                  /db_xref="taxon:6239"
                                                                                                                                                                                    /organism≖"Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:1627952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at 1 in this sequence. The true in
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CDS

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complement(join(4270. .4339,4493. .4547,5071. .5295,
5368. .5662,5891. .6148.6204. .6752_6818. .7287,7546. .7676,
8104. .8184,12576. .12775,13246. .13384,13931. .14132,
14183. .14294,14341. .14457,14994. .15155,15198. .15311))
//gene="F5386.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKFIWKVSEEYTACASNODDIVDWSGAGRSIASTSQPIVYCVNAITGRVVPEKLCADK
LRPKVEBARPCPHLICPSRWMAADWTECVPHCGEGTKREEVYCVGAHNVTVHYPDTFC
ENGTRPAAEENCVSTSCGRWEAAKWSKCTASCGQVRRHVACVGGSDCDEGGRPRQE
TTCYAGIPCSLATNSLDWDRAYLDGNTFGSBUDHNDWQAPRLVAGEBSTCSSTCGTG
VMSRTVECVAVNPISSAPIKLEMSECQDQEQPKLFESCEVRSCPLQEDSKLSEDEAPY
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RRPDVECDANTKPQTVEVCSFGSCSRPELLSNRVFEQNAEQKKLTLGTGGVATLYQGT
RRPDVECDANTKPGTVEVCSFGSCSRPELLSNRVFEQNAEQKKLTLGTGGVATLYQGT
RRPDVECDANTKPGTVEVCSFGSCSRPELLSNRVFEQNAEQKKLTLGTGGVATLYQGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQGNVTLNFKYRDFPASRVDLAPKPQIPSTKNRQRVQVSKEDVLREQASVLHKMNVSL
IEALLTAPNDEKAREQLRKYGNELVARRDIGHWSECRQKTCHVAGYQARGISCKVTFH
GEIRNVDNSICESLASVRPPETRPCHREDCPRWEASQMESSQRCVSSNCVSSMLOTT
TCRFTMGTSVDIGHCDITNRPATTMDCPNQNCKAEWRTSDWGSCSSECTGGYQLRLL
SCVWISSGRPAGRNCEQMRRPHSARACVADEPLPPCMPTASALYQRDASCQDQSRFCD
IIKLFHSCDSLEVRQKCCSTCTFVERKKF"
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GANFLWRYDDGTPCQAATSRAVCSKGSCQIVGCDGLISSSFRFDACGVCGGRGDTCDN
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/gene="F53B6.2"
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SKWYMHQRAPKLLIPESCCIPSEIERCRSNPFDQDAPPPYYTSTCYEPLQNDLLHVMN
VASWLCITNAIVQVIFVSLKTIKLLNFILLKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKSAIGEEGRKKNQLLKRDFSKLANPLSEFSLYREQPDTQFLKNRKIKNVDQODSRLFSLLEKYIFHSLSINLTIYLKALHFQTRVFPFKSFPHFNTLKFTFQLKMGALGDSAYGARGRLIKFSYIVTALISILFSISCICYGIMLLARRQYAELYSPS
                                                                                                                                                                      /note="predicted using Genefinder; cDNA EST yk193h3.3 comes from this gene; cDNA EST yk193h3.5 comes from tis gene; cDNA EST yk411f5.3 comes from this gene; cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(19892. .20022,20241.
/gene="F53B6.8"
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platelet-endothelial tetraspan antigen (SWLPET3_HUMAN)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(20516. .20602,20648. .20953,20999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(20516. .21818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGYYQSNYWGKRK"
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                                                                                                                  k411f5.5 comes from this
                                                                                                                                                                                                                                                                                                                                      /gene="F53B6.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F53B6.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MDFGILLVFLMAVAGTFAGISVSFSHSHEFPRHGLLGGGGFNPY/
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                                                                    codon_start=
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.3308,3430. .3649)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                      CATTTTCCTTCACAATGATCACCTCGTTTCATCCATTCTTTGTGACGGGAATGGATCGAG
catatcgagtacaatgcttttacatggaagctgataaaacagttagtgcacagattgagg 572
                                                                                                                                                                                                                         ttgtaacaacaactgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtg 512
                                                                                                                                                                                                                                                                                                                                                                                                                                       cacticcatitgaticatgcaatgitgcgcgtacacgatctctgaatccacgtggtattt 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.2%;
59.3%;
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gene

0,:

Score 74.8; DB 34 Pred. No. 0.00056; Mismatches

DB 34;

Length 32412; Indels

0;

Gaps

0

gene

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GYPINIQYLPSQGFIRAENIEDYNLRIQAFFKKNIAKIEQKQYVVISDNYMYDLTRNE
HVETYDDILQCIKKPTCQMNFISLKKGEAQIMDSPILPLTKSLYLYKPFYWTDVPLQL
SVPNIPPELNQN"
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vpltaly"TTSLD#VAALAFCAKNRKTVHAKNKNKNKSSKSAKSSTRCASKSGKSGKSRR
SSKAKH5KRSSKSSKKGTSGKSGKGSKKGGKSSKSKSKKKKTATTSGSQVSTV5AA
TGVSDKOSNSSKSSKSSKSKSRKNRELDSDAQKKMEKSGKSGKVALIFKTQOTTGS
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HFFFYTGMDRAFSIRCFFLESIKGLNAEIDVGTLAPQHVDQEYSLPVCAYHLKDGIEG
                                                                                                                                                                                                                                                                                                                                                                                 complement(join(27666. .27862,27919. 28905. .29001,29330. .29417,29467. ... 30107. .30301,30478. .30589))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MILSDQNFLQTQWKEPQTAQSKNTESKCEFHGNSNEVKPIGSLN
GQSIAQCRIHTEKTVPIVKGGEQARMEENEIYAIETFGSTGKGVFHDDMETSHYMKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F53B6.5"
23555. .24160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(27666. .30589)
/gene="F53B6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary prediction; 26276. .26348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein (SW:I2A6_RAT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F53B6.7"
/note=""-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELADEK I PLRLQKSKGLLNLI DKNFATLAFCRCWI DRLGETKY LMALKGKCSY STASR
LMLI LTLFTDRWMAMVGAC I LQSFAGKI I GKRANLLLNL I I "
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PQIEYEHGAISAYTNAHVFKYADKVQLYFTCTVQLCYKHDGGCEGITPPQCSGHSHGI
                         HVLRFAQVGQKVTHVWRCDQDASHVYGILIHSCYADDGHGNKFELVDDRGCSTDPFLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="TTT Lys K-tRNA; predicted using tRNAscan-SE-1.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F53B6.t1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F53B6.7"
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Matches 164
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ttcgtttgttattatcattatcaacttgtcctattttattctaacagtttatcattt 1641
                                                                                                                           gtgatattttcatcaaaaacttcttctatcgcttttatagcttctgaaaagcttattcatt 1521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (27-OCT-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
On Oct 19, 1999 this sequence version replaced gi:6016917.
Order of segments is not known; 800 n's separate segments.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 614429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans chromosome III clone
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                                                                                                                                                                                                                                                                                                                                                                          IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone Y18D10A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bin/display?ab=wormace&class=Sequence &object=Y18D10A Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-DEC-1998) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Hifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
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Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
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Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vanchen, R., Sulston, J., Thierry-Mieg, J., Thierry
                                                                                   neighbouring submissions.

The true left end of clone F08A8 is at 152766 in this sequence. The true right end of clone B0019 is at 105 in this sequence. The st of this sequence (1. .105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 152878)
Harris, B.
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
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94150718
The end of this sequence (152766. .152878) overlaps with the start
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 152878)
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cosmid Y18D10A, complete sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berks, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MDGSGEKAIGFLIQFSLNARFWTDKQLLATDEPFSSENYQMVRRFIISERPKSVDKLYKTGEIPARGRGKKVGGRVFSKNEISKNELSLVKLKQTPIIQOFYKNNGKKSTMVHLISKKTYSFIGOKLAAQIDEQLFRYKGFKVEQLMBELGLAAAQIFIAAAHYPKSNVAVLCGPGNNGGDGFVCARHLQQFGFTPSIVYPKESRNELMKSLVVQCE
                                                                                                                                                                                                                                                                                                                                          complement(join(29879. .30346
34557. .34852,35323. .35351))
/gene="Y18D10A.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(26502. .29006)
/gene="Y18010A.2"
complement(join(26502. .26573,27346. 27624. .27788.28732. .29006))
/gene="Y18D10A.2"
/note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MDEDIAEAQCASEGCANVRKNIGLLLMQNKQRAAEMQDFSKVQA
ECEVLRMKLVSTDAAYRESVQREAEAINAKEIAEASLKQGQYDSEFYKKKSASLQEQA
DDAEKHKDQANYWRNKYDSVCALTERLEANNIDIKSKYESTVKLLETAGKRMTSLDNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complement(join(7920. 8081,9752. 9924,10879. 11164, 12369. 12599,13906. 114204,15129. 11655,17748. 118104, 19860. 119949,20008. 20088. 20709. 20807,22205. 23127, 24486. 24744,25724. 25909,26020. 26130,26236. 26256))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="momnpnksppisinfplftmskfllfisisavatasdlyevfgi
srcpdtskfihnolvpfyonykgnlsdglkldfhavptgghqvdgkyvnrclhgalec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNVLRVMIDNPFSSHSHAIFAALKQISPQVSQLREIIESSEINQYVEMTGEDAIRDAV
QNLVDLISIYTNFPLKPTTLPPSS"
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                                       TSSIPITATLPTNLQAFPLIVDALFGFSFHPPTREPFTEMLKTVRASGIHVFSIDVPS
                                                                                                                                                                                                                            /protein_id="CAA22319.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNDENSYRYNVAPHSAWLPWIQVNGERNRNAEFKLKDFSSVFRLFFEVFLQKCLKRSI
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                                                                                                                                                                                                                                                                                                              /codon_start≈1
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/db_xref="GI:3979930"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                     .30346,31220. .31296,31346. .31522,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .27405,27490. .27580,
Query Match
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TSGINRFALKTALSICIFLLIFQTVDSDSSDSSASASVVSGAVKSEDTVVAVNKTTVVL
GEAIDANATSLEQHGAAIVGNVSEEKKRSLAIFFILVLLPPIFENAYNLNKGYFFSN
FSLATVALGALIGSILAYSRRDWSEIEALSPDVFTLVLLPPIFENAMISAVDPVGTLAI
FVPLITFAIFGTTISANVIGAGLYILGAIGLIFEFTFEECFAFAMISAVDPVGTLAI
FVPLITFAIFGTSSANVIGAGLYILGAIGLIFEFTFEECFAFAMISAVDPVGTLAI
FQAVKVESLLYMLVFGESMLNDAVSIVLAATALRHAKPSFNSLPASEIITSAFVTFTE
MFFFSACLGVOIGLLSALFFHFNTISFVAFTSTFAYIGMRGAVCFFALVLYMDL
LFCGISMSQFTRHNVSDIAQITFRHTFRTISFVAFTSTFAYIGMRGAVCFFALVLYMDL
DKEKKSILLTTVLFTTIFLGGSALPFISFINGCYBERQKRRRFTFRNKESTGN
CSALMWSGTTSTANVSDIAQITGNTATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTFATATSTTATSTFATATSTFATATSTFATATSTFATATSTFATATSTTATATSTTATATSTTAT
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DIKPQNILLIDPESGVLKLCDFGSAKYLVRNEPHVSXICSRYYRAPELIFGATWYTNSI
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KAHPWNKYFRVHTPAEALDLISKIIEYTFTSRFTPQAACQHAFFDELRNDARLPSGR
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/gene="Y18D10A.7"
/gene="Y18D10A.7"
/gene="Y18D10A.7"
/note="predicted using Genefinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47525 . .53224

/gene="YIBDIDA.6"

join(47525 . .47593,48112 . .48208,48610 . .48751,49616 . .5

50501 . .50818,51553 . .51971,52106 . .52364,52847 . .53224)

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YPWPFIIIPLIITICLSMGIILNFKIVRGVNYLYAPLNATWKTEEAVFGENWAKDDDH
FYPGKDILRRQGIYLIVNAKDGGNVLRQEYAQDFLKILDWILNVKLLSSAGRIFTYKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVSGEHHLLISSGSDSSTNEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSALMMSKTQEMSFFGSDDWGPKKSALDATSSAGRIMRQLFVRKFTAIERLENRDKLAALTKRALASDQMTDSDDVEFGGGGGGVGGGGRMKDDVTPTRGRSGSRNSSDVIISAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39072. .44375
/gene="Y18010A.5"
join(39072. .39164,40245. .40513,41360. .41936,44226. .44375)
/gene="Y18D10A.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTGERQTEAVSKRSNVVSERCGGPPCLRLVDGRTLSVCVSDDSS
HIDGSIGYHFFSLDCLSLSLTLSTAAVVATATSSSSSPKAFGVSVSLFLWSLLVAWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQYPGFEQIVKLED"
35614. .36138
/gene="Y18D10A.4"
                                                                      DYDGHVENASAWLILYQLKNEKWQLSRDFEDGLAEKIQSGEAPSELLNLYYFHSATFD
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                                                                                                                                                                                                                                                                   /protein_id="CAA22312.1"
/db_xref="GI:3979933"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/db_xref="GI:3979931"
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       /chromosome="I"
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Direct Submission
Submitted (12-NOV-1999) Louis, MO
jes@sanger.ac.uk or rw@nematode.wu
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E-mail:

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1392 catccttctaataactaattttagctaacaaatatatagtatgtaggaaataattactgt 1451
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                                                                                                                                                                                                                                                                           atttcctattctgtaaacaattcacttatttgcattattgcaattaaaaagtatttcatt
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                                                                                                                                                               ATTCATTTATTTAATTTATTTATTTATTTAATTAATTTATTTATTTATTTAATTAA
                                                                                                                                                                                                                                                   TTTAATTAATATTTATTTATTTAATTTAATTAATATTTATTTGTTTATTTAATTAATATATTT 77352
                                                                                                                                                                                                                                                                                                                                   TATTTAATTAATATTTATTTATTTATCTAATTAATATTTATTTATTTAATTAATATTTAT
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FEATURES
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTIANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone Y111B2D. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between the secure we arrange for a small overlap between the secure we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neighbouring submissions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKKIRKIKEKGGEKSSKSSSSSSSSSSSBEDAAGPPRMTGAPPSILMYSSSSSIKK

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                                                                                                                                              KDRIEAKKFEERMKKEQEKGEEKERKEREKERKERKEREIREIMERKKREEDDRIAA KLQIAQQLENDRKMREAEESGAEKETERAKMETEAANALGGLEEDLLANDIDEMTQQQ TKVDEERKVAEARRAVEEROJEKARPAQOLAPAPHTQKIQVKNEPU DHSFDILKEAEKVAEARRAVEEROJEKARRAQOLAPAPHTQKIQVKNEPU DHSFDILKEAEKDAHIIPTKSIKAEPLDVQKPLSAFEKLASLRGRTOSADMRRGGDST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVQAKKPRHFEIFWWKLVKNGLISTKFCVKNHKSKKITIFTPRPISDSPRPLFNQSNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQLPKLKHHSPPVEGLAKKQVIAANAIKEGVRKQISLFENKKDRLPGDPVYVFQFTEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="VDDEPTTSKKGGFYVGKGDVKDSNDEDEEEEEETDVEESIQEVP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(<616. .1221,2288. .2593,3842. .4122,6454. .6687,
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4404. .9723,10796. .11001,11112. .11276,11362. .11438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ∕organism≖"Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(58932. .59150,59217.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(58932. .59820)
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                                                                                                                                                                                      SRSRSASRSPSRSPSPQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSSSEDESDVGDDDDKDD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLTGCDGSVGSVCGCVEDGRKVVAAAWVRFRIAKKAAASHLHSACRKKTTKNQEKPCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(43452. .44114,45282. .45329))
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.
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                                                                                                                                                                                                                                              SHEGETAYIRVREDNSSGGGSGGGGRDRSRSRSPRAERRASPKYSPRRSRSRSRSRSRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSEVGVIKSTSERRHQKPITVLKRLKSSEIVADEFVTGGVDSRVVLWKLRGEHVEYVA
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                                                                                                                                                                                                                                                                                          ETSEEDVVVVVEDLKDHMRDAGDVCYADVARDGTGVVEFTRYEDVKYAVRKLDDTKFR
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Search completed: April 16, Job time: 10352 sec
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ORIGIN
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Copyright (c) 1993 - 2000 Comp
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T62359
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2 cttttatagcttctgaaaagcttattcattattcagt	######################################	standard; cDNA; 605 B);)) 3' apolipoprotein B SAI opoietin; EPO; anaemia ld attachment region; enic animal; ss. enic animal; ss. 1996, CAN696. 1995; CAN696. 1994; US-35891B.	45.6 2.6 110000 1 X20248_0 45.6 2.6 110277 1 X20249_4 45.4 2.6 2338 1 O54656 45.4 2.6 110000 1 T58840_4 45.2 2.5 2430 1 V22750_4 45.2 2.5 2430 1 V22733 44.8 2.5 4053 1 X52266 44.6 2.5 144 1 Q12515 44.6 2.5 5852 1 Q11710 ALIGN
atches 205; Indels 2; Gaps 1; taactaattttagctaacaaattatatagt 1431	aps 1431 133 1491 193	R element clone Rh32.; gene therapy; vector; gene therapy; vector; sare element; apolipoprotein B; sand for gene therapy, e.g. of sell disorders glish.) scaffold attachment region (SAR) and Rh10 (T31531) respectively carry and Rh10 (T31531) respectively carry tand the distal 1212 bp 5' human apoB imal sequence. These SAR elements f the human apoB gene chromatin DNA molecule adapted for transfection srythropoietin (EPO) cDNA (T31529) or Jy linked to an expression control SAR elements. The SAR elements ecombinant EPO in stable, long-term 18 C; 35 G; 274 T;	248_04 248_04 Borrelia burgdorfe 656 640_4 640_4 Continuation (5 of RA0_4 Babesia microti BM 733 Babesia microti BM Protein PR036 cDN 515 CSP-2 peptide from Sequence encoding Dictyostelium plas ALIGNMENTS

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Proclaim 20; Fig lA-E; 69pp; French.

CC laim 20; Fig lA-E; 69pp; French.

CC frist sequence corresponds to the genomic sequence encoding a Plasmodium flat sequence was isolated by screening a protein (W24790). The gene sequence was isolated by screening a protein (W24790). The gene sequence was isolated by screening a protein (W24790). The gene sequence was isolated by screening a protein (W24790). The gene sequence were from a missionary treated by prophylaxis (for strain 76/96 see FR9101286). Of 20 clones isolated, clone 729s was used to screen a library generated from Thai strain K1. One clone contained a 6.85 kb insert including the sequence presented here. The gene organisation comprises a first exon, a short of the prophylaxis of the second exon containing a 1.8 kb region encoding to be intron and a 5 kb second exon containing a 1.8 kb region encoding corresponding to a glycosyl-phosphatidylinositol membrane anchoring sequence. The invention relates to new polypeptides of at least 10 amino acids derived from the LSA-3 polypeptide with the exception of peptides w24791-4. The LSA-3 peptides can be used to raise antibodies and as vaccines for immunotherapy of malaria.
                                                                                                                      Query Match
Best Local
                                                                                                         Matches
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12-JUN-1996;
13-JUN-1995;
                                       5728
1430 gtatgtaggaaataattactgtaatacaataagtgatattttcatcaaaacttcttctat 1489
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P. falciparum liver stage antigen-3 genomic sequence.

Plasmodium falciparum; pre-erythrocyte; liver stage a
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                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum poly:peptide(s) and related nucleic acids - derived from the liver stage antigen-3, useful for malaria vaccine
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WPI; 97-065464/06
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prophylaxis; Thai strain; gene organisation; exon; intron; hydrophob
glycosyl-phosphatidylinositol membrane anchoring sequence; antibody;
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uence 6152 BP; 2725 A; 463 C; 1
                                     ATATATATGTATCTTTTACAAAATTTTAAAATTTTAAAATTTATATATATATATATTTA
                                                                     atatatattcgtttcttcttatcatccttctaataactaattttagctaacaaatatata 1429
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77. .274
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PT Claim 4; Page 56-61; 96pp; English.

CC This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to the Duffy binding like (DBL) family of genes which have homology to the CC the Duffy binding like (DBL) family of genes which have homology to the CC Buffy antigen binding protein (DABP) and sialls acid binding protein (CC (SABP) conserved regions (see T72889 and T72888 respectively). The var CC family of genes modulate cytoadherence and antigenic variation of CC Plasmodium infected erythrocytes. SABP and the Duffy antigen binding CC protein (DABP) are soluble proteins that appear in the culture CC supernatant after infected erythrocytes release merozoites. DABP and SABP CC mediate the binding of merozoites and schizonts to the erythrocyte ccurface. These proteins are necessary for erythrocyte invasion by the CC parasite. This sequence can be used in the compositions of the invention.

The compositions are for the treatment and prevention of malaria, and
   RESULT
T72882
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WPI; 97-
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Chitnis
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Plasmodium var-7 gene.
Plasmodium var-7 gene.
DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;
Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response
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                                                                                                                                                                                                                                                                                            P-PSDB; W22475
                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1996;
07-JUN-1995;
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19-DEC-1996.
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S C, Miller LH,
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Best Local Similarity
WO9641877-A2.
27-DEC-1996; F00894,
12-JUN-1995; FR-007007
13-JUN-1995; FR-007007
(INSP ) INST PASTEUR.
Daubersies P, Druilhe
WPI; 97-065464/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OB-OCT-1997 (first entry)

P. falciparum liver stage antigen-3 genomic sequence.

Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum;

prophylaxis; Thai strain; gene organisation; exon; intron; hydrophob
glycosyl-phosphatidylinositol membrane anchoring sequence; antibody;

vaccine; immunotherapy; malaria; ds.
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Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
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ersies P, Druilhe P;
97-065464/06.
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Proclaim 20; Fig 1A-E; 69pp; French.

Calaim 20; Fig 1A-E; 69pp; French.

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Best Local Similarity
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Q11710;
30-JUL-1991 (first entry)
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WO9106644-A
16-MAY-1991
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                                                                                                                                             Dictyostelium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mould; replication; Rep gene;
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                                                                                                                                                                                           plasmid Ddp2
                                                /product=
                                                                                              2378. .5041
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                                                                                                                Location/Qualifiers
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                                                involved in
                                                                                                                                                                                                                                                                        ВP
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                                                extrachromosomal replication
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Claim 15; Fig 1; 90pp; English.
CThe sequence of Ddy2 has been found to contain the putative open creading frame indicated in the Features Table. The possible ORF is C flanked by regions with similarity to promoter and poly adenylation CC signals of known Dictyostellum genes. The RNA and polypeptide product of the Rep gene have not, however, been detected. It is C believed that the product is produced in low amounts to positively CC regulate initiation of plasmid replication. The polypeptide may also contain regions that act as negative regulators of plasmid copy CC contain see also Q11711 and Q11712.
Seguence 5852 BP; 2298 A; 651 C; 708 G; 2195 T;
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Best Local S
Matches 218
                                                                           malaria; ss
Plasmodium
 WO9412643-A.
                                                                                                     Carbamoyl-phosphate-synthetase Carbamoyl-phosphate-synthetase
                                                                                                                                           Q62924 standard;
Q62924;
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Slade MB, Chang AC
WPI; 91-164194/22.
                                                                                                                                06-DEC-1994
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91-164194/22.
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                                                                           falciparum.
                                                                                                                             (first entry)
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                                                Location/Qualifiers 1226. .8401
                         /*tag= a
/EC_number= 6.3.5.5
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Pred. No.
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                                                                                                      CPSII;
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0.021;
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                                                                                                    psCPSII gene;
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RESULT
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ID 090204
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DT 1-
DE MA
DE MA
CO P1
PN EPP
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Best Local S
Matches 195
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03-DEC-1992; AU-006206.
16-DEC-1992; AU-006380.
(UNIX) UNISEARCH LTD.
Flores MV, Osullivan WPI; 94-200271/24.
                                                                                                                                                                                         EP-322712-A.
05-JUL-1989.
20-DEC-1988;
30-DEC-1987;
                                                                                                                                                                                                                                                                                                  Malaria-specific DNA insert of clone 41-2. DNA; malaria; clone 41-2; Plasmodium falciparum; Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1730
New antigenic proteins from Plasmodium falciparum - new encoding nucleic acid sequences and derived antibodies, useful in vaccines, diagnosis etc Claim 1; Table 17; 25pp; German.
                                                                              (BEHW) Behringwerke.
Knapp B, Hundt E, Enders
WPI; 89-194071/27.
P-PSDB; P90417.
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Sequence 8920 BP; 3836 A; 774 C; 1232 G; 3078 T;
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Disclosure: Page 6-16; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         1-NOV-1989 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  N90224
                                                                                                                                                                                                                                                                                                                                                                                                                                         N90224 standard; DNA;
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P-PSDB; R55694.
Nucleic acid encoding
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DE-831351.
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Pred.
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Sequence 1052 BP; 394 A; 93 C; 88 G; 477 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection;
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                                            /transl_except=
5546. .5548
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3461. .3
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656. .658
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2909. .2911
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prevention; pa
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Arginine
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Matches
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                                                                                                                                                                                                                                                                                     A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte membrane protein 1 (PfEMPI) or active fragments or analogues of that protein can be used in the treatment or prevention of symptoms of a malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaria. Nucleic acids derived from the PfEMPI gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different P. falciparum strains. Antibodies specifically immunoreactive with the PfEMPI polypeptide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the pfEMPI protein of the MC type of Plasmodium falciparum. An
                                                                                               8319
                                                                                                                                             8379
                                                                                                                                                                   1288
                                                                                                                      1348
                                                                                                                                                                                                                                                                 alternative, truncated version of the coding sequence is given in {\tt T41853}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 malaria parasite infections
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                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Plasmodium falciparum erythrocyte membrane proteins develop products for the diagnosis, treatment or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-1995; US-430908.
(AFFY-) AFFYMAX TECHNOLOGIES
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les 217; Conserv
                                                                                                            tcgaagcaataataaaactgccatatattcgtttcttcttatcatccttctaataact 1407
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                                               aattttagctaacaaatatatagtatgtaggaaataattactgtaatacaataagtgata
ttttcatcaaaacttcttctatcgcttttatagcttctgaaaagcttattcattattcag
                                                                                              Howard RJ,
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/transl_except=
6257. .6259
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5269. .6271
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275. .6277
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                                                                                                                                                                                                      Score 51.8; DB Pred. No. 0.063;
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on of
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                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 59-60; 849p; English.

Human apolipoprotein B (apoB) scaffold attachment region (SAR) element clones Rh32 (T31530) and Rh10 (T31531) respectively carry the 3' human apoB SAR element and the distal 1212 bp 5' human apoB SAR element and the distal 1212 bp 5' human apoB SAR elements of the human apoB gene chromatin domain. A novel recombinant DNA molecule adapted for transfection of a host cell comprises an erythropoletin (EPO) cDNA (T31529) or genomic clone (T31532) operably linked to an expression control sequence and to the 5' and 3' SAR elements. The SAR elements increase expression of the recombinant EPO in stable, long-term mammalian cell cultures.
1564 cattaggccatgaatagtttcgtttgttattatcatcattattcaacttgtcctattttat
                                                                               1506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA molecule expressing mammalian erythropoietin useful to transform cell lines, and for gene therapy, e.g. of anaemia and other red blood cell disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CANG-) CANGENE CO
Delcuve G;
WPI; 96-309587/31.
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scaffold attachment region; SI
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Human 3' apolipoprotein B SAR element clone Rh32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-1995; CA0696.
19-DEC-1994; US-358918.
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                                                                          gaaaagcttattcattattcagtaatcttttatatgcatactattgt--aaatgtttcat 1563
                                                                                                                                         tactgtaatacaataagtgatattttcatcaaaaacttcttctatcgcttttatagcttct 1505
                                                                                                                                                                       TATAAACATTTTAATTATAAAATATGTAATTATAAACATTTTAATTATAAAATATGTAAT
                                                                                                                                                                                                     tottatcatcottotaataactaattttagotaacaaatatatagtatgtaggaaataat 1445
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                                                                                                                                                                                                                                                                                                                    Similarity
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BP; 278 A;
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SAR element; apolipoprotein
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                                                                                                                                                                                                                                                                                                                    Score 51;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                 DB 1; Length 605
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PT binding proteins

SC claim 4; Page 56-61; 96pp; English.

CC This sequence represents the var-7 gene of plasmodium. Var-7 belongs to the Duffy binding like (DBL) family of genes which have homology to the CC the Duffy binding like (DBL) family of genes which have homology to the CC the Duffy binding like (DBL) family of genes which have homology to the CC plasmodium infected erythrocytes. SABP and T72888 respectively). The var CC family of genes modulate cytoadherence and antigenic variation of CC plasmodium infected erythrocytes. SABP and the Duffy antigen binding CC protein (DABP) are soluble proteins that appear in the culture CC supernatant after infected erythrocytes release merozoites. DABP and SABP CC compositions are for the treatment and prevention of malaria, and CC compositions are for the treatment and prevention of malaria, and CC compositions are nocleotide sequence or encoded polypeptide of the CC var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP. The CC compositions are used for the treatment and prevention of malaria. They care also used in the preparation of vaccines for inducing a protective immune response in a mammal to plasmodium merozoites (especially CC plasmodium falciparum or plasmodium vivax).

So Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
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07-JUN-1996; UO9508.
07-JUN-1995; US-487826.
(USSH) US DEPT HEALTH & Chitnis C, Miller LH, Wellems TE; WPI; 97-052231/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium var-7 gene.

DBL gene family; SABP; sialic acid binding protein; vaccine; therapy; Duffy binding like gene; Duffy antigen binding protein; erythrocyte; DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                  New malaria vaccines - cont
binding domains homologous
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15140. .16205
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Peterson DS, Sim
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Query Match
Best Local Similarity
Matches 180; Conserv

Conservative

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45.6%;

Score 51; I Pred. No. 0. Mismatches

DB 1;

Length 19124;

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RESULT 11
X20248_02/C
Continuation (3 of 10) o
WP Sequence split into 1
WP Fragment Name
WP X20248_01
WP X20248_02
WP X20248_03
WP X20248_05
WP X20248_05
WP X20248_06
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                                                                                                                                                                             ccgtcattattaccatttcgtttaaatttcgtccaaatcagaaggcataaaaataatgtt 1340
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nilarity 44.8%;
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Pred. No. 0.16;
0; Mismatches 292;
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Best Local S
Matches 203
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11-SEP-1984; AU-007066.

11-SEP-1985; AU-007066.

10-SEP-1985; AU-047326.

(HALL-) HALL INST MED RES.

Kemp DJ, Anders R, Coppel R

WPI; 86-094055/14.
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27-MAR-1986
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WP1; over P-PSDB; P60569.

DNA coding for Plasmodium falciparum DNA coding for Plasmodium falciparum antigenicity (
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The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp, to all or a portion of the base sequence coding RESA (N60472) or FIRA (N60473). RESA and FIRA lantigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.

Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
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agtttcgtttgttattatcatcattatcaacttgtcctattttattctaacagtttatca 1638
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Best Local Similarity
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11-SEP-1985; 006960.
11-SEP-1984; AU-007067.
11-SEP-1984; AU-007066.
10-SEP-1985; AU-047326.
(HALL-) HALL INST MED RES.
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Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
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24-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 1; 55pp; English
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taatcttttatatgcatactattgtaaatgtttcatcattaggccatgaatagtttcgtt
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1199. .4225
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801. .995
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No. 0.14;
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Best Local
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WO9845328-A2.
15-OCT-1998.
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                                                                                                                                                                                                                                      V68900 to V68998 represent nucleotide sequences which encode human breast tumour specific polypeptides. Detection or measurement of human breast tumour specific polypeptides and nucleotide sequences, or the corresponding RNA in a sample, is used for diagnosis and monitoring of breast cancer. Human breast tumour specific polypeptides and nucleotide sequences, and the vectors containing the DNAs, are a useful in vaccines for inhibiting development (for prevention or therapy) of breast cancer. The polypeptides may also be used to raise monoclonal antibodies, used as immunoassay reagents. Sequence 715 BP; 183 A; 131 C; 86 G; 294 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA sequences isolated from endogenous human retroviral element - and related vectors, transformed cells, proteins and antibodies, useful for diagnosis, treatment and prevention of breast cancer Claim 1; Page 127; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frudakis TN, Reed SG, Smith JM; WPI; 98-557473/47.
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11-DEC-1997; US-991789.
09-APR-1997; US-838762.
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Human; breast cancer; breast tumour tissue; diagnosis; treatment
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22-JAN-1999
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3568/c Q03568 standard; DNA; 6124 Q03568; 02-AUG-1990 (first entry)

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3082. .3151
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121. .128
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Best Local Similarity 47.8%;
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding SERA antigen of Plasmodium falciparum - also DNA encoding signal and regulatory sequences of SERA gene, for diagnosis, prevention and treatment of malaria.

Disclosure; p; English.

Disclosure; p; English of antigenic malarial proteins, useful diagnosis, prevention and treatment of the disease. The sequence may bused in an expression vector, and signal and regulatory sequences may used to stimulate production of other products.

Sequence 6124 BP; 2567 A; 602 C; 801 G; 2137 T; 17 Others;
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Inselburg JW, Bzik DJ;
WPI; 90-083508/11.
P-PSDB; R05526.
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2030
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Search completed: April 16, Job time: 9747 sec 2000, 04:40:48

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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
6: /cgn2_6/ptodata/
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Match
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1285.535 Million cell updates/sec
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         GenCore version 4.5
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/CTUS9_COMB.seq:*
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45 summaries
                     US-08-883-795A-36
US-08-887-775-1
US-08-487-826B-13
US-07-867-106-2
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Sequence 36, Appli Sequence 13, Appli Sequence 2, Appli Sequence 36, Appli Sequence 37, Appli Sequence 14, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 19, Appli Sequence 19, Appli Sequence 10, Appli Sequence 20, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 23, Appli Sequence 24, Appli Sequence 24, Appli Sequence 27, A
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US-08-883-795A-36
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Best Local Similarity
Matches 217; Conserv
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ALIGNMENTS	US-07-991-867B-32	US-08-451-405A-2	US-08-544-332-8	US-08-107-755A-8	US-07-991-867B-8	US-08-544-332-1	US-07-991-867B-1	US-08-980-060-3	US-08-544-332-41	US-07-991-867B-41	PCT-US95-16216-2	US-08-353-700-2	PCT-US93-07261-10	US-08-647-351B-1	US-08-795-475-4	US-08-795-475-2	US-08-451-405A-2	5340934-5	
	Sequence 32, Appl	Sequence 2, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 41, Appl	Sequence 41, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Patent No. 5340934	

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; IMMEDIATE SOURCE:
; CLONE: Rh 32
US-08-883-795A-36
                                                                                                                                      CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION UNMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 361-1398
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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Patent No. 5985607
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APPLICANT: Delouve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 40 King CITY: Toronto STATE: Ontario COUNTRY: Canada
                                                                                                                           TOPOLOGY:
                                                               ORGANISM:
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RESULT 2
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                                             TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                    REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1327
                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 273
                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,075
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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OPERATING SYSTEM:
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STRANDEDNESS:
                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                ENGTH:
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              nucleic acid
                                6243 base pairs
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Bradshaw, Marite
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; LOCATION: 3770..4013
; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
; OTHER INFORMATION: plasmid RP4"
US-09-056-075-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-487-826B-13
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Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Peterson, David S. APPLICANT: Su, Xin-zhaun APPLICANT: Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1221
                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1411 tttagctaacaaatatatagtatgtaggaaataattactgtaatacaataagtgatattt 1470
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1351 aagcaataataaaactgccatatattcgtttcttcttatcatccttctaataactaat 1410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1531 tcttttatatgcatactattgtaaatgtttcatcattaggccatgaatagtttcgtttgt 1590
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
                                                                    CLASSIFICATION:
                                                                                      APPLICATION NUMBER: FILING DATE: 10-SE
                NAME: Israelsen, Ned REGISTRATION NUMBER:
                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                   STATE: California
                                                                                                                                                                                                                                                                                                      STREET:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                          PatentIn Release #1.0,
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                                                                                                        US/08/487,826B
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NIH121.001CP1
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                                                                                                                                          Version
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16th
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US-07-867-106-2
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                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07867106 Patent No. 5389526 GENERAL INFORMATION:
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Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1471
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1659
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                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No.
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                   APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
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TOPOLOGY: linear
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                                                                                                                   ZIP: 19103
                                                                                                                                     COUNTRY:
                                                                                                                                                     STATE:
APPLICATION NUMBER:
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47.1%;
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US/07/867,106
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RESULT 5
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Best Local Similarity 46.8%;
Matches 214; Conservative
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APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
                                                                     2003 TTTTACTTTGAAAAAAAAAAAAAAAAAAAAAAAAA
                                                                                        1632 tttatcatttgtgataatatcac-----aaattataccttgtattgcccaattttt 1682
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TOPOLOGY: li
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Sequence 1, Application US/08446855A Patent No. 5849573 GENERAL INFORMATION:
APPLICANT: Stewart, Thomas S

APPLICANT:

Flores, Maria V

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US-08-883-795A-36/c ; Sequence 36, Application US/08883795A
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Best Local Similarity 47.6%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-
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MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
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                                                                                                         600
                                                                                                                                                                                                                                                                        480 CCATCCTATATATATACACAATATATAATACTCCCCAATATTGTGGGTTCCTATAATTTT 539
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                         ttgcccaatttttatgggcatcatttcctattctgtaaacaattcacttatttgcattat 1729
                                                                                                                                                                                                                                                                                                         ttgtcctattttattctaacagtttatcatttgtgataatatcacaaattataccttgta 1669
                                                                                                                                                                                                                                                                                                                                                        TATTAATATTTTGATGTGTACACATTAATATAGTT----TTACACTTCTTATAATAAAA 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (416) 361-13
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Delcuve, Gen
APPLICANT: Awang, Grego
TITLE OF INVENTION: Rec
TITLE OF INVENTION: VE
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       | 1386 tottatcatccttctaataactaattttagctaacaaatatatagtatgtaggaaataat 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                              1328 taaaaataatgttagaatcatcgaagcaataataaaactgcca--tatatattcgtttct 1385
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CLONE: Rh 32
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APPLICATION NUMBER: US/0
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
                                                                         1624 tctaacagtttatcatttgtgataatatcacaaatta-----taccttgtattgccc 1675
                                                                                                                                                    1564 cattaggccatgaatagtttcgtttgttattatcatcattatcaacttgtcctattttat 1623
                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gravelle, Micheline REGISTRATION NUMBER: 40,261 REFERENCE/DOCKET NUMBER: 78 TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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1676 aatttttatgggcatcatttcctattctgtaaacaattcacttatttgcattattgcaat 1735
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ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 665 base pairs
                                       TATAAACATTTTAATTATAAAATATGTAAATTATAAACATTTTAATTATAAAATATTTAAT 284
                                                                                                                                                                                                                                                                                                      tactgtaatacaataagtgatattttcatcaaaacttcttctatcgcttttatagcttct 1505
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US-08-487-826B-13/c
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Best Local Similarity
Matches 180; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                     REFERENCE/DOCKET NUMBER: NI TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                         LENGTH: 19124 base pairs
TYPE: nucleic acid
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ctgtaatacaataagtgatattttcatcaaaacttcttctatcgcttttatagcttctga 1507
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Miller, Louis H.
Peterson, David S.
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Wellems, Thomas E.
                                                                                                                                                                                      Conservative
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US-08-232-463-14
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US-08-232-463-14
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Best Local Similarity 4.3%; Pred. No. 0.016; Matches 16; Conservative 204. Minute.
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                                                                                                                                                                                                                                TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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                                                                                                                             IMMEDIATE SOURCE:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                      DB 1;
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TELEPAX: 703-816-4000
TELEPAX: 703-816-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.00
                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855
FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl TITLE OF INVENTION: phosphate synthetase II NUMBER OF SEQUENCES: 2
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                                                                                              TOPOLOGY:
                                                                                                          STRANDEDNESS:
                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington
                                                                                                                                         LENGTH: 8920 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                              linear
                                                                              genomic
                                                                                                        single
 2.7%;
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Maria V
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                                                                                                                                                                                                                                       47-80
 Score 48.6;
Pred. No. 0
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              ω
              Length 8920;
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US-07-638-431-1
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                                                                                                                                                                                                                                  TELEFAX: (301) 295-40 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/638
FILING DATE: 19910110
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Spevack, Avrom D.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PEREASE #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20814-5044
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                MOLECULE TYPE: D
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4673 base pairs
                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                ANTI-SENSE:
                                                                                                              HYPOTHETICAL:
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                                       ORGANISM: Fig. 17X(NL)
                                                                                                                                                                                                                                       TELEPHONE: (301) 7
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                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Bethesda
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                                                               Plasmodium yoelii
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                                                                                                                                                  linear
erythrocytic stage
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                                                                                                                                 DNA (genomic)
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; OTHER INFORMATION:
US-07-638-431-1
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Best Local Similarity 48.1%;
Matches 165; Conservative
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APPLICANT: Charoenvit, Yupin
APPLICANT: Hedstrom, Richard
APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
                                                                                                                                                                                              ZIP: 20814-5044
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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             ATTORNEY/AGENT INFORMATION:
NAME: Spewack, Avram D.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                 CLASSIFICATION:
                                                                                             APPLICATION NUMBER: POFILING DATE: 19920103
                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                 Bethesda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application PC/TUS9200018
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                                                                                                                                                                                                                                                                                                 Medical Center
                                                                                                                                                                                                                                                                                                                NMRDC Building 1
                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                Floppy disk
295-4033
                                                                                                                                                                                                                                                                                                                                                                             Protective malaria sporozoite surface protein immunogen and gene encoding
                                                                                                                PCT/US92/00018
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                                                                                                                                                                                                                                                                                                                T-12 National Naval
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RESULT 12
US-08-484-105-15/c
"~~"ence 15__Application US/08484105
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; OTHER INFORMATION:
PCT-US92-00018-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7%;
Best Local Similarity 48.1%;
Matches 165; Conservation
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
718..3195
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                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE: erythrocytic stage IMMEDIATE SOURCE:
                               TITLE OF INVENTION: ORIGIN OF NUMBER OF SEQUENCES: 24
                                                                              APPLICANT:
                                                                                                                                                                          APPLICANT:
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 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTTTGTATGATTAAGTTATTTTAAATTAACAGTTTGATAAATTGTCATCTTTTTATGT 3458
                                                            LAURENSON, Patricia
HERSKOWITZ, Ira
LI, Joachim J
GAVIN, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4673 base pairs
                                                                                                                                              RINE, Jasper
FOSS, Margit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Py-lambdagt11-2-7 kb genomic expression
                                                                                                                             MCNALLY, Francis J
                                                                                                                                                                            KOBAYASHI, Ryuji
                                                                                                                                                                                                             STILLMAN,
FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blood
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                                                                                                                                                                                         MAN, Bruce
, Stephen P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47.4; DB Pred. No. 0.043;
                                                REPLICATION COMPLEX GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 176; Indels
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                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08484106 Patent No. 5614618
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Best Local S
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15:
                                APPLICANT: LI, JOACHIM J
APPLICANT: GAVIN, Kinberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2504 base pairs
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ATTORREY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                           APPLICANT:
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                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATAGCTTTTATGCTATCCCAGCAAGTT 2190
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Similarity 45.5%; Pred. No. 0.044;
95; Conservative 17; Mismatches
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4 Embarcadero Center, Suite
                                                                                                                                                                                                                                       BELL, Stephen P
KOBAYASHI, Ryuji
                                                                                                                                         HERSKOWITZ, Ira
                                                                                                                                                                                MCNALLY, Francis J
                                                                                                                                                                                                RINE, Jasper
FOSS, Margit
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                                                                                                                                                       LAURENSON, Patricia
                      FLEHR,
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  HOHBACH, TEST, ALBRITTON & HERBERT Jero Center, Suite 3400
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US-08-323-170B-1/c
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                         APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1631 gtttatcatttgtgataatatcacaaatt 1659
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ATTORNEY/AGENT INFO
NAME: Osman Ph.I
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                     ZIP: 94111-3834
                                                                                                      COUNTRY:
                                                                                                                              STATE:
                                                                                                                                                 CITY: San Francisco
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAATAGAAGTAGTAGTATCKKWWTWWWYWYKYKTTTWYWKYTTYKTTWTCATGGGCAAA 2339
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                                                                                                                            California
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45.5%;
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Pred. No.
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6483 GGTTTTAATGAAAA 6470
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                                                                                                                                           6603 TTATCAAAAGTAAAAATTCGATTTCCATAAACCCCTTTCAAAGCTAAACTAATAGATACT
                                                                                                                                                                                    1630
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LENGTH: 9636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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APPLICATION NUMBER: US 08/010,409
ETLING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                          agtitatcattigtgataatatcacaaattataccitgtatigcccaatiittiatgggca 1689
                                                                                                                                                                                                                                                                                                                  cttattcattattcagtaatctttta--tatgcatactattgtaaatgtttcatcattag 1569
                                                                                                                                                                                                                                                                                                                                                                                         tttgtgaaaaaaaa 1763
                                                                                                                                                                                                                                                       gccatgaatagtttcgtttgttattatcatcattatcaacttgtcctattttattctaac 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catccttctaataactaattttagctaacaaatatatagtatgtaggaaataattactgt 1451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGTATCTTGTTTTATTGGAGGTATAAAAAAACTAATTCCTTCTCCTTTTTTTCCATTT
                                                                                                                                                                                                                                                                                                                                                                    TGTGAAATCA -- CATAATTTAAATGAATTTTCTGATACATTTTTCCTAACAAAAATATAT 6724
                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAGTGCACTTTTTTTCTTTTACTTGACTATTTAATTCCATTAATGAAGTCGAACCTGT 6782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAAATATAGCAAAACCTTTAGGACATTTCAATCCAAAAATATCTCCTTTTTTAATTTT 6842
                                                                                                                                                                                                                                                                                             TCATTTTTTTCTTTTCCTATAACTTTAATATCATTATTGTTATCATCAAAAACTAATGAT 6484
                                                                                                       tcatttcctattctgtaaacaattcacttatttgcattattgcaattaaaaagtatttca 1749
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Best Local Similarity 52.3%;
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
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LENGTH: 5181 base pairs
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                    1756 aaaaaaaaaaaaaa 1770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 143
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                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: signopology: linear
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de Taisne, Charles
Tine, John A.
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11-JUN-1993
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Search completed: April 16, 2000, 04:35:02 Job time: 9676 sec

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Title:
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SUMMARIES

23 4		No.	Result		
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williams, S.A., Lizotte-Waniewski, M., Laney, S. and Genes expressed in molting L3 larvae of Onchocerca Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi: Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences Smith College Department of Biological Sciences College, Northampton, MA, 01063, USA
Tel: 413853386
Fax: 4135853786
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Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                       AII11196 665 bp mRNA EST: 31-AUG-1998 SWOV3MCA1232SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVmL3) Onchocerca volvulus cDNA clone SWOV3MCA1232 5',
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AA655023 SWOV3MCAM
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                                           ggatggtggaccaaccagttcaactagttatcatttggtcagccagtttatca
                                                                                                                                                                                    aacaactgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtgcatatcg
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                          TGATGGTGGACCATCCGGACAACCTGTTCAATTTGCTACCATTGGTCAACCAGTGT-CCA
                                                                                                                            ATCAGTTGTTGTCATCTCATTCCATCCATTGTTTGTGACAAAAGTTGATCGAGCATATCG
                                                                                                       AATGACAACTGCATTTGCAACACAAATTGTCCCGATGCCTGTATGCCGATATGAGATTCT
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//lab_host="XII-Blue 
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/dev_stage="molting"
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/db_xref="taxon:6282"
/clone="8y003M(A1232"
/clone_1ib="Onchocerca volvulus molting L3 larva
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Pred. No. 1.1e-
0; Mismatches
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                                                                                                                                                                                                       Local
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                                                                            TACTGATATTATCATGCTTCGGTTAATAAGCGTATTGCTATTTATCACTGCTGTAAATGC 115
                                                                                                                                                                               453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes expressed in molting L3 larvae of Onchoc Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Sep 19, 1997 this sequence version replaced gi:1517220 Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWOV3MCA1144SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCA1144 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Filarioidea;
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                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Eco RI; Site_2: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Eco 
                                                                                                                                                                                                                                                                                                                               slustigm@nybc.org)."
121 c 125 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The
                                                                                                                                                                                                                                                                                                                                                                            library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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                                                                                                                                                                          Score 373.8; DB 3
Pred. No. 4.3e-65;
D; Mismatches 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggatggtggaccaaccggtcaaccagttcaatttgctattcatttggtcagcc--agtttat 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aatcacaactgcttttcaaactcaaattgtcccgatgccagtatgccgttatgaaatttt 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATACAATGCTTTTACATGGAAGCTGATAAGACAGTTAGCGCTCAACTTGAAGTTTCCGA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aacaactgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtgcatatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes expressed in molting L3 larvae of Onchocerca volvulu
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797212.
Contact: Steven A. Williams
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SWOV3MCAM12G08SK Onchocerca volvulus
(SL96MLW-OvmL3) Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                    Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
                                                                                                                                                                                                                                                                                                                                                            Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Filarioidea; Onchocercidae; Onchocerca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Onchocerca volvulus.
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                                                                                                                                                                                                                                                                                 primer: pBluescript SK.
                                                                                                                                                                                                                                                                                                            genome@smith.edu
                                                                                                                        /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOv3MCAM12G08"
                     /dev_stage="molting L3"
/lab_host="XL1-Blue MRF"
                                                                           (SL96MLW-OvmL3)"
                                                                                                /clone_lib="Onchocerca volvulus molting L3
/note="Vector: Lambda Uni-ZAP
                                                                                                                                                                                                         /organism="Onchocerca volvulus"
                                                                                                                                                                                                                                                   Location/Qualifiers
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XR; Site_1: Eco RI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                              acatggaagctgataaaacagttagtgcacagattgaggtatctgaaatcacaactgctt 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tttcgtttcatccattatttgttaccaaagttgatcgtgcatatcgagtacaatgctttt 533
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                                                                                                                                                                                                                                                                 TTGCAACACAAATTGTACCGATGCCTGTATGCCGATATGAGATTCTTGATGGTGGACCAT
                                                                                                                                                                                                                                                                                                                                                                      ACATGGAAGCTGATAAGACAGTTAGCGCTCAACTTGAAGTTTCCGAAATGACAACTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTCATTCCATCCATTGTTGTGACAAAAGTTGATCGAGCATATCGAATACAATGCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTTCGGTTAATAAGCGTATTGCTATTTATCACTGCTGTAAATGCTATTCCGGTTGATA
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AA618895 672 bp mRNA EST 12-NOV SWOV3MCA1879SK Onchocerca volvulus molting L3 larva cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.8%;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                    103
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   CGATCAGGCAGGATGCCGAAATGATGAAGGTGGACGTCAGGTAGCCGGAATTGAACTTCC
                                                                                                                                         TACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATGTATACGTGAAAGGCTTATA
                                                                                                                                                                                                                                                                                       TATTCCGGTTGATAACGGTGTAGAAGGTGAACCACAAATTGAATGTGGTCCAACATCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                TACTGATATTATCATGCTTCGGTTAATAAGCGTATTGCTATTTATCACTGCTGTAAATGC 162
                                     tgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaattttcacttcc
                                                                                                                                                                                  ttctgaaatgatgattcgtcttattgctttctgtactacacttattgcattgtcttattc 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439;
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1 (bases 1 to 672)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes expressed in molting L3 larvae of Onchocerca volvulu
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405188.
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                          Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853726
                                                                                                                                                                                                                                                                                                                                     Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I genes expressed in molting L3 larvae of Onchocerca Unpublished (1997) On Oct 30, 1997 this sequence version replaced gi:
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
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ll: genome@smith.edu
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Brugia malayi
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Filarioidea; Onchocercidae; Brugia.
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SW3D9CA349SK Brugia malayi L3 molting-day 9 larva cDNI
(SAW97NLW-BmL3d9) Brugia malayi cDNA clone SW3D9CA349
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a 106 c 138 g 178 t 1 others
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                                                                                    atatcattgatgtacgaactgatatcaacacccttgaaattagcgatgataatcaagctt 1142
                                                                                                                                                                                                                                                                                                                                                                                     caaaacctgctgcagctgcgcaacttcgtttactcaagaaaagatctgcagaaccggaga 1082
                       gcattgcattgattgctgccgtcattattaccattttcgtttaaatttcgtccaaatcaga 1322
                                                                                                                                                                                TACCAGTTGACTTACGTCATCGTGCACGTTTGCATCTCGGTGGACAACCAGTGGTACTCG
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Smith College Department of Biological Sciences
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Unpublished (1997)
On May 5, 1995 this sequence version replaced gi:797827
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biological Sciences, C. College, Northampton, MA, 01063, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="third stage larvae, nine days after infection"
/lab_host="p. coli xll-Blue MRF'"
/note="vector: LambdaZap II (UniZAP XR); Site_1: Eco RI
(5' end); Site_2: Xho I (3' end); Brugia malayi is a
lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi
isolated from the peritoneal cavity of jirds nine days
after infection. The mRNA was converted to double
stranded cDNA using reverse transcriptase and oligo (dT)
followed by Rnase H and DNApol I. The library was
constructed by Michelle Lizotte-Waniewski. The library is
available from the Filarial Genome Project Resource
Center: contact Dr. S.A. Williams, Clark Sclence Center,
Smith College, Northampton, MA 01063 USA phone +1 413
585-3826 fax +1 413 585-3786 email genome@smith.edu"

07 a 174 c 139 g 243 t 13 others
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(SAW97MLW-BmL3d9)"
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/db_xref="taxon:6279"
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Pred. No. 8.7e-58;
0; Mismatches 120;
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Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
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Seq primer: pBluescript SK
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   157
                                                                                            //dev_stage="molting L3"
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//lab_host="XL1-Blue MRF/"
//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
//note="Vector And Lambda Uni-Zap XR vector and has 1 x 10E6 independent
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a 102 c 106 g
                                                                         The library is available from
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                                                                         Dr. Sara Lustigman (email:
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Query Match Best Local Similarity

17.7%; 78.9%;

Score 314; DB 37; Pred. No. 3.7e-53;

Length 537;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374;
                                                                                                                                                                                  Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                               AI322068 552 bp mknn sWOv3MCAM12A04SK Onchocerca volvulus molting L3 larva cDNA creakuru-nvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM12A04 5',
                                                                                                                                                                                                                                                   Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797124.
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                          Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
                                                                                                                                                                                                                                                                                                                                                                                                 AI322068
AI322068.1 GI:4056219
                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                     (bases 1 to 552)
                                                                                                                                primer: pBluescript SK.
   Location/Qualifiers
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                                                                                                                                                           genome@smith.edu
                                                                      /db_xref="taxon:6282"
           /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                       (SL96MLW-OVML3)"
                                                  /clone_lib="Onchocerca volvulus molting
                                                               /clone="SWOv3MCAM12A04"
                                                                                                        /organism="Onchocerca volvulus"
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Lambda Uni-ZAP XR;
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Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XX vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigmanybc.org)."
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DEFINITION
                                          KEYWORDS
                                                                         ACCESSION
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                          mRNA sequence.
AI317885
AI317885.1 GI:
EST.
Onchocerca volv
                                                                                                AI317885 615 bp mRNA EST 17-DEC-1998 SWOVJMCAM06H125K Onchocerca volvulus molting L3 larva cDNA SWOVJMCAW06H25 Onchocerca volvulus cDNA clone SWOVJMCAM06H12
             Onchocerca
 Eukaryota;
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 Metazoa; Nematoda;
                             volvulus.
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Secernentea; Spiruria; Spirurida;
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                                                                                                                                                                                                                                                                                                                                                aacaa-ctgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtgcatatc 518
                                                                                                           atttgattcatgcaatgttgcgcgtacacgatctctgaatccacgtggtattttttgtaac 459
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                                                                                                                                                                                                  tgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcacttcc 399
                                                                                                                                                                                                                                                           TACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATGTATACGTGAAAGGCTTATA 237
ATCAAGTTGTTGTCATCTCATTCCATCCATTGTTTGTGACAAAAGTTGATCGAGCATATC
                                                                                  GTTTGATTCCTGTAATGTAGCACGTACACGTTCGTTAAATCCACGTGGTATTTTTTGTCAC
                                                                                                                                                                         CGATCAGGCAGGATGCCGAAATGATGAAGGTGGACGTCAGGTAGCCGGAATTGAACTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                         TACTGATATTATCATGCTTCGGTTAATAAGCGTAGGGCTATTTATCACTGCTGTAAATGC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Steven A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 4135853786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            slustigm@nybc.org)."
124 c 123 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR;
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(SL96MLW-OvmL3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Underwood,K. and Marra,M.
Molecular Parasicology OvmL3
Unpublished (1998)
On Jan 19, 1998 this sequence version replaced
Contact: Steven A. Williams
Volume of the contact 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams, S.A., Lizotte-Waniewski, M., Laney, S., Lustigman, Hillier, L., Allen, M., Bowles, L., Gelsel, S., Jost, S., Kuca Martin, J., Steptoe, M., Theising, B., White, Y., Wylie, T., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                College, Northampton, Tel: 4135853826 Fax: 4135853786
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1 (bases 1 to 531)
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                                     /dev_stage="moiting L3"
/lab_host="XL1-Blue MRF/"
/lab_host="XL1-Blue MRF/"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1: Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
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/db_xref="taxon:6282"
/clone="onch17"
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SWOv3MCAM03B05
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                                                                                                                                                                                                                                         sequence.
AA625020
AA625020.1 GI:2537422
EST.
Onchocerca volvulus.
Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda; Secernentea;
           College, Northampton, MA, Tel: 4135853826 Fax: 4135853786
                                                                                                                   Genes expressed in molting L3
Unpublished (1997)
On May 9, 1995 this sequence v
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                       AA625020 363 bp mRNA EST 12-NOV-1997
SWOV3MCA691SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO691 5', mRNA
                                                                Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
                                                                                                                                                                                           Williams, S.A., Lizotte-Waniewski, M.,
                                                                                                                                                                                                            Filarioidea; Onchocercidae; Onchocerca.
1 (bases 1 to 363)
Email: genome@smith.edu
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Pred. No. 6.4e-49;
0; Mismatches 99
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                                                                    Clark Science Center,
                                                                                                                                                                        Laney, S. and Lustigman, S. of Onchocerca volvulus
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                   sequence.
AA625024
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                                                    (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

a 71 c 77 g 110 t 1 others
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/lab_host="XL1-Blue MRF'"
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(SL96MLW-OvmL3)"
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/db_xref="taxon:6282"
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273 GNTTGATTCCTGTAATGTAGCACGTACACGTTCGTTANNTCCACGTGGTATTGTTGTCAC
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nes 327; Conservative
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                                                                                            CGATCAGGCAGGATGCCGAAATGATGAAGGTGGACGTCAGGTNGCCGGAATTGACCTTCC
                                                                                                                     tgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcacttcc 399
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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On May 9, 1995 this sequence version replaced g1:802407
Contact: Steven A. Williams
Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome@smith.edu
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//lab_host=="XLI-Blue MRF'"

//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho i; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2 or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded CDNA using
reverse transcriptase and ollgo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is -1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
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/clone_lib="Onchocerca volvulus molting L3
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/db_xref="taxon:6282"
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Pred. No. 3e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jan 19, 1998 this sequence version replaced g1:2285052. Contact: Blaxter ML Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Labs, King's Buildings, West Mains Road, Edinburg 3JT, UK. 131 650 6760 Tel: +44 131 650 6760 Fax: +44 131 670 5450
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MB3D6AA4G10T3 Brugia malayi day 6 post-infection third stage larvae
SAW96MLW-BmL3d6 Brugia malayi cDNA clone 3D6AA4G10 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The ABI trace of this sequence can be viewed at http://www.sanger.ac.uk/brugia/3D6/MB3D6AA4G10T3.html Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mark.blaxter@ed.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Jones, S.J.
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             105
/dev_stage="third stage larvae, six days after infection"
/lab_host="E. coli XLI-Blue"
/note="Vector: lambdaZapII (Unizap XR); Site_1: Eco R I
(5' end); Site_2: Xho I (3' end); Brugia malayi is a
lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi isolated
from the peritoneal cavity of jirds six days after
infection. The mRNA was converted to double stranded cDNA
using reverse transcriptase and oligo(dT) followed by
RNase H and DNApol I. The library had 2 x 10E5 independent
recombinants and average insert size was 900 base pairs.
The library was constructed by Michelle Lizotte-Waniewski.
The library is available from The Filarial Genome Project
Resource Center: Smith College, Northampton, MA 01063 USA phone +1
413 585 3826 fax +1 413 585 3786 email genome@smith.edu."
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="mixed"
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larvae SAW96MLW-BmL3d6"
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/strain="TRS Labs"
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On Sep 12, 1996 this sequence version replaced gi:1405277.
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, S
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Onchocerca volvulus
Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea;
Charonidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA618952 459 bp mRNA EST 12-NOV-1997 SWOV3MCA2020SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO2020 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                     Fax: 4135853786
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primer: pBluescript
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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by
                                                                                                             /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                 /clone_lib="Onchocerca volvulus
(SL96MLW-OvmL3)"
                                                                                                                                                                                       /clone="SWmL3C02020"
                                                                                                                                                                                                     /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                             /organism="Onchocerca volvulus"
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Matches 318; Conservative
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Unpublished (1997)
On May 9, 1995 this sequence version repl
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sc
Department of Biological Sciences, Clark
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                           Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea;
Filarioidea; Onchocercidae; Onchocerca.
1 (bases 1 to 395)
                                                                                                                                                                                                                                                                                                                                                           AA625010 395 bp mRNA EST 12-NO SWOV_MCA318SK Onchocerca volvulus molting L3 larva cDNA
                                                                                                                                            Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
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a 85 c 91 g 150 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6000 molting larvae (mL3),2000 larvae from day 1,
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77.88;
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Pred. No. 2.7e-43;
0; Mismatches 91;
                                                                                                          version replaced
                                                                                                                                                                                                                                                                                                                                            cDNA clone
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                                   acaatgttcagaaccacaaggattcggagctgttaaaacaggtggtgccgcagcaaaacc 1029
                                                                                   Email: genome@smith.edu
Seq primer: pBluescript
                                                                                                                                                                                                                                                  118
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                             /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                r: pBluescript SK.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              clone="SWmL3CO318"
                                                                                                                                                                                                              14.6%;
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Search completed: April 16, 2000, 03:08:58 Job time: 6182 sec

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                                                                                                                                                                                                                                                                                                                                                 Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                            Genes expressed in molting L3 larvae of Onchocerca volvulu
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405277.
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onchocerca volvulus.
Onchocerca volvulus
Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Onchocerca.
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AA618952
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                                                                                                                                                                                                                                                                                                                                  Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular Parasitology
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EST. .
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                                                                                                                                                                                                                                                                            Conservative
/dev_stage="moiting L3"
/lab_host="xL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O; volvulus molt to fourth-stage larvae by
                                                                                                                                                         /clone_lib="Onchocerca volvulus molting L3 larva
(SL96MLW-OvmL3)"
                                                                                                                                                                                                         /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                       /clone="SWmL3CO2020"
                                                                                                                                                                                                                                            /organism="Onchocerca volvulus"
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Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826 Fax: 4135853786
                                                                                                    Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae Unpublished (1997) on May 9, 1995 this sequence version Contact: Steven A. Williams
                                                                                                                                                                                                                                                                Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                      AA625010 395 bp mRNA EST 12-NOV-1997 SWOV3MCA318SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVmL3) Onchocerca volvulus cDNA clone SWmL3CO318 5',
                                                                                          Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                         GI:2537412
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Pred. No. 2.7e-43;
0; Mismatches 91;
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seq primer: pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
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Cameroon (forest strain). The L3 were cultured in 20% FCS
Cameroon (forest strain). The L3 were cultured in 20% FCS
Cameroon (forest strain). The L1 were day 1, 2, or 3 in
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in IMDM+ NCTC 135 and collected after form approximately
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Search completed: April 16, 2000, 03:08:58 Job time: 6182 sec

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Query length: 1779
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Database sequences: 188963
Database length: 23686106
Search time (sec): 139.2000
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_Geneseq_36:P81184
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Bovine peptidyl-glycine alpha-a
Newcastle disease virus immunog
Newcastle disease virus glycopu
Haematopoietin receptor Hu-B1.2
Haematopoietin receptor Hu-B1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus terreus triol poly Protein encoded by sequence whi Type B alpha amidating enzyme. Bacillus thuringiensis PS167P Nematode toxin 167P protein. B Nematocidal toxin 167P. New Ba
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GAP protein Ira2. Blocking Ras

Enzyme involved in eicosapenta

S. putrefaciens EPO biosynthes

Lambda gt10ch2 encoded C-termin

Lambda gt10ch201 encoded C-termin

Lambda gt10ch201 encoded C-termin
Candida albicans histidine Mouse protease-activated rec Human secreted protein clone
                                                                                                                                                                                                                                                                                                                                                                                                                     Segment of desmosomal cadherin, C-terminal amidation enzyme. cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast transcription regulatory
Biosynthetic enzyme of icosape
Sequence of human bone proteogl
Feline infectious peritonitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human neurotrophic biglycan. pa
Expression plasmid pUCPIC1799 :
C-terminal prepro-C-terminal al
Peptidyl C-terminal alpha-amida
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Bovine neurotrophic biglycan. I
Rat neurotrophic biglycan. Pro
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                                                                                 Oat phytochrome A apoprotein Carbamoyl-phosphate-synthetas
                                                                                                                1367
                                                        548
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seq_documentation_block:

ID R20112 standard; Protein; 935 AA AC R20112;

DT 06-APR-1992 (first entry)
DE AE-III (peptidylhydroxyglycine N Amidation; PHL.
OS Xenopus laevis. Location/Qualifit FT protein 1.935
FT 1.935
FT 1.935
FT 1.935
FT 2.9465404-A.
PD 08-7AN-1992
PP 01-7UN-1990; JP-141678.
PP 01-7UN-1990; JP-141678.
PR 10-AUG-1990; JP-210535.
PR 10-AUG-1990; JP-229911.
PA (CIBA) CIBA GEIGY AG.
PI Iwasaki Y, Shimoi H, Suzuki K, G FI Kawahara T, Kangawa K;
DR WPI; 92-010570/02.
PR Novel DNA encoding peptidyl hydroused to prepare PHL which can be peptide(s) e.g. human calcitonin PS (Laim 4; Page 18; 28pp; English. CC The sequence was deduced from a (PERM BP-3172). The vector servence comprise only residues 383-706 or reaction: R-GlyOH -> R.NH2. It camidated C-termini, e.g. calcito SQ Sequence 935 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_36:R06426
A_Geneseq_36:R11110
A_Geneseq_36:R10322
A_Geneseq_36:R80530
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US-09-323-427-2/rev x R20112
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                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: R20112 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                   1467 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel DNA encoding peptidyl hydroxy:glycine N-C lyase (PHL) - used to prepare PHL which can be used in the amidation of peptide(s) e.g. human calcitonin.

Claim 4; Page 18; 28pp; English.

The sequence was deduced from a CDNA insert from pAE-III-202-4 (PERM BP-3172). The vector serves as a source for a DNA fragment encoding PHL for the construction of an expression vector for the prepn. of recombinant PHL. The protein may be truncated to comprise only residues 383-706 or 383-713. The PHL catalyses the meadated C-termini, e.g. calcitonin, growth hormone, LH-RH.
                                                                                                                                                           542 lAlaAspGlyTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amidated C-termini, e.g. calcitonin, Sequence 935 AA;
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                                  AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                     TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1468
                                                                                                                        ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                                                                                                 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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/note=_"including
383..935
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Gaps: 18
Percent Identity: 19.437
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! В. sphaericus SLP. Host cel
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nPheValLys...GlnIleLysHisGinGluPheGlyArgGluValPheA 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aspargGluasnGly...argIleGlnCysPheH1salaGluThrGlyAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGT.....
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                                                                                                                                                                                                  TGATATCAACACCCTTGAA.....ATTAGCGATGATAATCAAGCTT 638
                                                                                                                                                                                                                                    alGluLysGlnThrGlnGluLysGlnGlnLys......GlnLysAsnSer
                                                                                                                                                                                                                                                                                                                                                                      rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV 742
                                                                                                 lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGly
                                                                                                                                                                      aGlyValProThrGlnGluLysGlnAsnValValGlnGluSerSerAlaG
                                                                                                                                                                                                                                                           GCA......GAACCGGAGAATATCATT...GATGTACGAAC 679
                                                                   GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT 538
                                                                                                                                   TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCT 588
CTCAATGTTTATGGGTTTAAGCATTGCATTGATT...GCTGCCGTCATTA 491
                                  ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVa
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p81184 standard; Protein; 1594 AP
P81184;
AC P81186;
AC P91186;
AC P91186;
AC P81188;
AC P81188;
AC P81188;
AC P81188;
AC P81188;
AC P81188;
AC P81189;
AC P81189;
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US-09-323-427-2/rev x P81184
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Vaccine; peplomeric protein; E2 gene.
Feline infectious peritonitis virus.
Ep-264999-A.
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WPI; 88-114147/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1586 ACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGA 1537
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                                                                                                            1386 ACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCAC 1337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuLysGluLysGluLeuAsnGluMetVal.....valGlyLeuLe 92
                                                                                                                                                                                                                              uArgLysGlyLysLeuLeuIleArgAsnAsnGlyLysLeuLeuAsnPheG 109
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27
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671 396	712CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA	
713 380	761 GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGAT. ::: ::::::::::::::::::::::::::::::	
762 363	811 CACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCC ::: ::	
812 348	852 CAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGAC :::: ::: ::::::::: 333 laLeuLeuProGlyAsnThrValLeuHisMetLeuThrLysValPhe	
853 333	CACAGCTTTTCTATCAATGCCAGAT	
894 316	TTTAATGGCTGGCCAAGAAGCTCACGTATAC:::	
944 312	993 GGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATA ::: :::::::: ::: 298 erGlyMetMetThrLeuLeuGlnLeuIleLeuValValValLeu	
994 298	1036TIGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGT	😐
281	265 SerProProTh	
64	078AATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGG !!! !:: ::: 248 snMetGly***CysAla***LeuLysIleAlaIleLeuThrMetAsnAsn	یس ب
1079 248	he***A	<u> </u>
1083 231	2 GACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTAT ::: ::::: ::::: :: ::::: 5 MetHisValValAsnHisTyrTyrPheMetCysMetValSerLeuLeuVa	<u> </u>
1133 214	1141GGATGGTG	₩.
1142 198	CAGTATGCCGTTATGAAATTT	<u></u>
1163 181	1201 AAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGC	<u> </u>
1202 164	1245 CATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTG ::	_
1246 148	1291TATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTA :::::::::::::::::::::::::::::::::	μ
1292 131	1336 GTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCAT	н-

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seq_documentation_block:

ID R87953 standard; Protein; 332 AA AC R87953;

DT 20-MAR-1996 (first entry)

DE Bovine neurotrophic biglycan.

KW Biglycan; proteoglycan; chondroi

KW neurotrophic; central nervous sy

learning.

OS Bos taurus.

Location/Qualifi

FT region 7. 23

FT region /label= Hypervar

PN W09530432-Al.

PD 16-NOV-1994; E01479.

PF 09-MAY-1994; WO-E01479.

PF 09-MAY-1994; WO-E01479.

PA (BOEF ) BOEHRINGER MANNHEIM GMB;

PI Hasenoehrl R, Huston J, Jungha

MPI; 95-403938/51.

PT proteoglycan cpds., partic. chor

PT memory deficit(s) in the elderl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: A_Geneseq_36:R87953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R87953;
R87953
Mueller HW; 95-403938/51. WPI; 95-403938/51. Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia
                                                                                                                                                                                                           W09530432-A1.
16-NOV-1995.
09-MAY-1994; E01479.
09-MAY-1994; WO-E01479.
(BOEF ) BOEHRINGER MANNHEIM GMBH.
Hasenoehrl R, Huston J, Junghans U,
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percent Similarity:
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Bovine biglycan (R87953) is a chondroitin sulphate proteoglycan with Bovine biglycan (R87953) is a chondroitin sulphate proteoglycan with Bovine biglycan (R87953) is a chondroit. It can be used to enhance neurotrophic activity for brain neurons. It can also be used for restore function nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients with damaging and selections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 568
                                                                                                                                                                                                                                                                                                                                                                lGluLeuArgIleHisAspAsnArgIleArgLysValProLysGlyValP 143
                                                                                                                                                                                                                                                                                                                                                                                                  CCAAATCAGAAGGCATAAAAATAATGTTAGA.....ATCA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT 468
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                                                                                                                                               rLeuArgIleSerGluAlaLys......LeuThrG
                                                                                                                                                                                 TATATTCGTTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAA 358
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                                                                                                         ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC
LeuAspHisAsnLysIleGlnAlaIleGluLeuGluAspLeuLeuArgTy
                                     ATCARAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA
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seq_documentation_block:
ID R87951 standard; Prot
AC R87951 standard; Prot
AC R87951 proteoglyca
AC R87951 proteoglyca
AC R87951 proteoglyca
AC Ratus sp. Locat
AC RATUS Sp. Masenoehrl R. Huston
AC Ratus sp. Masenoehrl R. Huston
AC Ratus sp. Masenoehrl R. Huston
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AC Cand function of CNS r
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SQ Seguence 369 AA;
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CC neurotrophic activity for brain neurons. Recombinant biglycan, concluded to encoding cona (T08768) in eukaryotic host could be used to enhance the survival and maintain the structure cand function of CNS neurons during normal ageing as well as after and function of CNS neurons during normal ageing as well as after complete the survival and manage. It can also compatible the complete compatible the complete compatible the compatible that the compatible
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US-09-323-427-2/rev x R87951
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Align seg 1/1 to:

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775 AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA 726

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seq_name: A_Geneseq_36:R87952
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seq_documentation_block:

ID R87952 standard; Protein; 369 AA AC R87952;
DT 20-MAR-1996 (first entry)
DE Human neurotrophic biglycan.
KW Biglycan; proteoglycan; chondroi
KW neurotrophic; central nervous sy
KW learning.

OS Homo sapiens.
FH Key 1..37
FT region /label= Sig_pept
FT region /label= Hypervar
PN W09530432-Al.
16-NOV-1995.
PF 09-MAY-1994; E01479.
PD 09-MAY-1994; WO-E01479.
PP 09-MAY-1994; WO-E01479.
PF NOWAY-1994; WO-E01479.
PF NOWAY-1994; Wo-E01479.
PF PO-WAY-1994; Wo-E01479.
PF PO-WAY-1994; Wo-E01479.
PF PO-WAY-1994; Wo-E01479.
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PF PO-WAY-1994; Wo-E01479.
PF CO-WAY-1994; Wo-E01479.
PF O-WAY-1994; Wo-E01479.
PF CO-WAY-1994; Wo-E01479.
PF CO-WAY-1995; English.
PF CO-WAY-1994; Wo-E01479.
PF CO-WAY-1994; WO-E01479.
PF CO-WAY-1995; English.
PF CO-WAY-1994; Wo-E01479.
PF CO-WAY-1994; WO-E01479.
PF CO-WAY-1995; English.
PF CO-WAY-1994; Wo-E01479.
PF CO-WAY-1995; English.
PF CO-WAY-1994; Wo-E01479.
PF CO-WAY-1995; English.
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US-09-323-427-2/rev x R87952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia Claim 3; Fig 8; 60pp; English.

Human biglycan (R87952) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve-learning efficiency and memory in the elderly and in patient with demenria.
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                                                                                                                                                                                                                                                                                                                                                                           137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1994; WO-E01479.
09-MAY-1994; WO-E01479.
(BOEF) BOEHRINGER MANNHEIM GMBH.
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Biglycan; proteoglycan; chondroitin sulphate; neuron protection; neurotrophic; central nervous system; CNS; memory loss; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 LysGluIleSerProAspThrThrLeuLeuAspLeuGlnAsnAsnAspIl 103
GCATTGCATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT
                                                                                                                                         AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAA 518
                                                                                                                                                                                                                       sAsnHisLeuValGluIleProProAsn....
                                                                                                                                                                                                                                                                                  CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 568
                                                                                                                                                                                                                                                                                                                                                     ProLeuArg.....LysLeuGlnLysLeuTyrIleSerLy 148
                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA
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/label= Hypervariable_region
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Gaps: 13
Percent Identity: 20.401
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Seed of the seed o	180 421 197 407 21: 35: 25 25 26 26 27 27 27 28 28 28 28 28 29 30 30 30 30 30 30 30 30 30 30 30 30 30	158 46 16
p94856 standard; protein; 693 AA. p94856; p94856; p27-JUN-1990 (first entry) p27-JUN-1990 (first entry) p27-JUN-1990 (first entry) p27-JUN-1990 (protein; 693 AA. p27-JUN-1989; pAX799; alpha amide; ds. synthetic. synthetic. p29790-A. 18-JUN-1989; J0-17184. 15-JUL-1987; JP-306867. 15-JUL-1987; JP-306867. 15-JUL-1987; JP-306867. 15-DEC-1987; JP-306867. 15-DEC-1987; JP-306867. 16-DEC-1987; JP-306867. 17-JUL-1988; Suntony Ltd. 17-JUL-1988; J0-17279/03. N-PSDB; N94527. Recombinant C terminal alpha amidating enzymes of Xenopus laevis on their precursors deoxyribonucleic acid encoding sequences. Althouries of Xenopus laevis on their precursors deoxyribonucleic acid encoding sequences. and their precursors deoxyribonucleic acid encoding sequences. bisclosure; 7pp; English. pisclosure; 7pp	GluAsnSerGlyPheGluProGlyAlaPheAspGly TATATTCGTTTCTTCTTATCATCCTTCTAATAACTI ::::::::!!! **TLEUARTGIATGTAGGAAATAATTACTGTAATACTI ::!!! **TLEUARTGIATGTAGGAAATAATTACTGTAATACAI ::::::::!!! **TLEUARTAGTATGTAGGAAATAATTACTGTAATACAI ::::::::!!! **TCAAAACTTCTTCTATCGCTTTTATAGCTTTCTAAAACI TLEUASPHISASNLYSILEGINALaIlEGIULEUGI 7*TCAGTAATCTTTTATGCATACTATTGTAAATG 1!!! **::::::::::::::::::::::::::::::::	8

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US-09-323-427-2/rev x P94856
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Percent Similarity:
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seq_name: A_Geneseq_36:P94854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1467 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also N93060.
Sequence 693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1417 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1367 AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA..... 1323
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513 Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl 528
                                                                                                                                                                                                                                                                                                                                                1183 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 1134
                                                                                                                                                                                                                                                                                                                                                                                                        1230 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 545
                                                                                                                                                                                                                                                                             1133 GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 1084
                                                                                                                                                                                                                                                                                                                                                                            : |||::: |||||::: :::|||:::
577 uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 593
                                                                                                                                                                                                                                  1083 TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTG 1034
                                                                                                                                                                         1033 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 984
                                                                                                                                                                                                                                                             ||| :::|||::: |||:::|| || 600 Gly......valLeuTyrAlaValAsnGlyLysProTyrTy 611
                                                                                                                                                                                                                                                                                                                       629 .....IleLeuAspThrPheIleProAlaArgLysAsnPh
                                                                                                                  983 AATGCTGATGGATGTGCTCTTGATAAATATTTG......CTAAATAATTT 940
                                                          939 GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC 894
                             640 eGluMetProHisAspIleAlaAlaGlyAspAspGlyThrValTyr 655
                                                                                                                                                Quality:
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0.945
43.103
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Gaps: 12
Percent Identity: 21.552
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seq_documentation_block:

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alignment_scores:
Quality:
Ratio:
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EP-299790-A.
18-JAN-1989.
15-JUL-1988; 306508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546
 632 laValSerTyrAlaPro....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.

Plasmid pAx799 contains a sequence derived from Xenopus laevis. The plasmid was screened from an E coli library using plasmid pXA457 to screen a larger library.

Although the gene product is similar to that of pXA457 at the N-terminus, it has an area of hydrophobic elements suggesting a membrane function. See also N93060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUNR) Suntory Ltd.
Obsuye K, Kitano K, Tanaka S, Matsuo H, Mizuno
WPI; 89-017279/03.
N-PSDB; N90791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
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P94854;
27-JUN-1990 (first entry)
C-terminal prepro-C-terminal alpha-amidating enzyme of pxA799.
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                                                            uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA
                                                                                                                                                                                                                                                                 nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 584
                                                                                                                                                                                                                                                                                                                                                                    AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lAlaAspGlyTyr.....
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                              AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 1134
                                                                                             AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 1184
                                                                                                                                AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                                                                                              AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 1231
                                                                                                                                                                                                  leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                   ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
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Identity:
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12
21.552
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638
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alignment_block:
US-09-323-427-2/rev x R73053
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                                                                                                                                Align seg 1/1 to: R73053 from: 1
                                                                                                                                                                                                                  Percent Similarity:
                          1467 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
                                                                                                                                                                                                                                                                                                               N-FSDB; 087970.

Increasing protein prodn. from cultured animal cells - by adding a trichostatin to the medium, effective at low concn. and not injurious to host cells
Injurious to host cells
Disclosure; Page 10-15; 19pp; English.
3mu-1S cells (i.e. CHO cells expressing a peptidyl C-terminal alphamidase enzyme (AE)) were suspended in F-12 medium to which aliquots of trichostatin were added. Cells were cultured for 3 days at 37 deg and then assayed for AE. Without trichostatin, AE productivity was 708 U/ml. At 10, 50, 100 and 200 nM trichostatin, AE productivities were respectively 866, 1897, 1894 and 3359 U/ml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1133 GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 1084
546 lAlaAspGlyTyr...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1033 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1083 TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptidyl C-terminal alpha-amidating Peptidyl C-terminal alpha-amidating trichostatin; CHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FURU/) FURUKAWA K. (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R73053 standard; Protein; 875 AA. R73053;
                                                                                             TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGCTGATGGATGTGCTCTTGATAAATATTTG.....CTAAATAATTT 940
                                                              CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC 894
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                                                                                                                                                                                                                                   Ratio:
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0.945
43.103
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21.552
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Sequence of the property of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast transcription regulatory factor SRB8.
Transcription regulatory factor; suppressor of RNA polymerase SRB8; RNA polymerase II; holoenzyme; SWI/SNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        679
                                                                                                                                                                                                     06-MAR-1997.
28-AUG-1996; U14192.
31-AUG-1995; US-521872.
11-OCT-1995; US-540804.
26-JAN-1996; US-590399.
(WHED) WHITEHEAD INST BIOMEDICAL RES.
(WHED) KOLESKE AJ, Thompson CM, Young WPI; 97-179258/16.
purified RNA polymerase II holo:enzyme - comprises RNA polymerase II and one or more regulatory proteins, pref. suppressor of RNA polymerase B proteins or SWI/SNF proteins Claim 11; Fig 10a-b; 154pp; English. Claim 12; Fig 10a-b; 154pp; English. Novel yeast SRB (suppressor of RNA polymerase B) proteins SRB4, SRB5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces
W09708301-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspArgGluAsnGly...ArgIleGinCysPheHisAlaLysThrGlyGl 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG 1034
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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRB6, SRB7, SRB8, SRB9, SRB10 and SRB11 (W13821-28) are transcription regulatory factors that act as positive and negative regulators of RNA polymerase II activity, and are components of the RNA polymerase II identified using methods designed to II holoenzyme. They were identified using methods designed to Crearminal domain (CTD) function. SRB8 and SRB9 appear to repress Crearminal domain (CTD) function. SRB8 and SRB9 appear to repress CTD activity. Genomic clones (T59904-11) for the SRBs have been obtd. SRBs can be used to treat diseases resulting from alteration or SRBs can be used in in vitro transcription of DNA and to identify can also be used in in vitro transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1267 CATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTA..... 1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1103
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                                                                                                                                                                                                                                                                                                                                                                           TyrMetMetProSerLeuTyrArgLeuLeuAsnIleLeu.....
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                                                                                                                                                                                                                                                                                               TCACGTAT.....ACAAATATGCGGATCGAT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....PheSerAlaGlnLysArgValValSer 356
                                                                                                                                                                                                                           CAC...AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA 831
                                                                                                                                                                                                                                                              eulleSerSerGlyLeuLeuTyrLeuGlnAspSerAsnAspLysPheVal 400
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CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG
                                                                                                                                                 A.....ATAGCGAATGTGTTCGACCACAATGTTCAGAACCACA 793
                                                                                                                                                                                      HisvalGlnLeuLeuIleAsnLeuLysIleSerProLeuMetLysSerGl 417
                                                                                                            \verb"nTyrasnMetValLeuArgAsnValMetGluTyrAspValLysPheTyrG"
                                    luIlePheAsnPheAspGlnValValGluIleThrGluGinIleLysMet
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Ratio:
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                                                                           .GATTCGGAGCTGTTAAAAACAGGTGGTGCCGCAGCAAAACCTG
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0.393
47.648
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Gaps: 24
Percent Identity: 19.632
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                                                                                                                                                                                                                                                                                                                                                                                                                                   369
                                                        450
                   699
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	CATTATTGCAATTAAA 41 ::: ::::: nLeuIleSerLeuLys 714 A_Geneseq_36:R99462	GCATTATTGCAATTAAA 41 ::: ::::			TCAACTTGTCCTATTTTA	TTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC	SerAsnGlnAlaValGlyGlnThrTrpAsnPheProGluValPheGlnVa	SerAsnGlnAlaValGlyGlnThrTrpAsnPheProGluValPheGlnVa			TCTA :::: LysL	GTAGGAAATAATTACTG ::: ValleuLysValaspAsnAspLeuAr	.CTGCCATATATATTCGTTTCTTCTTATCATCCTTCTAATAACTAA ::: ::: ::: ::: ::: pValProAlaTyrAsnValThrSerPheMetProPheTrpLys	AAAATAATGTTAGAATCATCGAAGCAATAATAAAA 416 	11 5	ATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCG 4 ::: :: ::: ::: PIleGluSerLeuGluAlaLeuMetAsp 5	വ വ വ	AAT :: pLe	H U	98 AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 649 :::: ::: 61 nLeuSer	451 ArgIleLeuSerAsnAspIleThrAsnLeuGl 461
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seq_documentation_block:
ID R99462;
AC R99462;
DT 30-JAN-1997 (first entry)
DE Blosynthetic enzyme of icosapentaeno;
KW Icosapentaenoic acid synthase; EPA; of foodstuffs; animal feed; lipid balanc antiinflammatory; anticancer agent.
SS Shewanella putrefaciens.
PN W09621735-A1.
18-JUL-1996.
PP 13-JAN-1996; J00030.
PP 13-JAN-1996; J00030.
PP 13-JAN-1996; J00030.
PF 
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US-09-323-427-2/rev x R99462
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    Quality:
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Percent Similarity:
                                                                                                                                                       1446 TCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTG 1397
                                                                                                                                                                                                                                                                                                                           1496 ATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGG 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1545 TGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA.... 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1645 TTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATT 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1695 AATAATAACCCCCATCAAGTGGAGGAAGAAGAAGGAAGCAATCTTAGTTT 1646
            1396 CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1595 GCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAA 1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         932 ......GlnAlaAlaMetGlnLeuA 938
                                                                                                                                                                                                                                         916 IleSerIleAsnProAsnProLysValAspSerAspLeuGlnLeuLys.. 931
                                                                                                                                                                                                                                                                                                                                                                                                             899 lnLysLeuValGlnGlyThrLeuValAsnThrGluAsnGluValCysThr 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  884 pGly.....AlaargValPheValGluPheGlyProLysAsnIleLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              873 ArgPheThrSerGlnLeuGluAlaMet.....TyrAsnAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  827 ProPheAlaLysAlaIleAspAlaAlaLysPheThrLysThrSerArgAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 83-94; 145pp; English.

The DNA sequence (T34137) which encodes the biosynthetic enzymes of loosapentaenoic acid (EPA) can be used to transform Escherichia coli. The DNA sequence allows efficient microbial production of EPA, which is a raw material for drugs, agrochemicals, foods and animal feedstuffs. EPA is also useful for lipid balance correction and as an antihypertensive, antiinflammatory and anticancer agent. Sequence 2756 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of icosapentaenoic acid using transformed DNA coding for icosapentaenoic acid synthase derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JAN-1996; J00030.
13-JAN-1995; JP-004299.
(SAGA ) SAGAMI CHEM RES CENTRE.
KATO S, KONDO K, Yamada A, Yazawa WPI; 96-342288/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1997 (first entry)
Biosynthetic enzyme of icosapentaenoic acid synthase.
Icosapentaenoic acid synthase; EPA; drugs; agrochemicals;
foodstuffs; animal feed; lipid balance correction; antihypertensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; anticancer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ysIleLysAlaSerPheLysLysHis.....MetLeuGlnSerVal 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aLeuTyrSerAsnAlaThrGlyGly...LeuTyrGluSerThrAlaAlaL 859
.....GGAATTTCACTT.......CCATTTGATTCATGCAAT 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.00
0.389
46.800
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Gaps: 23
Percent Identity: 18.400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....ACA 1497
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from Shewanella
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682 GAACTGAT	71. 11 68 12	CAANGETGITCHC COLORD TO THE COLORD TO THE COLORD TO THE COLORD TO THE COLORD		TGATAAATATTTGCTAAATAATTTGGAA	998 ACTGTGGAAATTCTAAATGCTGATGGAT 998 ACTGTGGAAATTCTAAATGCTGAT 1 1 100 GATGATTATATCOMETTATGLUGINALALYSLEUALASETSETGLYV	.042 GCGC	092 GCCAGTTT	5 4 2	1192 CTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATT 1143 :: ::: ::: :: ::: ::: 1037 snalaileGlnThrargSerValValalaproValIleGluAsnGlnVal 1053		ACATGGA 124 ::: alvalG1 102	100	970 aAsnHisIleSerLysAlaThrArgAlaLysMetAlaLysSerLeuGluT 987	29	1364 GTTGCGCGTACACGATCTCTGAATCCACGTGGTATT	AspProTyrGlnAlaAsp 9
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seq_documentation_block:
ID R05159; standard; prot
AC R05159; standard; prot
AC R05159; (first e
DT 09-CCT-1990 (first e
DT 17-APR-1990 (first e
DT 17-APR-1990 (first e
DT 3-NOV-1989; US-432044 (first e
DT 3-NOV-1989; US-432044 (first e
DT 4-APR-1990 (first e
DT 17-APR-1990 (first e
DT 18-CT 1
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Quality:
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US-09-323-427-2/rev x R05159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: R05159 from: 1 to: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              582 ACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 TGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bone matrix DNA and proteins used in detection, diagnosis and treatment involving skeletal and/or connective tissue disease states.

and/or connective tissue disease states.

pisclosure; p: English.

probes and Abs raised to the proteins can be used to determine probes and Abs raised to the proteins can be used to determine their levels useful in diagnosis of associated conective tissue their levels useful in diagnosis of sosteo/rheumatoid arthritis, diseases states such as osteoporosis, osteo/rheumatoid arthritis, paget's disease, artherosclerosis and periodontal disease.

Proteins may also be used to induce or block biological function. Sequence 368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of human bone proteoglycan I (biglycan).
Osteoporosis; rheumatoid arthritis; Paget's disease;
atherosclerosis; periodontal; human bone matrix; proteoglycan.
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3-NOV-1989; US-432044.
(USSH) Nat Inst of Health.
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                                                                                                                                                                                                                                                                                                                                                           712
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                                                                                                                                                                                                                                                                                            119
                                                                                                                                                                                                                                                                                                                                                                                                                                 102 eSerGluLeuArgLysAspAspPheLysGlyLeuGlnHisLeuTyrAlaL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    725 CTCA.....AGAAAAGAT......713
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86 LysGluIleSerProAspThrThrLeuLeuAspLeuGlnAsnAsnAspIl 102
                                                                                                                                                                                                                                                                                            euvalLeuvalAsnAsnLysIleSerLysIleHisGluLysAlaPheSer 135
                                                                                                                                                                                                                                                                                                                                                           .....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 668
                                                                                                                                            ProLeuArgAsnVal......GlnLysLeuTyrIleSe 146
                                                                                                                                                                                                                  CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC 618
                                                                      CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.50
0.730
41.472
Length: 299
Gaps: 14
Percent Identity: 19.732
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146 rLys......

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seq_name: A_Geneseq_36:R88469
                                                                                                                                                                                                                                                               documentation_block:
R88469 standard; Protein; 1464 AA.
DNA encoding feline infectious peritonitis I virus spike protein - used in a vaccine for prevention and treatment of FIPV-I infection claim 1; Page 14-17; 23pp; Japanese.
                                                                                                                                                                             Feline infectious peritonitis 1 virus spike protein. Feline infectious peritonitis 1 virus; FIPV-I; spike protein; vaccine; prevention; treatment.
                                                                10-JUN-1994; 129300.
10-JUN-1994; JP-129300.
(KITA) KITASATO KENKYUSHO
WPI; 96-072341/08.
                                                                                                                                                                                                                             R88469;
14-AUG-1996 (first entry)
                                                                                                                                                                  Feline infectious peritonitis 1 virus
                                                                                                                                                                                                                                                                                                                                                   312
                                                      N-PSDB; T10166
                                                                                                                                     J07327683-A
19-DEC-1995
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                                                                                                                                                                                                                                                                                                                                           leThrLysValGlyValAsnAspPheCysProMetGlyPheGlyVal 327
                                                                                                                                                                                                                                                                                                                                                                           TCACAAATTATACCTTG.....TATTGCCCAATTTTTATGGGCATC 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                           .....ATTTTATTCTAACAGTTTATCATTTGTGATAATA 130
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                             1035 TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1390 TTTCACTTCCA.....TTTGATTCATGCAAT......GTTGCGCGT 1356
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                                                                                                                                                                   985 TA.....AATGCT.....GAT
                                                                                                                                                                                                                 890 r.....TyrValCysAsnGlyAsnThrHisCysLeuLysLeuL
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                                         920 GlyAlaArgLeuGluSerLeuMetLeuAsnAspMet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  772 alAsnGlnThrAspLeuPheGluPheValAsnAsnThrGlnAlaArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               739 LysasnSerThrThrGlyGluIlePheThrValValProCysAspLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the feline infectious peritonitis 1 virus (FIPV-I) spike protein. The FIPV-I spike protein may be used in the production of a vaccine for the prevention and treatment of FIPV-I infection. The spike protein may be produced by transforming a host cell with the spike protein DNA and expressing the sequence such that the spike protein can be isolated. Sequence 1464 \mathrm{AA}_{i}
euThrGlnTyrThrSerAlaCysGlnThrIleGluAsnAlaLeuAsnLeu
                                                                                                                                                                                                                                                                                                      TyrIleGlnIleGlnValLysProValValAsp.....CysAlaTh
                                                                                                                                                                                                                                                                                                                                                  TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT 1036
                                                                                                                                                                                                                                                                                                                                                                                            hrGlyAsnIleSerIleProLysAsnPheThrValAlaValGlnAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r {\tt His Val Glu Ile Val AspAsp Ser Ile Gly Val Ile Lys Pro Val Ser Terminal}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                            ..GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTA 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oGlnPheTyr.....TyrIleThrLysTrpAsnAsnAspThrSerSerA 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rAlaGlnValAlaValIleAsnAspGluIleValGlyAlaIleThrAlaV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAA 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerSerPheAlaIleCysAsnThrGlyGluIleLysTyrValAsnValTh 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  snCys.....ThrSerAlaIleThrTyr 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerArgSerSerThrProAsn.....PheValThrSerTyrThrMetPr 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
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0.508
46.597
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Percent Identity:
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16
19.895
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US-09-323-427-2/rev x W88310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: W88310 from: 1 to: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1552 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1461 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1502 ATAACAATCAATTTTAATACACGTAATGCATTCGAAGGAC......A 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1361 GCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGT 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1411 GTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTT 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1311 TGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTG...ATCGTGCAT 1265
                                                                                                                                                                                                                                                                                                                                                                 1164 GCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAG 1115
::: |||||||:::::||| :: :: ::::::
138 erLysGluAlaValGlnGluPhe......IleAlaArgLysAlaThrPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1214 ATTGAGGTATCTGAAACTGAAACTGCTTTTCAAACTCAAATTGTCCCGAT 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1264 ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAG 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 ThralaHisAsnLysAsnGluGlyGlyAsnAlaArgMetPheCysTyrAr 125
                                                                                                                                                                                                                1048 CTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGAT 999
                                                                                                                                                                                                                                                                                                                                                                                                                              63 erPhePheArgAlaLeuPheGlnValLysLysIieIleValAlaLeuLys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 ......ileHisTyrValAsnMetAspLysAsnPheArgS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 LysasnLysIleValGluIleProAsnPheIleAsnThrAsnLysPheAs 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 lePheSerArgPheileArgMetLeuIleProAlaValProLeuIleCys 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              998 ACTGTGGAA.....ATTCTAAATGCTGATGGATGTGC 967
                                                                                                                                                                                    966 TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGAT...... 924
                                                            209 aIleAsnHisLeuIleLeuSerLysThrSerAsnCysAsnAspPheIleL 226
                            euLeuIleAlaGlyAspGlyAlaLeuArgAsnLysLeuLeuAsp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 AA;
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0.533
46.281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 363
Gaps: 18
Percent Identity: 21.763
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1742 ACTGCAGCAACAACAACAACAAACAACAACAACAACAACAA
Align seg 1/1 to: R59926 from: 1 to: 3079
alignment_block: US-09-323-427-2/rev x R59926
alignment_scores: Quality: 89.00 Length: 752 Ratio: 0.264 Gaps: 42 Percent Similarity: 44.814 Percent Identity: 18.617
me: A_Geneseq_36:R59926 cumentation_block: 59926 standard; protein; 3079 AA. 59926 protein Ira2. 2-FEB-1995 (first entry) AP protein Ira2. 38; GTPase activating protein; GAP; GAP relat AS2; v-Ras; heat shock; neurofibromatosis typ accharomyces cerevisiae. 09416069-A. 1-JUL-1994. 2-JAN-1994 UG0198. 2-JAN-1994 UG0198. 2-JAN-1994 UG0198. 2-JAN-1995 UG-004824. 2-JAN-1995 UG-
TGCACTTCTGCAACATAAT 597.
671ACACCCTTGAAATTAGCGATGATAATCAAGCTTTG 636 ::: ::: 321 laGluLysIleAlaGluThrLeuLysIleAspAspAsnAlaArgLys 336
714 ATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATC 672 ::: :::::::: :::
764 GCCGCAGCAAAACCTGCTGCAGCTGCGGCAACTTCGTTTACTCAAGAAAAG 715 ::: ::: ::::: ::::: 288 AlaCysGluargProValValAlaThrAspSerGlyGlyValLysGluVa 304
803TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGT 765 :: :: 271 alleuSerSerGluTrpGluGlyPheGlyLeuValValAlaGluAlaMet 287
836 .GAACCAAATAGCGAATGTGTTCGACCACAATGT
241LeuValCysGlnLeuAsnLeuValAspLysValPhePheLe 254

6 TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGC 917	966 TO
	2575 ri
GATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	1016 G
6 ATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGCTTTTGTC 1017 :::	1066 A: : 2561 L
6 AGTTCAATTTGCTAT ::::::::: 4 luLeuThrIleLeuV	o 4
ATGCCAGTA	
6 AGATTGAGGTATCTGAAATC ::::: 5 LysIleArg	U 0
alLeuProThrThrGluValAlaAsnAsnIle	37
9 GTACAATGCTTTTACATGGAAG	
ດ .	
	1344 G 2458 s
88 TCACTTCCATTGATTCATGCAATGTTGCGCGTACACGATCTCT 1345 :::::::: ::::::::: nlleSerHisIlePheArgIleLeuIleArgLeuSerValArgGluThrA 2458	1388 T 2441 n
23GTAATGATGAAGGTGGACGTCAAGTTGCCGGAATT 1389 :: :: 25 AsnLeuTyrGlnHisValTyrLeuAlaAspAspGluGluGlyProGluAs 2441	
32 GAAAGGTCTTTATGATCAAGAAGGTTGCC	1452 G 2408 r
	1499 A : 2392 A
44GGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA 1500 ::: ::: 75 heLeuGlyValIleGlyLysSerLeuAlaGluSerAsnProGluLeuThr 2391	1544 . 2375 h
rHisF	1559 . 2358 r
07 ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCG. 1560 :::: ::::::::::::::::::::::::::::::	07 42
48 TTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATG 1608 	1648 1 1 2325 a
98 AGCAATAATAACCCCCATCAAGTGGAGGAAGAAGAAGAAGAAGCAATCTTAG 1649 ::::: ::::::::::::::::::::::::::::	1698 <i>I</i> 2316 1

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ID R42452 standard; Protein; 1634 AA.

RA2452;
AC R2452;
DT 27-MAY-1994 (first entry)
DE Enzyme involved in elcosapentaenoic a
KW EPA; elcosapentaenoic actions.

So shewanella putrefaciens.

OS Shewanella putrefaciens.

PN W09323545-A.

PN W09323545-A.

PN ENGY-1993; J00641.
PN 15-MAY-1993; J90641.
PN 15-MAY-1993; J9-147945.
PR (SAGA) SAGAMI CHEM RES CENTRE.

PA (SAGAMI CHEM RES CENTRE.

RAMA (SAGAMI CHEM R
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                                                                                                  alignment_block:
US-09-323-427-2/rev x R42452
                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                            Ratio:
percent Similarity:
Align seg 1/1 to: R42452 from: 1
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25.NOV-1993; J00641.

14-MAY-1993; J00641.

(SAGA) SAGAMI CHEM RES CENTRE.

(KATO S, KONDO K, YAMADA A, YAZAWA K;

KATO S, KONDO K, YAMADA A, YAZAWA K;

RWPJ; 93-386577/48.

RWPJ; 93-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2874 GluHisGlnIleAsnGlnLysSerAspHisTyrLeuCysTyrMetPheLe 2890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2857 ysSerThrAlaPheAspPheLeuLysMetMetPheArgAsnSerTyrPhe 2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2924 LysIleLeuLeuGluTrpLeuSerSerAspAsnGluAsnAlaAsnIleTh 2940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2940 rLeuTyrGlnGlyAlaIleLeuPheLysCysSerValThrAspGluProS 2957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2988 gLys 2989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2974 IleCys.....AlaLeuArgPheTyrSerValIleArgAsnGluIleAr 2988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2957 erargpheargphealaLeuIleIleargHisLeuLeuThrLysLysPro 2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 CTTGTAT ...... TGCCCAATT ..... 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 AATAGTTTCGT.....TTGTTATTATCATCATTATCAACTTGTCCT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzyme involved in elcosapentaenoic acid (EPA) synthesis. EPA; elcosapentaenoic acid synthetase; drug; anticoagulan hypolipemic; hypoglycemic; antihypertensive; anticancer; foodstuff; additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 52-63; 106pp; Japanese.

EPA is useful as a drug, having anticoagulant, hypolipemic, hypolycemic, antihypertensive and anticancer activity. It is also a pesticide and is useful as a nutritional foodstuff and animal feed additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AAAA 8 '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .........GCTTCTGAAAAGCTTATTCATTAT...TCAGTAATCTTTTA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTTATTCTAACAGTTTATCATTTGTGATAAT...ATCACAAATTATAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alAspPheGluGlyGluMetValAsnIleGluAsnLysAsnThrIlePro 2923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                               88.00
0.376
46.800
                                                                                                                                                                                                                                                                    Gaps:
Percent Identity:
                                  to: 1634
                                                                                                                                                                                                                                                                              : 500
: 23
: 18.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anticoagulant;
anticancer; pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is isolated for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pesticide;
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VT 999 : : 1096	GCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGA	042 081
T 1043	GCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTC::::::::::	068
2A 1093	GATG(054
TT 1143	er	.192
AA 1193 :: aA 1037	GTTAGTGCACAGATTGAGGTATCTGAAATCACA :::::::: algluvalGluAlaprovalAsnServalGlnAla	N ii
3A 1240 31 1020	TGTTACCAAAGTTGATCG ::: uValGluLysLeuValGl	0 8
TA 1290 :: al 1003	TTTGTAACAACAACTGT ::: ::: ::: !yIleValThrSerGlnI!	1328 987
uT 987	AsnHisIleSerLysAlaThrArgAlaLysMetAlaLysSerLeuGl	970
3		1329
1329 Al 970	GTTGCGCGTACACGATCTCTGAATCCACGTGGTATT	1364 954
AAT 1365 ::: Asp 953	CCGGAATTTCACTTCCATTTGATTCATGCA	1396 938
TG 1397 : :NA 938	TCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGT	932
931	ATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAA :::::: ::: SerIleAsnProAsnProLysValAspSerAspLeuGlnLeuLys	1 9
r – :	lnLysLeuValGlnGlyThrLeuValAsnThrGluAsnGluVal	9
C	A	1499
1500 uG 899	TGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA:::::	1545 884
AA 1546 :: AS 884	GCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGAC	1595 873
NTT 1596 :: 7al 872	TTCTAAAAATCGAATTTACTAAATCT ::: :: ysIleLysAlaSerPheLysLysHis	1645 859
TTT 1646	AATAATAACCCCATCAAGTGGAGGAAGAAGAAGAACAGGAAGCAATCTTAGT	1695 843
AGC 1696 	CCGRCIGCHGCHACHACHACHACHACHACHACHACHACHACHACHACHAC	827

532	582	632	682	713	761	811	861	911	935	969	998
1249	1236	1228	1211	1197	1181	1173	1163	1147	1130	1113	1097
		GTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACATGTAAT 5	GAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCA (ATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTGTCGAC	CAAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCA ::::::	TATCCAACAGATTTAATGGCTGGC	TGCTCTTGATAAATATTTGCTAAATAATTTGGAA	ACTGTGGAAATTCTAAATGCTGATGGATG
483	533	583	633	683	714	762	812	862	912	936	970
1265	1249	1236	1227	1211	1197	1180	1173	1163	1146	1130	1113

.50 112.59 81.50 112

112.59

2.49

1911

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Database: Issued_Patents_AA:*
Database sequences: 133990
Database length: 13297546
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Query: US-09-323-427-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  About: Results were produced by Copyright (c) 1993-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: Apr 16, 2000 4:46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM of: US-09-323-427-2 to: Issued_Patents_AA:*
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-Q-Cgn21/USPTQ_spool/US09323427/runat_14042000_170513_19887/app_query.fasta.1
-DB-Issued_Patents_AA -CpMT-fastan -SUFFIX=backtrans.rai
-CAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=4.000 -GAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.000 -GAPOP=4.500 -GAPEXT=7.000 -YGAPD=10.000
-XGAPEXT=0.500 -GAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6:000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=20
-TRA_SCORE=pct -ALIGN=15 -MODE=LOCAL -CUTFMT=pfs -NORM-ext
-MINLEN-0 -MAXLEN-1000000 -USER-US09323427 -NCPU=6 -ICPU=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO_XLPXY -WAIT -THREADS=1
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/ the GenCore software,
Compugen Ltd.
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47 1.97
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0.0952
0.94 0.1491
0.49 0.1441
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alignment_block:
US-09-323-427-2 x US-08-415-751-6
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; NAME/KEY:
US-08-415-751-6
                                                                                                                     alignment_scores:
                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-415-751-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-800-825A-5 - 81.50
/cgn2_6/ptodata/1/iaa/PCTUS9_COMB.pep:PCT-US94-10166-5 - 81
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-872-302-5 - 81.00
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-392-806A-6 - 81.00
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 324-167
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION UNMEER: US/08/415,75:
FILING DATE: 03-APR-1995
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION UMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5
COMPUTER: PC
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GUT, JIRITITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: PHILLIPS, MOORE, LEMPIO & FINLEY
STREET: 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                 Quality:
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                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hana Dolezalova
                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
United States of America
                                                                                                                                                                                                                                                                                                                                                                      362 amino acids
                                                                                                                                                                                                                                                                                                                    linear
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NELSON, RICHARD, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PETERSEN, CAROLYN
                                                                                                                                                                                                identified as Xaa.
                                                                                                                                                                                                                Positions coded by nonsense codons are
                                                                                                                                                                                                                                                       Cryptosporidium parvum
                                                          121.50
1.095
40.659
                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND RNA ENCODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYPEPTIDES BINDING ANTI-
CRYPTOSPORIDIUM ANTIBODIES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/415,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30,518
                                                Length: 273
Gaps: 18
Percent Identity: 23.077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.5 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480.19-2 (HHD)
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Align seg 1/1 to: US-08-415-751-6 from: 1 to: 362
seq_documentation_block
                             seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1035 .....AACCGCGCAGAAAGTATCAACGGTTTCAGAATCGCATGTC 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1125 GGTTGGTCCACCATCCAA......AATTTCATAACGGCATACTGGCATCG 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1169 GGACAATTTGAGTTTGAAAAGCAGTTGTGATTTCAGATACCTCAATCTGT 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1357 CGCGCAACATTGCATGAATCAAA...TGGAAGTGAAATTCCGGCAACTTG 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1307 TGACAACAGTTGTTGTTACAAAAATACCACGTGGATTCAGAGATCGTGTA 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1269 ACG.....ATCAACTTTGGTAAC.....AAATAATGGATGAAACGAAA 1306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 eGlyLysProValLeuLeu***Val***ThrTrpGlu***IleAlaCysI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132
                                                                                                                                                      1595 CAATAAGACGAATCATCATTTCAGAAGATTTAGTAAATTCGATTTTTAGA 1644
                                                                                                                                                                                                                                                                                                                                                                    155
                                                                                                                                                                                                                                                                                                                                                                                                                              147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValValSerSerValSerThrValLyspheLeuAlaAlaArgTyrAspTh 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrLysLeuProAspPheGlySerAsnGlyArgProThrIleGlySerIl 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCACTAACTGTTTTATCAGCTTCCATGTAAAAGCATTGTACTCGATATGC 1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....val***LeuValTyrGly...Cys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACCTTTCACATAAACATGTCCTTCGAATGCATTACGTGTATTAAAAATTG 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGTCCACCTTCATCATT.....ACGGCAACCTTCTTGATCATAAA 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leSerTyrLeuSerCysLeuArgThrTrp......131
                                                                                                                                                                                                               AAAACTAAGATTGCTTCCTGTCTTCTTCCTCCACTTGATGGGGTTATTAT 1694
                                                                                                                                                                                                                                                                                                         .....AsnValThrAspIleArg***TrpCysArgCysCysCys..... 178
                                                                                                                                                                                                                                                                                                                                     АТТСТСААССССВААТССВАТААСАСААТССВАТААСТСТАСТАССАСАААС 1594
                                                                                                                                                                                                                                                                                                                                                                  ATTGTTATTGAAGTTGGTCCACATTCAATTTCTGGCTCACCTTCGACACC 1544
                                                                                                                                                                                   ......CysValLeuileG 155
                                                                                                                         u***CysCysCysCysCys 215
                                                                                          ....TGCTGCAGTCGGTGT 1748
                               /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-415-751-35
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NAME/KEY:
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NAME/KEY:
US-08-415-751-35
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                                                                                                                                                                                                                alignment_scores:
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                                                                                                                            alignment_block:
US-09-323-427-2 x US-08-415-751-35
                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                            Align seg 1/1 to: US-08-415-751-35
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 324-167
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Hana Dolezalova
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 480.
REFERENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
APPLICATION NUMBER: 0
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
      1706 TIGTTTGTTGTTTGTTTGTTGTTGTTGCTGCAGTCGGTGT 1748
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                      FEATURE:
                              STREET: 385 Shell CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                TECTTCCTCTTCTTCCTCCACTTGATGGGGTTATTATTGCTGTTGTTG 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94306-1840
                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
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NELSON, RICHARD, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PETERSEN, CAROLYN
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                                                                                                                                                                                                                                                                                                                                                                                                              362 amino acids
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                                                                                                                                                                                                                                                                                                                       Cryptosporidium parvum
                                                                                                                                                                                                                                                                               identified as Xaa.
                                                                                                                                                                                                                                                                                           Positions coded by nonsense codons
                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBL...
June 1, 1993
TIMBER: 07/891,301
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                                                                                                                                                                           109.00
6.056
58.065
                                                                                                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRYPTOSPORIDIUM ANTIBODIES, DNA AND RNA ENCODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND METHODS FOR IMMUNOTHERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYPEPTIDES BINDING ANTI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/071,880
35
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                                                                                                                                                                              percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480.19-2 (HHD)
                                                                                                      from: 1 to: 362
                                                                                                                                                                                  31
0
51.613
                                                     151
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151 sCys***LeuTrpTyrAsnCysCysCysCysPheCysCys 165

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SEQUENCE CHARACTERISTICS:
LENGTH: 3200 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-451-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-323-427-2 x US-08-477-451-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 101.00
Ratio: 0.537
Percent Similarity: 41.501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-477-451-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-477-451-8 from: 1 to: 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08477451
Patent No. 5928865
GENERAL INFORMATION:
APPLICANT: COVACCI, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEPHONE: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
  749 CAGGTTTTGCTGCGCACCACCTGTTTTAACAGCTCCGAATCCTTGTGGT 798
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||||||||:::
804 uProTyrAsnThrGlnThrThrCysTyr.......813
                                                                                                                                                                                                              655 CTAATTTCAAGGGTGTTGATATC......AGTTCGTACATCAATGATATT 698
                                                                                                                                                                                                                                                                                                                                                                                            564 ATTTTGTACTGCAGCAAGTAT......TACAGGTTGTCCATTATGTT 604
                                                                                                     791
                                                                                                                                                                                                                                                                                                                 605 GCAGAAGTGCACGGTGACGTAAATCAACTGGCAAAGCTTGATTATCATCG 654
                                                                                                                                     699 CTCCGGTTCTGCAGATCTTTTCTTGAGTAAACGAAGTTGCGCAGCTGCAG 748
                                                                                                                                                                                    774 alAsnPheLeuSerGlnPheLeuIleProLysProTyrLeuThrGluIle 790
                                                                                                                                                                                                                                                                         745 IleValPheCysArgIlePheGluLeuValTyrArgLeuLeuIleAlaLy 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                         IleAsnPheIleMetProPhe......GlnArgGluAlaArgCysLe 804
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Gaps: 24
Percent Identity: 22.075
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1585 1020	TCGACACCATTGTCAACCGGAATCGAATAAGACAATGCAATAAGTGTAG ::: ::: :AspThrIlePheHisArgThrPheLysGlyPheCysPhePheCysLe	1005
ōω	TTGATTGTTATTGAAGTTGGTCCACATTCAAT::: :::	99
1488 995	GACCTTTCACATAAACATGTCCTTO	- α ω
1438 989	AATTCCGGCAACTTGACGTCCACCTTCATCATTACGGCAACCTTCTTGAT:::	1389 982
1388 981	GGATTCAGAGATCGTGTACGCGCAACATTGCATGAATGAA	1339 969
1338 969	ATAATGGATGAAACGAAAATGACAACAGTTGTTGTTGTTACAAAAATACCACGT ::::::::::::::::::::::::::::::::::::	1289 957
1288 956	TTCCATGTAAAAGCATTGTACTCGATATGCACGATCAACTTTGGTAACAA ::::::::: :: TyrArgLeu	1239 946
1238 945	GATTTCAGATACCTCAATCTGTGCACTAACTGTTTTATCAGC	N O
1196 929	GCATCGGGACAATTTGAGTTTGAAAAGCAGTTGT	1163 917
1162 916	TGGTCCACCATCAAAATTTCATAACGGCATACTG ::: ::: :::: IleTyrPheArgPhePheSerSerIleGluThrPheIlePhe	1128 903
1127 902	TGATAAACTGGCTGACCAATGATAGCAAATTGAACTGGTTGACCGGT ::::: :: ::	1081 886
1080 886	GGACAACCGCGCAGAAAGTATCAACGGTTTCAGAATCGCATGTCCATTTA	1031 873
1030 873	ATCACCGTTACCATCATCGAC	999 857
998 856	AGCAAATATTTATCAAGAGCACATCCATCAGCATTTAGAATTTCCACAGT :: SerIleAsnGlyPheValPheGluSer	949 848
948 847	CGTGAGCTTCTTGGCCAGCCATTAAATCTGTTGGATATTCCAAATTATTT:::::: eileasnPhe	899 844
898 844	ACTGATCTGGCATTGATAGAAAAGCTGTGATCGATCCGCATATTTGTATA :::::: ::::: LeuSerValAsnGlyPhePheLysAlaSerCysLeuProCysPheLeuPh	849 828
848 827	TCTGAACATTGTGGTCGAACACATTCGCTATTTGGTTCTTTAATGGTAAT ::: ::: :::: ::: ::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: :::: :::: :::: :::: ::: ::::	799 814

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-070-301-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,301
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1
FILING DATE: 15-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     840 leAlaIleAlaIlePheIleArg 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490 TTACCATTTCGTTTAAATTTCGT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            823 lSerPheValLeuIleIleThrLeuLeuIleIleProIleAlaValLeuI 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          537 CTCAATGTTTATGGGTTTAAGCATTGCATTGATT...GCTGCCGTCATTA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   807 ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          742 alGluLysGlnThrGlnGluLysGlnGlnLys.....GlnLysAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   790 lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGly 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             773 aGlyValProThrGlnGluLysGlnAsnValValGlnGluSerSerAlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        810 ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           725 rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV 742
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                                                                     FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 20036-8218
                                                                                                                                                                                                                                                                                                                              STREET: 1233 20t
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o, Application US/08070301
5871995
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KATO, Ichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KISHIMOTO, Jiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YANAGI, Mitsuo
OKAMOTO, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIDA, Toshio
KAMINUMA, Toshihiko
                                                                                                                                                                                                                                                                                                                                                                Wegner, Cantor, Mue
233 20th Street, N.W.
                                                                                           24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masahiro
                                                                                                                                                                                                                                                                                                                                                                                               Cantor, Mueller & Player, P.C
                          JP 1-209687
                                                                                                                                                               #1.25
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alignment_block:
US-09-323-427:2/rev x US-08-070-301-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 440706
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 989 aming
                                                                                                                                                                                                                1322
                                     1230 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 1184
                                                                                                                                                                                                                                                                                                                                                                             1367 AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA..... 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1467 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1517 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1468
                                                                                                                                                                                                                                                                                                                                              664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1417 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 1368
                                                                                                                                                                                                                                                      679 nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            658 lAlaAspGlyTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEFAX: (202) 835-0605
                                                                                  713 AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                642 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-APR-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Player, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 2 FILING DATE: 02-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 1-FILING DATE: 31-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 744
                                                                                                                            AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 1231
                                                                                                                                                                                                                                                                                                                                          Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl 679
                                                                                                                                                                      leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla 712
                                                                                                                                                                                                            .....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 128
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0.965
43.103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP 2-76331
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12
21.552
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US-08-540-804-12

7	LENGTH: 1226 aminc TYPE: amino acid TOPOLOGY: linear	X: 617-861-95 N FOR SEQ ID N CHARACTERISTI	TRATION NUMEROCE/DOCKET		ų	OR APPLICATION DATA PPLICATION NUMBER:		ARE: Patentin Release #1.0, APPLICATION DATA:	TYPE: Floppy disk ER: IBM PC compatible	02173 ER READABLE FORM:	CITY: Lexingcon STATE: Massachusetts Conver. IISA	ET:	ITLE OF INVENT ITLE OF INVENT UMBER OF SEQUE	APPLICANT: Young, Richard A. APPLICANT: Koleske, Anthony J. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M.	ion US/08	eq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-540-804-12	939 GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC 894 	983 AATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTT 940 111111 ::::: 780	1033 TCCATTCCTGCTTTGTCGATGATGGTARCGGTGATACTGTGGAAATTCTA 504 ::::::::::::::::::::::::::::::::::::		108 762	1183 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 1134 :::::: :::!!! 744 laValSerTyrAlaPro
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alignment_block: US-09-323-427-2/rev x US-08-540-804-12 alignment_scores: Quality: 93.50 Ratio: 0.403 Percent Similarity: 47.444 Align seg 1/1 to: US-08-540-804-12 from: 1 to: 1226 1267 CATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTA..... 1223 1222GTGCACAGATTGAGG......TATCTGAAATCACAAC 1192 1141 TGGATGGTGGACCAACCGGTCAACCAGTTCAAT.....TTGCT 1104 1191 TGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTT 1142 279 TyrValAspGlnAsnProLeuThrMetHisLysIleIleGlnLeuIleLe 295 1003 GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT 954 1053 TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG 1004 312 euValAlaLysLeuLeuLeuLeuArgIleAsn......322 295 uTrpSerIleHisProSerArgGlnPheAspHisTyrGluSerAsnGlnL 312 323 ...SerThrAspGluAspLeuHisGluPheGlnIleGluAspAlaIleTr 338 357 TyrMetMetProSerLeuTyrArgLeuLeuAsnIleLeu.......... 369 401 HisValGlnLeuLeuIleAsnLeuLysIleSerProLeuMetLysSerGl 417 877 CAC...AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA 831 903 TCACGTAT.....ACAAATATGCGGATCGAT 878 953 TIGCTAAATAATITGGAATATCCAACAGATITAATGGCTGGCCAAGAAGC 904 830 A.....ATAGCGAATGTGTTCGACCACAATGTTCAGAACCACA 793 792 AG.....GATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG 749 472 etValAlaGluTrpTyrLeuSerHisLeuCysSerGlyIleLeuSerSer 488 648 TAATC.....AAGCTTTGCCAGTTGATTTACGTCACC 617 461 nLeuSer.....LysThrProLeuSerIleLysIleM 472 698 AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 649 451 ArgIleLeuSerAsn.... 748 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAGATCTGCAGAACCGGAG 699ileThrTyrGlyIleIleLysValProThrTyrIleArgLysL 384pheSerAlaGlnLysArgValValSer 356 Length: 489 Gaps: 24 Percent Identity: 19.836AspIleThrAsnLeuGl 461

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seq_documentation_block:
; Sequence 12, Application
; Patent No. 5922585
                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-218-265-12
Sequence 12, Application US/08218265
Patent No. 592585
GENERAL INFORMATION:
APPLICANT: Young, Richard A.
APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5922585e1 Factors which modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 SerAsnGlnAlaValGlyGlnThrTrpAsnPheProGluValPheGlnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 gIleGluLeuGlnSerValTyrAsnAspGluLysLeuLysThrGluLysL 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 ysAspValProAlaTyrAsnValThrSerPheMetProPheTrpLys...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 eLeuPheThrLysThrPheIlePheIleTyrLysLysValLeuLysGluL 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             616 GTGCAC.....TTCTGCAACATAAT 597
                                                                                                                                                                                                                                                                                                                                                     lnLeuIleSerLeuLys 714
                                                                                                                                                                                                                                                                                                                                                                                                   GCATTATTGCAATTAAA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCAATTITTATGGGCATCATTTCCTATTCTGTAAACAATTCACTTATTT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTAACAGTTTATCATTTGTGATAATATCACAAATTATACCTTGTATTG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erLysGlnPheGlnLysAlaArgAsnAsnVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAATAGTTTCGTTTGTTATTATCATCATTATCAACTTGTCCTATTTTA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euLysAsnAspLysSerGluValLeuLysValTyrSerMetIleAsnAsn 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAATACAATAAGTGATATTTTC.....ATCAAAACTTCTTCTA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                 tSerIlePheLeuLysArgLysAspPheThr...AsnLysAsnLeuIleG 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lAsnIleArgPheLeuLeuHisAsnSerGluIleIleAspThrAsnThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGCTTTTATAGCTTCTGAAAAGCTTATTCATTCAGTAATC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....MetLeuIleAlaThrAsnLeuLysGluTyrIleLysPheMe 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCATTATTACCATTTCGTTTAAATTTCGTCCAA...ATCAGAAGGCAT.. 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \tt uGluValPheHisHisPhePheLysTrpIleGluPheIleValTyrHisG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....TTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PhePheMetLysAsnPheProPheValLeuLysValAspAsnAspLeuAr 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTAGCTAACAAATATATAGTAT.....GTAGGAAATAATTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....AAAAATAATGTTAGAATCATCGAAGCAATAATAAAA.... 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleLeuLeuCysTyrGlnLysLeuPheSerGlnPheIleAsnAspHisIl 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lnLeuLeuSerAsp......IleGluSerLeuGluAlaLeuMetAsp 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValAsnArgThrValLeuLeuLysIlePheLysIlePheCysIleAspLe 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....CTGCCATATATATTCGTTTCTTCTTATCATCCTTCTAATAACTAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
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alignment_scores:
Quality:
Ratio:
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US-09-323-427-2/rev x US-08-218-265-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-218-265-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-218-265-12 from: 1 to: 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                      1003 GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT
                                                                                                                                                                                                        1053 TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1191 TGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTT 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1222 ......GTGCACAGATTGAGG......TATCTGAAATCACAAC 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1267 CATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTA.....
                                       295 uTrpSerIleHisProSerArgGlnPheAspHisTyrGluSerAsnGlnL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 TyrValAspGlnAsnProLeuThrMetHisLysIleIleGlnLeuIleLe 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,265
FILING DATE: 25-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Lexington STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                           TGGATGGTGGACCAACCGGTCAACCAGTTCAAT.....TTGCT 1104
                                                                                                                                                                                                                                                pSerLeuValPheGlnLeuAlaLysAsn.....
                                                                                                                                                                                                                                                                                                                                     ...SerThrAspGluAspLeuHisGluPheGlnIleGluAspAlaIleTr 338
                                                                                                                                                                                                                                                                                                                                                                                                                     .....IleThrTyrGlyIleIleLysValProThrTyrIleArgLysL
                                                                                     TyrMetMetProSerLeuTyrArgLeuLeuAsnIleLeu
                                                                                                                                                                  .....PheSerAlaGlnLysArgValValSer
                                                                                                                                                                                                                                                                                            ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MA
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617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.50
0.403
47.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHI94-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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24
19.836
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384

830 A.....ATAGCGAATGTGTTCGACCACAATGTTCAGAACCACA 793

792 AG.....GATTCGGAGCTGTTAAAAACAGGTGGTGCCGCAGCAAAACCTG 749

451 ArgIleLeuSerAsn......AspIleThrAsnLeuGl 461

CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG 699

698 ANTATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 649

596 GGACAACCTGTAATACTTGCTGCAGTACAAATGGAATCTGCATGTCACC 547

505 uGluValPheHisHisPhePheLysTrpIleGluPheIleValTyrHisG 522

::||| |||::: :::|||::: |||::: ||522 || InLeuLeuSerAsp......IleGluSerLeuGluAlaLeuMetAsp 535

536 IleLeuLeuCysTyrGlnLysLeuPheSerGlnPheIleAsnAspHisI1 552

.....AAAAATAATGTTAGAATCATCGAAGCAATAATAAAA..... 416

370 TTTTAGCTAACAAATATATAGTAT.......GTAGGAAATAATTACTG 330

ysAspValProAlaTyrAsnValThrSerPheMetProPheTrpLys... 584CTGCCATATATATTCGTTTCTTCTTATCATCCTTCTAATAACTAA 371

569

gleGluLeuGlnSerValTyrAsnAspGluLysLeuLysThrGluLysL 618

651 lAsnIleArgPheLeuLeuHisAsnSerGluIleIleAspThrAsnThrS 668

......TTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC 208

ATGAATAGTTTCGTTTGTTATTATCATCATTATCAACTTGTCCTATTTTA 158

635 SerasnGlnAlaValGlyGlnThrTrpAsnPheProGluValPheGlnVa 651

291 TCGCTTTTATAGCTTCTGAAAAGCTTATTCATTATTCAGTAATC..... 248 496 TCATTATTACCATTTCGTTTAAATTTCGTCCAA...ATCAGAAGGCAT.. 452

451

903 TCACGTAT.....ACAAATATGCGGGATCGAT 878

|| ::||| :::::: | euIleSerSerGlyLeuLeuTyrLeuGlnAspSerAsnAspLysPheval 400

alignment_scores: Quality: 93.00 Ratio: 3.000 Ratio: 3.000 Percent Similarity: 40.260 Percent Identity: 28.571 alignment_block: US-09-323-427-2/rev x US-07-906-349A-6 Align seg 1/1 to: US-07-906-349A-6 from: 1 to: 801 Align seg 1/1 to: US-07-906-349A-6 from: 1 to: 801 798 ACCACAAGGATTCGGAGCTGTTAAAACAGGTGCTGCAGCAAAACCTG 749	Sequence 6, Application US/07906349A Sequence 6, Application US/07906349A Patent No. 5474064 Patent No. 5474066 Patent No. 5474064 Patent No. 5474066 Patent No. 5474	57 GCATTATTGCAATTAAA 41 ::: ::::: 709 lnLeuIleSerLeuLys 714 seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-07-906-349A-6	### 107 CCCAATTTTTATGGGCATCATTTCCTATTCTGTAACAATTCAACAATTCAACAATTTTCTAATCAGGTTTTTTATGGGCATCATTTCCTATTCTGTAACAATTCAACAATTCAACAATTTATACCTTGTATTG 107 CCCAATTTTTATGGGCATCATTTCCTATTCTGTAAACAATTCACTTATTT 108

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-415-751-35
                                                                                                                                                                TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/415,75:
FILING DATE: 03-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: HAND DOLEZALOVA
                                                                   TOPOLOGY: lin
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GUT, JIRI
TITLE OF INVENTION: POLYPEPTIDES BINDI
TITLE OF INVENTION: CRYPTOSPORTIOUM AN
TITLE OF INVENTION: AND RNA ENCODING TITLE OF INVENTION: VECTOR AND TRANSFC
TITLE OF INVENTION: METHODS FOR IMMUNC
TITLE OF INVENTION: DIAGNOSIS AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        648 TAATCAAGCTTIGCCAGTIGATITACGICACCGTGCACTTCTGCAACATA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 ATGGACAACCTGTAATACTTGCTGCAGTACA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAAACCGGAG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
          NAME/KEY:
                                                                                                                            STRANDEDNESS:
                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306-1840
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                                                                                                                                                 amino acid
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Positions coded by nonsense
                                              Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEECH, JAMES
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                                                                                                         linear
                                                                                                                                                                                                                                                      (415)
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                                                                                                                              single
                                                                                                                                                                                                                                                      324-1677
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-303-238-3
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US-08-415-751-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                    Sequence 3, Application Patent No. 5654270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-415-751-35 from: 1 to: 362
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                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                       APPLICANT:
                                                       APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING
NUMBER OF SEQUENCES: 8
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 yMetArgAsn***ProHisArgGluLeuLeuHisGluLeuValValLysG
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                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ACCTGTAATACTTGCTGCAGTACAAAATGGAAT.........
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                                                                                                                                                                                                                                                                                                                    Application US/08303238
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4370 LA JOLLA VILLAGE DRIVE, SUITE 700
NN DIEGO
                                                                                                                                                                                       HARPER, JOHN R.
                                                                                                                                                                                                           WHITBY, DAVID J.
                                                                                                                                                                                                                                  RUOSLAHTI, ERKKI I.
LONGAKER, MICHAEL T.
                                          CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identified as Xaa.
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1.220
49.669
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467 CCAAATCAGAAGGCATAAAAATAATGTTAGAATCA 433	ଜ	AAATGGAATCTGCATGTCACCATTTGGCTTCTCA ::: ::::: ::::AsnHisLeuValGlu	GTGCACTTCT	e 14	AACA 66	/1 AlaL 11	775 AAACAGGTGGTGCCGCAAGCAACACCTGCTGCAGCTGCGCAACTTCGTTTA /20 :::::: ::: ::: :::::: ::: 102	: 368		ignment_scores: 91.50 Length: 299 Quality: 91.50 Gaps: 14 Ratio: 0.738 Gaps: 14 ercent Similarity: 41.472 Percent Identity: 19.732	INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 368 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein -08-303-238-3		FILING DATE: CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/978,931 FILING DATE: 17-NOV-1992 ATTORNEY-AGENT INFORMATION:	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: TOPE COMPATION PC COMPUTER: PATENTIAL Release #1.0, Version #1.25 SOFTWARE: PATENTION DATA: APPLICATION NUMBER: US/08/303,238	STATE: CALIFORNIA COUNTRY: UNITED STATES 7TD: 93132
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seq_documentation_block:
   Sequence 67, Application US/08325071
   Patent no. 5587311
   GENERAL INFORMATION:
                                                                                                                             seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-67
                                                                                                                                                                                                                                                                                                                       .279 LeuArgGluLeuHisLeuAspAsnAsnLysLeuAlaArgValProSerGl 295
    APPLICANT:
                                                                                                                                                                           312
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                                                                                                                                                                                                        TCACAAATTATACCTTG.....TATTGCCCAATTTTTATGGGCATC 89
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                                                                                                                                                                 leThrLysValGlyValAsnAspPheCysProMetGlyPheGlyVal 327
                                                                                                                                                                                                                                                                                                                                                                                                  isAsnGlnIleArgMetIleGluAsnGlySerLeuSerPheLeuProThr 278
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COBON,
Stewart Gary
Joanna Terry
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alignment_block:
US-09-323-427-2/rev x US-08-325-071-67
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                                                                                                                                                                                                    alignment_scores:
                                                   Align seg 1/1 to: US-08-325-071-67 from: 1
                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/242,196
FILING DATE: 06-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
1476 TGCATTCGAAGGACATGT......
                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/062,109
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27-NOV-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DAIL.
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: AU PI2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202
TELEFAX: 904136
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS;
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W.
CCITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: AU PI4912 FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20007-5109
                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                            650 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                           202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEMP, David Harold
SRISKANTHA, Alagacone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILLADSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOHNSON, Law Anthony York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                         protein
                                                                                                                                               90.00
0.612
40.947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: AU PH9196
27-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1987
                                                                                                                                             Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                     67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              60042/111 BIAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
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С
               .......TTATG 1454
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22
21.727
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seq_documentation_block:
    Sequence 22, Application US/08477451
    patent No. 5928865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-477-451-22
                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-08-477-451-22
                                                                                                                                                                                                 alignment_block:
US-09-323-427-2/rev x US-08-477-451-22
                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94608-2916
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.30
SOFTWARE: PATCHTIN DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                      Align seg 1/1 to: US-08-477-451-22 from: 1 to: 485
                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Helicobacter Pylori Cagi Region NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysG1 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701 GAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGA 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||:::||||||:::||||||| |||| |||| 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 yGlnAsnLysCysValLysValAsp 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 TGATAATCAAGCTTTGCCAGTTGAT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
REFERENCE/DOCKET NUMBER: 035.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                  1447 GTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTT 1398
                                      1397 GCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTA...... 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4560 Hort
CITY: Emeryville
STATE: CA
                                                                             10 ValileLeuValTyrProlleLeuPheLeuPheAlaLeuIleIleLys.. 25
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acids
                                                                                                                                                                                                                                                                89.50
0.393
40.426
                                                                                                                                                                                                                                                              Length: 564
Gaps: 28
Percent Identity: 18.085
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13	AACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGAT 7	754
26	rgLeuT 3	9
55	7	790
109	SerIleLysAsnMetGlySerAlaLeuValGlyAsnGlyPheGlySerSe 3	293
91		799
800 292	TTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAG 8 ::: :: ::: ::::: ::: ::: :::	841 276
276		259
842	TCTATCAATGCCAGATCAGTATTACCA. 8	868
259	LeuMe	243
869	:	910
911 243	TAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC	960 226
226	ProAsnLysGlnGluLeuThrGlnProLysIleLysGlyLeuIleMetGl	210
61		1010
09		196
.011		1033
	uLeuIleAlaPheHisGluSerTyrGlnIleGlnGluPheSerLeuVal.	179
1034	······································	1064
179	euValTrpTrp.GlnAsnIlePheValCysAspTrpTrpLe	166
١ ٥	TGGTCAGCCAGTTTATCATATCATCATCATCATCATCATCATCATCATCAT	1098
0	.TCAACCAGTTCAATTTGCTATCAT	1122
149	}sirecysvaiserashbeurnebeulleurp.TrpTrpPheSerLysLe	, ,
1123	CCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGG	1170
133	eTrpTyrSerAsnProLysThrProPheIleValSerValPheLysPheC	116
1171	CAAACTCAAATTGT	1184
1185 116	ATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTT :: ::: :::	106
105	ysProTyrLeuLysThrLysIlePheLeuSerAlaTyrThr	
1235	TACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTG	1284
N	: ::: serbeuPheProAsnIleSerIleL	75
1285	ACAACTGTTGTCATTTCGTTTCATCCATTATTTGT	1319
75	LeuIleIleLeuMetThrGlnTrpGlnAsnTrpPheLeuPheValGlnLy	59
ຸ ເ	אַרְעַרְאַרְעַיִּתְּיִתְּעַתְּיַיִּתְּעָתְּיַתְּיִיתְּעָתְּיַתְּיַתְּעָתְּיַתְּיַתְּעָתְּיַתְּעָתְּיַתְּעָתְּיַתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּיִנְּתְּעָתְּעָתְּיִנְּתְּעָתְּעָתְּיִנְּתְּעָתְּעָתְּיִנְּתְּעָתְּעָתְּיִנְּתְּעָתְּעָתְּיִנְּתְּעָתְּעָתְּעָתְּעָתְּיִנְּתְּעָתְּעָתְּעָתְּעָתְּעָתְּעָתְּעָתְּ	1333
28 27 27	erIleIleSerLysTyrTyrLeuLeuSerHisAlaLysPheThrMetLys	42
1334	······CACGATCTCTGAATCCACGTG	1354

seq_documentation_block: Sequence 61, Application US/08325071 Patent No. 5587311 GENERAL INFORMATION: APPLICANT: COBON, Stewart Gary APPLICANT: MOORE, Joanna Terry APPLICANT: WILLADSEN, Peter APPLICANT: WILLADSEN, Peter APPLICANT: KEMP, David Harold APPLICANT: SRISKANTHA, Alagacone APPLICANT: RIDING, George Alfred APPLICANT: RAND, Keith No. 5587311man TITLE OF INVENTION: DNA Encoding A Cell Membrane TITLE OF INVENTION: Glycoprotein Of A Tick Gut NUMBER OF SEQUENCES: 71 CORRESPONDENCE ADDRESS:	386	

WASHINGTON, D.C. TRY: USA 2007-5109 R 2007	AAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 113 ::::::::::::::::::::::::::::::::			to: US-08-325-071-61 from: 1 to: 549	/rev x US-08-325-071-61	: ity: 89.00 Length: 3 tio: 0.614 Gaps: tty: 40.390 Percent Identity: 22.	05-08-372-071-01	MOLECULE TYPE: prot	; LENGTH: 549 amino actus TYPE: amino actid	CHARACTERISTICS:	904136	TELECOMMUNICATION TELEPHONE: 202	29,768 BER: 60042/111	ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.	APPLICATION NUMBER: AN FILING DATE: 27-NOV-1986	:	u pj 987	600	PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA: APPLICATION UNMBER: PCT/AU87/00401	APPLICATION NUMBER: 0//242/150 FILING DATE: 05-JUL-1988	FILING DATE: 07-AUG-1992 PRIOR APPLICATION DATA:	PRIOR APPLICATION NUMBER: US 07/926,368 APPLICATION NUMBER: 1007	APPLICATION NUMBER: US 08/002/109 FILING DATE: 17-MAY-1993	FILING DATE: 14-0CT-1993 PRIOR APPLICATION DATA: 00/000 100	APPLICAT	M TYPE: Floppy disk M TYPE: Floppy disk TER: IBM PC compatible TING SYSTEM: PC-DOS/MS-DOS ARE: Patentin Release #1.0, Version #1.2	Z0007	197	: Foley & Lar
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-325-071-63
                                                                  APPLICATION NUMBER: AU PH9196

APPLICATION NUMBER: AU PH9196

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 60042/111 BIAU

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 672 5300

TELEPAX: 202 672 5399

TELEX: 904136

INFORMATION: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: 07/242,196
FILING DATE: 07-AUG-1988
PRIOR APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
PRIOR APPLICATION NUMBER: 07/242,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PI4912
FILING DATE: 16-CCT-1987
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

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PRIOR APPLICATION DATA:
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Sequence 63, Application US/08325071
Patent No. 5587311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: AU PI2570 FILING DATE: 19-JUN-1987 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 558731lman
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20007-5109
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MOORE, Joanna Terry
JOHNSON, Law Anthony York
WILLADSEN, Peter
                       protein
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alignment_scores:

			<u> </u>						_
35 THICLANCHATTINATIGGTTGGCCAAGAAGCTCACGTATACAAATATGC 886 ::: :: 351 PheaspSerAspHisCysLysTrpTyrGl 360 885 GGATCGATCACGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG 836	20 20 34	CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC ::: ::: ::: TTTGTCGATGGTGT	1163 CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGG 1123	1251 CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG 1211	ASPSETTyrCysseAACTGTTGTCAT. :: yGlnCysIleAsnAlaCysLysM yGlnCysIleAsnAlaCysLysM TTATTTGTTACCAAAGTTGATCG TSG1yCys.ArgserThrAlaLy	163 SGILLYSASDLEULEUGINATGASP	1476 147 147	Ratio: 0.614 Gaps: 22 Percent Similarity: 40.390 Percent Identity: 22.284 alignment_block: US-09-323-427-2/rev x US-08-325-071-63 Align seg 1/1 to: US-08-325-071-63 from: 1 to: 650	89.00 Length:

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pir2:S72278
pir2:D71606
pir2:T15789
pir1:A35269
pir1:A36054
pir2:S03356
pir2:S03356
pir2:S17855
pir1:T14850
pir2:F71615
pir2:F7161612
pir2:F716126
pir2:F71633
pir2:F71633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pir2:S72284
pir2:F71606
pir2:B26696
pir1:RNZOBF
pir2:S78177
pir2:A40970
pir2:C71607
pir2:G71613
pir2:G71618
                                                                                                                                    pir2:H71606
                                                                                                                                                                                             pir2:S23344
                                                                                                                                                                                                                           pir2:S32559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pir2:T03099
pir2:S52967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pir2:E71604
pir2:S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search information block:
Query: US-09-323-427-2
Query length: 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pir2:A49772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database sequences: 142080
Database length: 47169319
Search time (sec): 178.310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database: PIR_62:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                About: Results were produced by the GenCore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM of: US-09-323-427-2 to: PIR_62:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL=frame+_n2p_model -DEV=xlp
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-Q-/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19903/app_query.fasta.1
-DB-PIR_62 -OPMT=fastan -SUFFIX=backtrans_rpr -GAPOp=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPCXT=0.000
-QGAPEXT=0.000 -WINMATCH=0.100 -XGAPEXT=0.500
-PGAPOD=6.000 -GAPEXT=7.000 -YGAPOP=10.000 -XGAPEXT=0.500
-PGAPOD=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER-US09323427 -NCPU=6 -ICPU=3 -NO_XLDXY -WAIT
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10 | DNA-directed RNA polymerase (EC
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                                                                                                                                                                                                                     probable amine transporter PFH S-layer protein precursor - Baser protein precursor - Baser antigen/papain-like protein hypothetical protein precein (mulguanidine nucleotide exchange hypothetical protein 2136 - In probable chloroquine resistance in the protein 
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alignment_scores:
Quality: 1379.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: cut-1 a Caenorhabditis elegans gene coding for a dauer A; Reference number: A49772; MUID:91323673 A; Accession: A49772 A; Status: preliminary; not compared with conceptual translation and the conceptual tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Sebastiano, M.; Lassandro, F.; Bazzicalupo, Dev. Biol. 146, 519-530, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-423 <SEB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1242 GGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAA 1193
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cuticlin 1 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #te
C;Accession: S27799
C;Accession: S27799
R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P.
submitted to the EMBL Data Library, July 1991
submitted to the EMBL Data Library, July 1991
A;Description: CUT-1 a Caenorhabditis elegans gene cod
A;Reference number: S27799
A;Accession: S27799
A;Molecule type: DNA
                                                                                                                                               seq_name: pir2:S27799
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                                                                                                                                                                           uValSerGlu.....GluSerValArgArgAlaThrSerThrGlyI 387
                                                                                                                                                                                                                                                                                                   TCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA 560
                                                                                                                                                                                                                                                                                                                           IleMetGluGly.....AlaSerProSerAlaProGluAlaAlaAlaLe
                                                                                                                                                                                                   TTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCA 465
                                                                                                                                                                                                                           leSerSerThrProIleGlyLeuProSerPheLeuGlyMetArgThrIle
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                                               gene coding
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colla

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A;Residues: 1-308 <SEB>
A;Cross-references: EMBL:M55997; NID:g156271; PID:g156272
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: CUT-1
A;Introns: 245/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-323-427-2/rev x S27799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1253 TGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                            1203
                                                                                                                                                                                                                                                                                                                                                                                                                          1103 ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT 1054
                                                                                                                                                                                                                                                                                                                                               1003
                                                                                                                                                                                                                                                                                                                                                                                     1053
                                                                                                                                                                                                                                                                                   56 ThrileGlyGlnGlnValTyrHisLysTrpThrCysAspSerGluThrTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156
                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCC
                                                                                                                                                                                                                                                                                                                           GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT
                                                                                                                                                                                                     aHisValTyrLysTyrAlaAspArgSerGlnLeuPheTyrGlnCysGlnI 139
                                                                                                                                                                                                                                                               TCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGA 854
                                                                                                                                                                                                                         TCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGT
                                                                                                                      aHisAlaAlaAlaAlaProGlnAlaGlyValGluValGlnAlaAlaP
                                                                                                                                                              TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAA 754
                                                                              roValGlyAlaAlaProValAlaAlaProValAlaAlaAlaAlaAlaAla
                                                                                                                                          ACCTGCTGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
          AAGATCT...GCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA 671
ProAlaValProArgAlaThrLeuAlaGlnLeuArgLeuLeuArgLysLy
                                                                                                                                                                                                                                                       S27799 from: 1
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3.989
74.503
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Percent Identity:
                                                                                                     .GCGCAACTTCGTTTACTC...AAGAA 718
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5
60.596
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                                                                                         205
                                                                                                             741
                                                 222
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1250 TTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGAT 1213
1297 ATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGC 1251 ::: :::::: 58 IleTyrLeuLeuIleLeuTyrLysAsnLysIleAsnAsnIleTyrAsnAs 74
1335 TGGTATTTTGTAACAACTGTTGTCATTTCGTTTC 1298 :::::::: 41 yrSerPheLeuTyrAsnTyrSerLeuAsnIleLysAspPheSerAsnPhe 57
1385 CTTCCATTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACG 1336 ::::: :::
1435 AAGAAGGTTGCCGTAATGAAGGTGGACGTCAAGTTGCCGGAATTTCA 1386 :: :::::: :::::::: 16 LysLysLeuLeuIleIlePheLysTyrAsnIleSer
Align seg 1/1 to: S72284 from: 1 to: 960
alignment_block: US-09-323-427-2/rev x S72284
alignment_scores: Quality: 119.00 Length: 612 Ratio: 0.436 Gaps: 34 Percent Similarity: 44.608 Percent Identity: 21.078
A;Gene: rpoC2 A;Genome: plastid A;Genome: plastid A;Note: this apparently degenerate plastid is referred to as the apicoplast C;Keywords: nucleotidyltransferase; plastid; transcription
A;ReSidues: 1-960 <mil> A;Cross-references: EMBL:X95275; NID:g1171583; PID:e220245; PID:g1171589 A;Note: biosynthesis of this protein involves a -1 frameshift in the codon for residue 5 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996 C;Genetics:</mil>
A; Molecule type; DNA
J. Mol. Biol. 261, 155-172, 1996 A:Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fa A:Reference number: S72277; MUID:96346169
<pre>seq_documentation_block: DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid N;Alternate names: RNA polymerase rpoC2</pre>
seq_name: pir2:S72284
470 CGTCCA 465 302 ArgPro 303
520 TAAGCATTGCATTGATTGCCGGCGATTATTACCATTTCGTTTAAATTT 471 :: :::::::::::::::::::::::::::::::::
570 ACAAAATGGAATCTGCACTGTCACCATTTGGCTTCTCAATGTTTATGGGTT 521 ::::::::: 268 rSerThrGlyIleSerSerThrProIleGlyLeuProSerPheLeuGlyM 285
620 CACCGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGT 571 ::::::::::::::::::::::::::::::::
670 ACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGT 621 ::: ::: 239 snThrLeuAspIleMetGluGlyAlaSerProSerAlaProGlu 253

610	CGTGCACT	647
σ	<pre>LysTyrLeuIleTyrLysIieTyrLeuTyrLysLeuAsnIleAsnLysIl :</pre>	347
648	AT	697
698 346	TGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAAACCGGAGA	741 · 330
742 330	1F 60	791 316
316	nTyrLysGlnLeuTyrLysTyrAsnLeuGlyGlnHisIleGlyValIl	300
و د	SSerValTyrLeuCysAsnIleTyrAsnAsnIleCysAsnThrCysLeu	283 820
821	CAGTATTACCATTAAAGAACCAAATAGCGAAT	855
856 283	ACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCA ::: :::::::::::::::::::::::::::	895 266
266	GlyThrPheIleTyrThrLysAsnThrTyrIleThrLysTyrIleLe	G 6
4 0	GTHUS TO SHITTELE CONTROL OF THE STREET AND THE STR	o 4
- N	AAATATTTGCTAAATAATTTGGAATATCCAA	978
241	AAATGC ::: ysileL	224
N		1 20 8
	GGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCC	1075
207	ysArgLeuIleAsnIleThrSerAsnPheIle	191
1076	GGTCAGCCAGTTTATCATAA	1108
191	pThrAlaLeuLysThrAlaA	174
1109		1109
174	TyrIleLeuSer	158
1109	AACCAGITCAAT	1120
157	yrīle	141
1121	ATGAAATTTTGGATGGTGGACCAACCGGTC	1150
141	nAsnLys1leLysTyrSerGlnLeuGlnGlnLeuIleGlyTyrL	124
1151	AAACTCAAATTGTCCCGATGCCAGTATGCCGTT	1183
124	AsnProIleTyrSerAsnLeuPheLeuPhePhe	108
1184	·····TCACAACTGCTTTTC	1198
107	lIleAsnLysIleGlnGlyIleLeuAsnAsnA	91
1199	TGAGGTATCTGAAA	1212
91	nLysTyrTyrGluIleLysAsnAsnTyrIleAsnValPheLeuAsnAsnT	74

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seq_documentation_block:
probable multiple transmembrane domain protein PFB0770c - malaria parasite (Plasmodium probable multiple transmembrane domain protein PFB0770c - malaria parasite (Plasmodium probable multiple transmembrane domain protein PFB0770c - malaria parasite (Plasmodium probable multiple multi
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:F71606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATG 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eullepheLeuMetAsnLysIleLeuTyrAsnTyrAsnAsnIleLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGCAACATAATGGACAACCTGTAATAC.....TTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTCGTCCAAATCAGAAGGCATAAAAATAATGTTAGAATCATCGAAGCA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sCysAsnPheIleTyrAsnSerIleSerLysAsnPheLysTyrAsnLeuA 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTAATTTTAGCTAACAAATATATAGTATGTAGGAAATAATTACTGTAATA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAATAAAACTGCCATATATATTCGTTTCTTCTTATCATCCTTCTAATAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ysAsn.IleHisAsnLysTrpIleLeuTyrAsn.....IleTyrThrTy 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAATAAGTGATATTTTCATCAAAACTTCTTCTATCGCTTT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nTyrAsnPhelleAsnSerAsnTyrTyrPheLysLysMetAsnPhelleL 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGCTTATTCATTATTCAGTAATCTTTTATATGCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leIleLeuAsnAsnAsnAsnAsnLysTyrAsnValIleTyrPheLeuIle 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |||:::||| :::||| :::||| :::
rTyrLeuTyrTyrH1sI1eLysPheTyrAsnLeuTyrAsnLysGlyI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euLys......AsnPheAsnAsnIleGlnIleLeuAsnLysLeu 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTATTTGCATTATTGCAATTAAAAAGTAT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ysLysLeuPheIleTyrLeuAsnIleIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTTTATTCTAACAGTTTATCATTTGTGATAATATCACAAATTATACCT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGGCCATGAATAGTTTCGTTTGTTATTATCATCATTATCAACTTGTCC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACT ATTGTAAA.....TGTTTCATCA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTATTGCCCAATTTTTATGGGCATCATTTCCTATTCTGTAAACAATTCA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pheTyrValAsnAsnIlePheIle.....TyrTyrLys.TyrGluL
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A;Residues: 1-1122 <GAR>
A;Cross references: GB:AE001417; GB:AE001362; NID:g3845271; PID:g3845273; TIGR:PFB077
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0770c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-323-427-2/rev x F71606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1404 TCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTA 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1354 CACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATT 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1254 ATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTAT 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 sThrCysAsnAsnHisThr......CysAsnAsnHisThrCysAsn. 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 CysasnAsnHisThrSer...AspAsnAsnThrCysAsn....... 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGC 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AsnHisThrCysAsnAsnHisThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....TCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGAT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGC 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....AsnHisThrCys....AspAsnAsnThrCys.....
                                                                                                                                                                                                                                        CAGATTTAATG...GCTGGCCAAGAAGCTCACGTATACAAATATGCGGAT 882
                                                                                                                                                                                                                                                                                                                TGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAA
                                                                                                                                                                                                                                                                                                                                                    ......SerHisAsnAspThrGlnGluAsnAsnIleMetLysAsnLy 603
                                                                                                                                                                                                                                                                                                                                                                                                                       snLysLysGluThrHisAsnAsnPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....AsnAsnHisThrLeuGlyAsnPro 564
                                                                                                                                                                                                                                                                                                                                                                        GTCGATGGTAACGGTGATACTGTGGAA......ATTCTAAATGC 979
                                                                   sn.....SerLeuLeuAspIleAsnGluTyrAsnAsnAsnAsnSerAsnAsp
                                                                                                   AAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAG
                                                                                                                                      eLysLysIleIleGluLeuAsnThrThrLysLeuValGluGluArgAsnA 648
                                                                                                                                                                        CGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC
                                                                                                                                                                                                           CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT
LeuAsnGluTyrPhe.
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0.492
46.654
                                                                                                                                                                                                                                                                                     .....LeuTyrLeuAsnThrLysSerTyrAspA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 508
Gaps: 31
Percent Identity: 21.654
     .AspAsnLeuIleGluAsnAsnIleLe
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              676
                                                732
                                                                                     662
                                                                                                                     782
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seq_documentation_block:
hypothetical protein 1 (CYD-COII intergenic region) - Leishmania tarentolae mitochondric
C; Species: mitochondrion Leishmania tarentolae
                                                                                        seq_name: pir2:B26696
                                                                                                                                                                                                                                                          131
                                                                                                                                                                                                                                                                                                     887
                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   693 leMetAsnLysLeuMetTyrThrAsnValSerAsnAsnGluArgTyrArg
                                                                                                                                                                      81 ATTCTGTAAACAATTCA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731 CGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATA.....
                                                                                                                                                                                                           yrAsnAsnAsnAsnAsn
                                                                                                                                                                                                                                                                                                                                                                        nPheIleAlaTyrIleIleArgProPheIleLysAsp...... 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleIleArgAsn...IleTyrPhePheLeuCysAlaLeuSerGlyArgGl 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATTCAGTAATCTTTTATATGCATACTATTGTAAA.......
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|TyrAsnGluValPheGluIlePheLeuArgAsnIleLysGlnProAspL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGCATAAAAATAATGTTA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alPheTyrIlePheTyrIleLysPheAspIleSerTyrLeuLysLeuIle
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uMetIleProTyrIleThrTyrCysLeuGlyLysIleAlaMetSerIleV
                                                                                                                                                                                                                                                                                                                                        TCATTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATACAATAAGTGATAT.....300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheIlePheIleLysCysIleSerGluPheLeuPheLeuLeuLeuLeuVa 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATATAGTATGTAGG............AAATAATTACTGTA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....LeuTh 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCAATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATT 489
                                                                                                                                                                                                                                                                                                                                                                                                                    .....TGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....TTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCA 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 843
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A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: hypothetical protein 1 (CYb-COII intergenic region)
C;Keywords: mitochondrion
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A;Residues: 1-443 <SIM>
A;Residues: 1-443 <SIM>
A;Cross-references: GB:M10126; GB:J02707; GB:M10127; GB:M11022; GB:M64690; GB:N00030;
A;Note: the authors translated the codon ATT for residue 388 as Phe and TTC for resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Simpson, L.; Neckelmann, N.; de la Cruz, V.F.; Simpson, A.M.; Feagin, J.E.; Jasmer, J. Biol. Chem. 262, 6182-6196, 1987
A;Title: Comparison of the maxicircle (mitochondrial) genomes of Leishmania tarentola A;Reference number: A92643; MUID:87194837
A;Accession: B26696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-323-427-2/rev x B26696
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1059 AACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1550 GACAATGGTGTCGAAGGTGAGCCAG.....AAATTGAATGTGGACCAAC 1507
                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1406 CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCG 1357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 eIleIleLeuCysAspTyrThrSerLeuPheTyrLeuSerPheAspLeuI
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                                                                                                                                                                                                                                                                                                                                ATCTGAAATCACAACTGCTTTTCAAACTCAAATTG...TCCCGATGCCAG 1160
                                                                                                          TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA 1060
                                                                                                                                                                      TyrLysIleLeuIleLeuTrpTyr.....
                                                                                                                                                                                                                                                                                                                                                                                            eIleSerIleLeuPheGluLeuPhe..... 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTA 1257
                                                     \verb|nLeuIleAsnPheIleLeuLeuPheValLeuLeuTyrTyrMetIleLeu|.|
                                                                                                                                                                                                                        TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGT 1207
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                                                                                                                                                                                                                                                                              .....SerLeuLeuLeuPheLeuIleLeuIleSerSerArgPheGly 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heAspThrArgPheValPheMetIleIleIleMetGlnTyrIleIleIle 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....LeuPheLeuPheCysPhePhePheLeuPheCysPheLeuAsnP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTT 1457
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Ratio:
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0.463
44.485
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R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; W. J. Mol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium A; Reference number: S72277; MUID:96346169
A;Accession: S72282
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pNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Plasmodium falciparum plastid C;Species: plastid Plasmodium falciparum C;Date: 31-Dec-1990 #sequence_revision 15-May-1998 #text_change 11-Jun-1999 C;Accession: $72282; $10438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir1:RNZQBF
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A; Molecule: 1-1024 <WIL>
A; Residules: 1-1024 <WIL>
A; Residules: 1-1024 <WIL>
A; Residules: 1-1024 <WIL>
A; Residules: 1-1024 <WIL>
A; Cross references: EMBL:X95275; NID:g1171583; PIDN:CAA64572.1; PID:e220243; PID:g117
A; Cross references: EMBL:X95275; NID:g1171583; PIDN:CAA64572.1; PID:e220243; PID:g117
A; Cross references: EMBL:X95275; NID:g1171583; PIDN:CAA64572.1; PID:e220243; PID:g117
A; Cross reference EMBL:X95275; NID:g1171583; PIDN:CAA64572.1; PID:e220243; PID:g117
A; Cross references: EMBL:X95275; NID:g117
A; Cross references: EMBL:X95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X52177; NID:g9879; PIDN:CAA36427.1; PID:g9880
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A; Residues: 328-1024 <GAR>
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-323-427-2/rev x RNZQBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1633 AATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACT 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1583 ACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATG.....
1499 ACAATCA.....ATTTTAATACACGTAATGCATTCGAAGGACATGT 1459
                                                                                                                                                                                                                                                                                                               1544 ......
                                                                                                                                                                                                                               102 roPheIleTyrAsnAsnIleIleIleLeuAsnGlyLeuTyrLysThrCys 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::: :::::: :::||||:::::: :::
86 eAsn...IleAsnLysIleIleLysPheAsnIleLeuIlePheIleLeuP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATAATATCACAAATTATACCTTGTATTGCCCCAATTTTTATGGGCATCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCCTATTCTGTAAACAATTC
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                                                                       IleGlnLeuPheLysLysAsnAsnLysIlePheIleIleLysPheLysAs 135
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0.373
45.113
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Gaps: 28
Percent Identity: 17.594
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728	8	728
390	snThrAsnGluGlyLeuThrCysGlyLeuValAsnTyrLeuThrThrAs	37
728	CAGCTGCGCAACTTCGTT	4
	:: ::::::::::::::::::::::::::::	357
746	ACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTG	795
357	eLysIleAsnMetIleThrThrGlyLeuAsnSerLysPheIleLeuAsnA	340
796	5GTTCAGAACC	80
340	4 ValGlnTyrSerAspGlnValAsnAsnLeuSerGluIleAsnGlnLysPh	32
806	TTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAAT	847
323	rileAsnIleIleLeuGluAsnIleAsnIleAsnProLeu	310
848	ATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTA	897
310	gAsnIleTyrAsnAsnIleThrLeuLeuLeuAsnAsnLysLysT	295
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295	LysTyrLeuLysIlePheLysTyrGlnLeuLeuAsnIleAsnAr	281
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280	leLysSerLys	277
998	TTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATA	1047
277		σ,
. 6	4 leteurneseritetysteuAsnPheserTyrTyrSerAspPheTyrIl	1070
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243	6 snIleTyrIleAsnLeuLeuAsn	23
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1159 236	GTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGT:::: :::::::::::::::::::::::::::	1208 219
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204	l euPheIleTyrAsnAsnIleIleAsnLysLysIleLeuIle.	19
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191	9 rLeuAsnAsnleTyrIleAsnLysAsnIleSerL	17
1309	ACGATCTCTGAATCCACGTGGTATTTTGT	135
179	3 AspCysTyrPheAsnAsnPheLysPheAsnPheLeuIleLeuLeuTy	16
1359	8 GACGTCAAGTTGCCGGAATTTCACTTCCATTTGAT	140
O.	2 rgIleIlePheLysIleSerLysLeuAsn	15
4	8 TTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGG	145
152	5 nAsnAsnLysAsnIleI	13

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115 630	ATCATTTGTGATAATATCACAAATTATACCT ::: rGluTyrGluAspAlaIleIleIleSerArgLysIleLeuTyrAsnAsnL	. 145 613
146 613	TTATCAACTTGTCCTATTTTATTCTAACAGTTT	178 597
179 596	TAAATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCATCA	. 580
229 580	<−ດ	229 563
230 563	CTTATTCATTATTCAGTAATCTTTTATATGCATACTATT	0 4
269 546	CTGAAAAG ::: rgAsp	318 531
319 531	ATAGTATGTAGGAAATAATTACTGTAATACAATAA ::::::	353 514
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454 489	GCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGC::::::::::	503 473
504 473	TGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATT :::::: PheAsnTyrLeuLeuSerPh	553 467
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604 457	TTGCCAGTTGATTTACGTCACCGTGCACTTCTGCA :::	638 440
639 440	ATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCT::: ::::: :::::	688 424
689 423	TACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTG	727 4 07
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seq_documentation_block:

289 289 289 289 289 305 305 305 320 3770 3770 3770 3770 1370 A 697 I 370	266 TATTCATTATTCAGTAATCTTTTTATATGCATACTATTG 2	TTTTATAGCTTCTGAAAAGCT 2	ສ . H ທີ່ພ	LysA 4	YFATATATTCGTTTCTTATCATCC 3 ::: :::::::::::::::::::::::::::::::	euAsnArgIleLeuAsnThrAsnThrAsnIleIleAsnLysAsn 4	AATCAGAAGGCATAAAATAATGTTAGAANCATCAGAASCAAGGCATAAAAAATAATGTTAGAANCATCAGAASCA	CATTATTACCATTTCGTTTAAATTTCGTCCA 4b	:: ::: 41	GGACAACCTGTAATACTTGCTGCAGTACAAAAA100AAA1CACCTGTAATACACTTGCAGTACAAAA100AAA1CACCTGCAATTTCATTTCATTTCATTTCATTTCATT	TTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCAA	CTTGAAATTAGCGATGATA b	ATCTGCAGAACCGGAGAA 6 :: ::::: snLysileAsnGlnAsnGlnLysi 3	lleTyrTyrProLysVa 3	AAGGATTCGGAGCTGTTAAAACAG / ::::::::::::::::::::::::::::::::::	AAGAACCAAATAGCGAATG 8	TGCGGATCGATCACAGCTT 8 :: :::::::: euTyrIleGlnAsnAsnGl 3	TTGCTAAATAATTTGGAATATCCAACAGATTTAA 9 ::::: ::::: ::::: nasnThrThrIleTyrGlnIleLysHisProHis 2	
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22	768 TGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCA 7:	
55	46 lPheGlnThrGlyIleArgAsnLeuV 5	
69	TTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGG 7	
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30	9 AGAAGCTCACGGATACAAATATGCGGATCGATCACAGCTTT 8 : ::::: :::	
)10	38GGCCA 9	
197	85 TAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG 9 ::::::::::::::::::::::::::::::::::	
183	66	
1008 466	GTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTTGTCGATGATGGT:: ::: ::: ::: ::: ThrAspSerPheArgValThrTTpHisProLeuSerAlaAspGluGlyLe	
1056 449		
1106 433	TGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTG :::: :: :: ::	
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1241 384	ATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGG :::::::: ::::::::::::::::::::::::::	
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1341 363	TTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAAT::	
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1441 331	NTGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTA	
1488 318	erGlyLeuLeu	
152 302	TGAGCCAG yAspGluLysG	

	SThrPheValAsnMetThrLeu.LeuTyrGluI :::::: :::: ::::: ::::: ::::::
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C;Accession: G71613
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, I.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
                                                                                                                                   hypothetical protein PFB0470w - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                    seq_name: pir2:G71613
                                                                                                                                                                                                                                                                                                          879 luLysGluLys 882
                                                                                                                                                                                                                                                                                                                                                                                          862 uValLeuLysThrValGluGluGluLysGluGluGluGluGluLysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 TAAATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCATCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      774 eGluLysAsnLeuSerHisLeuLeuAsnIleTyrTyrGlnHisLysIleV 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleArgIleSerGluTyrValLeuSerLysTyrPhePheArgAsnGlyLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGCAATTAAAAAGTATTTCATTTGT..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euPhe.....ValCysGly 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTATGGGCATCATTTCCTATTCTGTAAACAATTCACTTATTTGCATT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eIleAsnAlaLeuSerLysMetCysTyrThrTyrGluMetTyrValValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACAAAT.....TATACCTTGTATTGCCCAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATAATAT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ······GATATTTTCATCAAAACTTCTTCTATCGCTTTTATAGC
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A;Accession: G71613
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Rolecule type: DNA
A;Residues: 1-1346 <GAR>
A;Cross-references: GB:AE001397; GB:AE001362; NID:g3845192; PID:g3845193; TIG:G:GenetLos:
A;Experimental source: clone 3D7
C;GenetLos:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-323-427-2/rev x G71613
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Ratio: 0.319
Percent Similarity: 46.036
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    1159 ...TATGCCGTTATGAAATTT
                                                                                                                                                              1244 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGG......T
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                                                                            ATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAG... 1160
                                                                                                                      {\tt sPhePheIleLeuLysGluAsnTyrTyrTyrLeuSerIleAspAsnLeuT}
                                                                                                                                                                                                        IleSerLeuSerLeuCysAspIleLysTyrLeuAsnLeuTyrAlaLeuCy
                                                                                                                                                                                                                                                                                         {\tt luGlnAsnLeuAsnHisGluAsnMetLysTyrIleIleHisAsnLeuMet}
                                                                                                                                                                                                                                                                                                                                                                          AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
                                                                                                                                                                                                                                                                                                                                                                                                                    TGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luGlnMetPheLeu...LysLysPheLysAspSerLysGlnSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAGGTGGACGTCAAGTTGCCG...GAATTTCACTTCCATTTGATTCA 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euTyrThrSerPheSer.SerLeuSerTyr.Val...ValLysTyrAsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLysGlyTyrCysAsnLeuPheGluIleLeuTyrGlyTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AsnSerGlyTyrAsn...... 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uHisAsnAsnLeuAspAsnLysAsnAsnAsnMetAspPheAsnAsnMetM
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.TGGATGGTGGA 1131
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48
21.280
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probable membrane protein YMR216c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM8261.10c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 06-Feb-1998
C;Accession: S55098
C;Accession: S55098
C;Ribedman, K.; Brown, D.; Bowman, S.
                                                                                                 R; Dedman, K.; Brown, D.; Bowman, S.
submitted to the EMBL Data Library, June 1995
A; Reference number: $55089
A; Accession: $55098
A; Accession: $55098
A; Molecule type: DNA
A; Residues: 1-742 < CDED>
A; Cross-references: EMBL: 249809; NID: 9854459; PID: 9854468; MIPS: YMR216c
A; Experimental source: Strain AB972
C: Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: pir2:S55098
A;Map position: 13R
C;Keywords: transmembrane protein
F;241-257/Domain: transmembrane #status predicted <TMM>
                                                            A;Gene: SGD:SKY1
A;Cross-references: SGD:S0004829; MIPS:YMR216c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1118 alTyrileAsnileMetLysIleValLysLysMetLysAsnTyrAspGlu 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1101 lasnGlnIleMetPheIleLeuAspPheIleLySIleIleAsnGluLySV 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1149 sTyrPheGlnLeuLysLysIleAspLeuGluTyrIleAsnSerAsnIleA 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1135 AsnIleLysArgLysAsnTyrPheThrThr.....TyrSerLysAsnLy 1149
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1166 snAsnLysLysAsnThrTyrAsnAspPhePheAsnGluAsnAsn 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 ...ATAAAACTGCCATATATATTCGTTTCTTCTTATCATCCTTCTAATAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 ATAATGTTAGAATCATCGAAGCAATA......422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1199 eSerAspAsnIleIleArgTyrSerHisAsnGluLysIleAsnThrHisT 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 CTAATTTTAGCTAACAAATATATAGTAT......GTAG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1216 yrLysAsnAsnLysTyrTleIleLysAspIleLysThrPheTyrLysLeu 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1249 sGluGlnIlePheTyrPheLeuLeuPheTyrProPheGluLeuLysGlnT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1233 AspAsnPheLeuIleSerAspIleLeuLeuIleLeuGluLysGlnAsnLy 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1279 TyrLysTyrAspGluThrPheLeuPheAssnMetGluIleLeuPheLeuTy 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTT...TATGGGCATCATTTCCTATTCTGTAAACAATTCACTTATTTGCA 55
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us-09-323-427-2.backtrans.rpr

	1094 CAGCCAGTTTATCATAAATGGACATGCGATTCTGATAACCGTTGATACTTT 1045	1144 TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT 1095 :: ::: 575 alleuLeuGlyAlaPro	1194 AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 1145 	1214 ATTGAGGTATCTGAAATCAC 1195 ::::::::::::	1237 CTGATAAAACAGTTAGTGCACAG 1215 ::::::::::: :: 529 erAsnSerAsnValSerThrAspIleAsnSerProGluAsnLeuIleGln 545	1287 TGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAG 1238 :::: 527Metasps 529	1337 CGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATT 1288 :::::::: 520GlyProTyrIleSerAsnThr	1387 CACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCA 1338	1437 TCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTT 1388 ::::	1487 AATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGA 1438 :::::: 	1537 AAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATCAAT	1587 TACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCG 1538 ::::: 465	1637 ATCGAATTTACTAAATCTTCTGAAATGATTGGTTTTGTTTG	1687 CCCCATCAAGTGGAAGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAA 1638 	1737 AGCAACAACAAACAACAACAACAACAACAACAACAACAAC	Align seg 1/1 to: S55098 from: 1 to: 742	alignment_block: US-09-323-427-2/rev x S55098	alignment_scores: Quality: 104.50 Length: 303 Ratio: 0.816 Gaps: 13 Percent Similarity: 42.244 Percent Identity: 20.462
114	119	12	11 12	11 13	11 15	11	Align	Perce	alignm	A;Cros A;Expe C;Gene A;Gene	A; Acce A; Stat A; Mole A; Resi	.; Per Scienc A;Titl A;Refe	C;Spec C;Date C;Acce R;Gard	seq_na seq_dc hypoth			···	

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Lecule type: DNA
sidues: 1-1712 <GAR>
DSS-references: GB:AE001386; GB:AE001362; NID:g3845148; PID:g3845151; TIGR:PFB031
perimental source: clone 3D7
                                                144 TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT 1095
                                                                                                                                                                                                                                      166
                                                                                                                                                                                                                                                                        244 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC 1195
                                                                                                                                                                                                                                                                                                                            150 LysTyrSerPheHisLysLeuArgIlePheTyrGluTyrLysIleGluMe 1166
                                                                                                                                                                                                                                                                                                                                                                                  294 CATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTAC 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                      133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 TC...CACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATC 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 rValTyrGluTyrValIleGluLysTyrLysArgValHisValLeuTyrL 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 ATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAA 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .441 ATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGA 1392
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)9-323-427-2/rev x C71618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rdner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, 1 ertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, ncc 282, 1126-1132, 1998

tle: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. ference number: A71600; MUID:99021743

cession: C71618
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ecies: Plasmodium falciparum
ecies: Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1031 .....CATTCCTGCTTTGTCGATGATGGTAAC...GGTGATACTGTGGAA 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ent Similarity:
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Quality:
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e: PFB0315w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      itus: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          documentation_block:
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| | | :::||||||::|||
625 LeuLeuGly.............GluLeuProSerTyrLeuLeuArgAsnG1 637
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                                                                                                                                                               AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 1145
                                                                                                                                                                                                                     tGluLysLeuLysLysAsnTyrIleHisCysIleTyrAspIleSerAspL 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                        euGlyArgLeuLeuGlnIleValGluLysLeuPheLysLysTyrIleLeu 1149
                                                                                                      ysLeuGluPheLeuIleLysLysLysMetGlnHisTyr...... 1195
.....PheAsnHisIleIleIleAsnSerTyrGl 1205
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0.477
44.422
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Gaps: 20
Percent Identity: 18.864
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555 C
605 CAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTG 556
CTG 60: 14
648 TAATCAAGCTT638 :: ::: 1412 euileLysPheLysArgLysGluCysLeuMetLysTyrPheTyrThrLeu 1428
4 4
GAACTGATATC 6
13
<u> </u>
Lysīl 1
IAAAGAACCAAATAGCG 8 ::: :: snArgIleAsnIleLys 1
μ @
eAsnTy 13
12 CCAAGAAGCTCACGTATACAATTATGCGGATCGATCAC
AACAGATTTAATGGCTG ;;;;;; leLysValSerLysLys
CTT 9
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CGT 1

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seq_documentation_block:
hypothetical protein PFB0870w - malaria parasite (Plasmodium falciparum)
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C;Dete: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C;Date: 13-Nov-1998 #sequence, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
C;Accession: M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
C;Accession: M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.
i.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.
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i.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.
i.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; Pertea, M.; Salzberg, S.; Labarder, M.; Salzbe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-323-427-2/rev x E71604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: E71604 from: 1 to: 2380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1484 eLysLeuLeuGlnValLeuVaiGlnLysLysGluLysLysSerVallieA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1501 spvalLeuGlnLeuTyrAspLysTyrProTyrIlePheGlnTyrLysAsp 1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1536 AsnArgLysLeuLeuLeuAsnPheLeu 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 TCATCAAAACTTCTTCTATCGCTTTTA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1652 TTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCG 1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1699 CAGCAATAATAACCCCCATCAAGTGGAGG...AAGAAGACAGGAAGCAATC 1653
                                                                                                                                                                                                                                                                                    1602 TCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTAT...TCGATTC 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 nAsnAsnAsnAsnGlyTyrLysLysLysIleLysAsnLysAsnLysAsnL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1505 TCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTA 1456
                                                                                                                                                                                                                                                                                                                                                                523 ysAsnLysLysLysAsnLysLeu.....Asn
                                                                       548 erIleAspAsnAsnVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......TTCGTCCAAATCAGAAGGCATAAAAATAATGTTA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......GTTTCTTCTTATCATCCTTCTAATAACTAATTTTAGCTAAC 360
                                                                                                                                            CGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACT 1506
                                                                                                                                                                                                                   AsnTyrAsnAspAsnPheValSer.ValAsnGlySerTyrAspAsnTyrS 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104.50
0.415
47.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 528
Gaps: 24
Percent Identity: 19.886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ......ThrLeuTyr 1535
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869	TTACGTCACCGTGCACTTCTGCAACAT	647
300	eSerAlaIleIleAlaSerCysAsnIleP	786
548	TCATTGATGTACGAACTGATATCAACACCCTTGAAATTAG	697
785	uAsnIleAsnAsnPheTyrAspAspAsı	774
869	GCTGCGCAACTTCGTTTACTCAAGAAAAGATCT	747
774	IleThrGlnIleLeuProTyrT	764
4	PAAAACAGGTGGTGCCGCAGCAAAACCTG	797
o,	:: lyAsnValPheValGly	751
798	TACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAG	847
750		737
848	AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAG	897
736	GlnLysLeuGluAsnIle	730
898	GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGT	947
729	nlleIleSerAsnValTyrLysHisGlyCys	714
948	TGCTGATGGATGTGCTCTTGATAAATATTTGCTA	985
713	erIleCysAlaCysCysLeuSerValGlyLeuSerValAsnLysCys	697
986	TGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC	1035
697	nIleLeuAsnMetHisThrSerIleAlaGlySerSerAlaG	683
1036	TATCATAAATGGACATGCGATTCTGAAAACCGTTGATACTTTCTGCGCGGT	1085
683	ProTyrHisLeuGlyValSerSerLeuLeuIleGluLysAs	670
1086	GTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT	1135
669	euGlyIleSerPheSerProAlaGlyLeuLeuIle	658
1136	TCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATG	1185
658	<pre>1ValLeuLeuAspAspThrLysGluLysAlaAspProMetAsnL</pre>	643
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1236	TTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCT	1285
626	sGlyMet.IleLysGlnGlnHisAsnAsnIleHisAsnThrHisAsnIle	610
1286	TGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTT	1335
610	IleLysAsnThrLeuSerLysValPheTyrLysAsnTyrValLysArgI	594
1336	GTTGCGCGTACACGATCTCTGAATCCAC	1364
593	ysLysTyrAspThrSerTyrSer	584
1365	GTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAA	1405
84	<pre>(::: :::::::::::::::::::::::::</pre>	567
4	TGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGA	1455
567	4IleAsnAspGluIleArgGluLysLysLysAsnAsnLysGl	55,

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A; Molecule type: DNA
A; Residues: 792-6839 CHEN2>
A; Cross-references: EMBL:X15423; NID:g6897; PIDN:CAA33463.1; PID:g6898
A; Experimental source: var. Bristol
R; Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
Nature 342, 45-50, 1989
A; Title: Sequence of an unusually large protein implicated in regulation of myosin ac
A; Reference number: S06797; MUID:90044042
A; Reference number: S06797
A; Status: nucleic acid sequence not shown
                                                                                                                A;Molecule type: DNA
A;Residues: 806-1175;1178-1998,'Y',2000-3040,'I',3042-3335,'I',3337-5693;5696-6359,'I
A;Cross-references: EMBL:X15423
                  A;Experimental source: var. Bristol
R;Benlan, G.M.; L'Hernault, S.W.; Morris, M.E.
Genetics 134, 1097-1104, 1993
A;Title: Additional sequence complexity in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Benian, G.
submitted to the EMBL Data Library, November 1989
A;Reference number: S07571
A;Accession: S07571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;MoLecule type: DNA
A;Residues: 1-6839 <BEN1>
A;Cross-references: EMBL:L10351
A;Experimental source: var. Bri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Reference number: S57242
A:Accession: S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, February 1993
A;Description: Additional sequence complexity within twitching of Caenorhabditis eleg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 #text_change 18-Jun-1999. C;Accession: S57242; S07571; S06797; S57218 R;Benlan, G.M.; L'Hernault, S.W.; Morris, M.E. submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: myosin-regulating protein N;Contains: protein kinase (EC 2.7.1.-) C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
twitchin - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: pir2:S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    902 ArgLysIlePheAspTyrTyrThrPheVal 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 TCAGTAATCTTTTATATGCATACTATTGTA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 TCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 TATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              868 LeuPheIleCys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           851 snAsnSerValIleSerProHisLeuIleLysTyrAsnHisIleLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             835 eLysValSerProPheAspSerAspTyrValGlyIle...GlyAsnLysA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 GTCATTATTACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGCATAAAA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            813 leAspGly.....PhePheSerThrLysLysLysAspPheGlyCysPro 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597 TGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCAC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATTCGTTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leGluLysAspTyrLeuPheLeuIleGluAsnLeuLysAspIleLeuGlu 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnThrArgThrGlu.....ArgIleIl 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .........ValLysAsnIlePheHisLysTyrIleAsnAsnLeuTrpI 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....SerAsnIlePheValAsnPheArgAsnLysLysCysI 813
sequence complexity in the muscle gene, unc-22, and its encoded p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bristol
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	TrpGlnGluValGlyThrPheProAspCysThrAlaLysValasnLy AGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCAC	63 TGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGC	1003 GTGATACT	1046	.085TATCATAAATGGACATGCGATTCTGAAACCGTTGATACT	.yLeuLeuAspLeuArgIleL CTATCATTGGTCAGCCAGTT ::: ::: ::: \lapheGluGlyGluProAla	142TTGGATGGTGGACCAACCGGTCAACCAGTT	1173 TGTCCCGATGCCAGTATGCCGTTATGAAATT	223 AGT	2 phisvalaspLeuGluTrpLysPr 1CGTGCATATCGAGTACAATGCT	431 J 310 (441
euging 3712 GCAGCT 741	CAT	rGGCTG 914 ::: 1yG1yT 3662 873 G1yThr 3678	lyThr 36 GCTCT 96 ::: ThrLe 36	se 21	ລັ ໝ ⋅	leLy GTT.		1aG 3	Ø ·· ⊢∃	In Ic	. 0

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A;Cross-references: GB:J03512
A;Experimental source: submaxillary gland
R:Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson Jr.,
J. Biol. Chem. 262, 11339-11344, 1987
A;Title: Structural properties of porcine submaxillary gland apomucin.
A;Reference number: A92606; MUID:87280230
A;Accession: B29789
A;Accession: B29789
A;Molecule type: protein
A;Residues: 1572-1607 <EC2>
C;Superfamily: pig submaxillary mucin
C;Keywords: tandem repeat
                                                          alignment_block:
US-09-323-427-2/rev x T03099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: mRNA
A:Residues: 12139-12167,'T',12169-13288 <EC3>
A:Residues: 12139-12167,'T',12169-13288 <EC3>
A:Cross-references: GB:M61883; NID:g454837; PID:g164374
A:Cross-references: GB:M61883; NID:g454837; PID:g164374

R:Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.; Hill, R.L.
J. Biol. Chem. 263, 1081-1088, 1988
J. Biol. Chem. 263, 1081-1088, 1988
A:Title: Porcine submaxillary gland apomucin contains tandemly repeated, identical seque
A:Reference number: A28528; MUID:88087170
                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 12139-12167, 'T', 12169-12641 <TIM>
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A;Residues: 1-13388 <ECK>
A;Residues: 1-13388 <ECK>
A;Cross-references: EMBL:AF005273; NID:g2581863; PID:g2581864
R;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
J. Biol. Chem. 266, 9678-9886, 1991
A;Title: Porcine sumbarillary mucin contains a cystine-rich, carboxyl-terminal domain A;Reference number: A40009; MUID:91236743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Eckhardt, A.E.; Timpte, C.S.; DeLuca, A.W.; Hill, R.L.
J. Biol. Chem. 272, 33204-33210, 1997
A;Title: The complete cDNa; Delucation of the polypeptide chain A;Reference number: 214839; MUID:98070526
A;Recession: T03099
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A28528
   Align seg 1/1 to:
                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N; Alternate names: apomucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:T03099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Species: Sus scrofa domestica (domestic pig);Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Sep-1999;Accession: T03099; A40009; A28528; B29789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in, submaxillary - pig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3746 sp...ArgIleAspIleLysTrpAsnProThrAlaAsnAsnGlyGlyAla 3761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3720 GluGluProIleIleAlaLys.....AsnGlnPh 3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  590 CCTGTA 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eAspValProAspProValAspLysProGluValThrAspTrpAspLysA 3746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ly......GluSerLysProLeuGluAla 3719
                                                                                                                                                                                                                                     Quality:
   T03099 from: 1
                                                                                                                                                                 104.00
0.654
39.259
                                                                                                                                                          Length: 405
Gaps: 20
Percent Identity: 21.975
to: 13288
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13029 erLysGluIleThrAlaSerProLysValSerSerProGluThrThrAla 13045
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                                                                                                                                                                                                                                                                                                                                    13073 euGlyGluGluLysSerProGlyAspValTrpThrAlaAsnCysHisLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1234 ATAAAACAGTTAGTGCACAGATTGAGGTATCTGAA...ATCACAACTGCT 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1331 ATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTAC 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1381 CATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGT 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1557
1707 AACAACAACAGCAATAATAACCCCCATCAAGTGGAGGAAGAAGACAGGAAG 1658
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                                          snAspThrCysCysGluIle......GlyHisCysGluLysArgThr 13136
                                                                                                                                                                                                                                                                                    TGGACATGC...GATTCTGAAACCGTTGAT.....ACTTTCTGCGC 1039
                                                                                          ACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAA 957
                                                                                                                                          oSerProProThrCysLysThrGlyGluArgLeuIleLysPheLysAlaA 13123
                                                                                                                                                                                  CysThrCysThrGluAlaLysThrValAspCysLysProLysGluCysPr 13106
                                                                                                                                                                                                                                                                                                                                                                                      CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyAlaThrGluAspGlnGluAsnGluAsnLysThrGlyCysProAlaPr 13062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAGTTGATCGTGCATATCGAGTACAATGCTTT...TACATGGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheLysGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lySerGlyThrThrSerSerProGlyGlyValLysThrGluAlaThrThr 12978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAA 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ro...GlySerGlyGlyValThrSerSerGlnGluGlyThrSerArgGlu 13010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCA.....CTTC 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCG 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGTGGACCAACTTCAATAACAATCAATTTTAATACACGT...AATGCA 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCGGTTGACAATGGTGTCGAA......GGTGAGCCAGAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGAT 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAATCTTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATG 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ······ValGlyThrThrGluAlaGlyIleSerSerGlyAsnSerP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rThrProThrGluValArgAlaAlaThrGlyAlaGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....AlaProArgIleSerAlaThrGlySerThrSerValS 13029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTCTATAACACCGACTGCAGCAACAACAACAACAACAACAACAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....ThrAlaValGlyAlaThrSerArgSerTh 12945
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696	744	772	806	856	906	13137
13211	13194	13177	13162	13145	13145	
696 TATCATTGATGTACG 682 ::: 13211 TyrAsnGlyCysThr 13215	744AGCTGCGCAACTTCGTTTACTCAAGAAAGATCTGCAGAACCGGAGAA 697 ::: ::: ::: :::	772 CAGGTGGTGCCGCAGCAAAACCTGCTGC. 745 	806 TGTTCAGAACCACAAGGATTCGGAGCTGTTAAAA 773 	856 AGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAA 807 ::::::::::::::::::::::::::::::::::::	AGCTCACGIAIACAAAIAIACCAAAA	::: ::: 13137 CysLeupheAsnAsnThrAspTyr

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SwissProt_38:CUT1_CAEEL - 1420.50 2216.62 106-116 42
SwissProt_38:RPOB_PLAFA - 112.00 155.32 0.0652 12
SwissProt_38:Y0H3_CAEEL - 109.50 155.32 0.0652 12
SwissProt_38:Y0H3_CAEEL - 109.50 155.32 0.0221 49
SwissProt_38:RPOB_PLAFA - 106.50 153.40 0.1581 34
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SwissProt_38:RMS_PLAFA - 103.50 143.90 0.3708 1150
SwissProt_38:RMS_PAPILI - 103.00 144.04 0.3498 55
SwissProt_38:RMS_PAPILI - 103.00 144.04 0.5809 56
SwissProt_38:RMS_PAPILI - 100.50 1139.96 0.5809 56
SwissProt_38:RGALDICDI - 100.00 144.63 0.5669 31
SwissProt_38:RGALD_PAPILI - 100.50 1139.90 0.7490 71
SwissProt_38:YAY3_SCHPO - 97.00 124.80 1.57 21
SwissProt_38:YAY3_SCHPO - 97.00 121.80 1.57 21
SwissProt_38:YAY3_SCHPO - 97.00 123.90 1.10 64
SwissProt_38:YAY3_SCHPO - 97.00 133.90 1.10 64
SwissProt_38:YAY3_SCHPO - 97.00 133.91 1.10 57
SwissProt_38:YAY3_SCHPO - 97.00 133.61 1.10 1.76 1.10 57
SwissProt_38:YAY3_SCHPO - 97.00 136.11 1.45 369
SwissProt_38:PGS1_RAT - 95.50 136.11 1.45 369
SwissProt_38:RGS1_RAT - 95.50 136.11 1.45 369
SwissProt_38:RGS1_RAT - 95.50 124.70 1.89 122
                                   SwissProt_38: PGSI_HUMAN -
SwissProt_38: XLIG_ECOLI -
SwissProt_38: AMD2_XENLA -
SwissProt_38: SRBB_YEAST -
SwissProt_38: SYLMS_CAEEL -
SwissProt_38: YLMS_CAEEL -
SwissProt_38: PYR1_SCHPO -
SwissProt_38: PYR1_SCHPO -
SwissProt_38: DYR1_SCHPO -
SwissProt_38: TUD_DROME -
SwissProt_38: YF61_METJA -
SwissProt_38: Y155_VEAST -
SwissProt_38: Y155_PARPR -
SwissProt_38: SYLS_PARPR -
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Database length: 29864866
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-Q-/cgn2_1/USPTO_spool/US09323427/runat_14042000_170514_19931/app_query.fasta.-
-Q-/cgn2_1/USPTO_spool/US09323427/runat_14042000_170514_19931/app_query.fasta.-
-DB=SwissProt_38 -QFMT=fastan -SUFFIX=backtrans.rsp
-GAPOP=12.000 -GAPEXT=4.000 -MINATCH=0.100 -LOOPCL-0.000
-COOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.000 -QGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DCCALIGN=200
-THR_SCORE=PCt -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-MINLEN=0 -MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3
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                    116 424 | Q03755 caenorhabditis elegar 1024 | P21421 plasmodium falciparu 1495 | Q09276 caenorhabditis elegar 1495 | Q09276 caenorhabditis elegar 1369 | P21809 bos taurus (bovine). 55 742 | Q03656 saccharomyces cerevis 150 | P17889 bacillus subtilis. tra 150 | P12021 sus scrofa (pig). apom 554 | P34855 apis mellifera liqust 1716 | P17889 bacillus subtilis. tra 1716 | P17889 bacillus scrofa (pig). apom 554 | P18091 bos taurus (bovine). 317 | P14188 dictyostelium discoid 369 | P16492 herpesvirus saimiti (del 1717 | P16492 herpesvirus saimiti (del 1718 | P17802 pacudomonas aeruginos per 1718 | P18653 mus musculus (mouse). 369 | P18890 xenopus laevis (africal 1718 | P1890 xenopus laevis (africal 1895 | P1890 xenopus laevis (africal 1890 | P1890 xenopu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | P47853 rattus norvegicus (rat)
| 8 | Q08853 plasmodium falciparum |
| 8 | P21810 homo sapiens (human) |
| 1 | P75802 escherichia coli hyp |
| 5 | P12890 xenopus laevis (afrid |
| 7 | P25648 saccharomyces cerevi |
| 61 | P47179 saccharomyces cerevi |
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| 62 | P41951 caenorhabditis elega |
| 63 | P41951 caenorhabditis elega |
| 64 | Q08794 schizosaccharomyces |
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i P25823 drosophila melanogast
i Q58956 methanococcus jannasc
i P05510 neurospora crassa. na
i P14772 saccharomyces cerevi
i P13837 paramecium primaurel
i P27801 saccharomyces cerevi
i P27801 saccharomyces cerevi
30938 rattus norvegicus (rat
029441 archaeoglobus fulgid
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SA PEREFERENCE AND SERVICE SER
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SwissProt_38:RMAR_CANGA -
SwissProt_38:UL52_HSV7J -
SwissProt_38:AMD_HUMAN -
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01-FEB-1994 (Rel. 28, C
15-JUL-1998 (Rel. 36, I
15-DEC-1998 (Rel. 37, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities reguires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBDITIES (APR-1995) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: COMPONENT OF THE CUTICLES. IT FORMS A RIBBON APPROXIMATELY 2 MICRONS WIDE RUNNING ALONG THE LATERAL LINES UNDERNEATH THE ALAE. CONTRIBUTES TO THE FORMATION OF EXTRACELLULAR ENVELOPES PROTECTING THE ORGANISM FROM THE ENVIRONMENT.

-I- SUBCELLULAR LOCATION: SECRETED

-I- TISSUE SPECIFICITY: LOCALIZED IN A NARROW BAND NOT EXPOSED TO THE EXTERIOR, RUNNING UNDERNEATH THE ALAE.

-I- DEVELOPMENTAL STAGE: EXPRESSED DURING DAUER LARVA FORMATION.

-I- DOMAIN: THE SMALL REPEATS A-A-P-[AVI] ARE ALSO PRESENT IN MANY PROTEINS CONSTITUTING THE PROTECTIVE ENVELOPE OF OTHER SPECIES.
                                                                                                                                                                                                                                           REPEAT
REPEAT
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MEDLINE; 91323673.
SEBASTIANO M., LASSANDRO F.,
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CUT-1 OR C47G2.1.
Caenorhabditis elegans.
Caenorhabditis elegans.
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IG -> MR (IN REF. 1).
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4 X 4 AA REPEAT OF A-A-P-[AVI].
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! ! P21358 candida glabrata (
! P52468 herpes simplex vir
! P19021 homo sapiens (human
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alignment_block:
US-09-323-427-2/rev x CUT1_CAEEL
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7)
                                                                                                                                                                                                                      MEDLINE, 95.07345.

GARDNER M.J., GOLDMAN N., BARNETT P., MOORE P.W., RANGACHARI K., GARDNER M.J., GOLDMAN N., BARNETT P., MOORE P.W., RANGACHARI K., STRATH M., WHYTE A., WILLIAMSON D.H., WILSON R.J.M.; STRATH M., WHYTE A., WILLIAMSON D.H., WILSON R.J.M.; Phylogenetic analysis of the rpoB gene from the plastid-like DNA of plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                               RPOB_PLAFA
                                                                              GARDNER M.J., WILLIAMSON D.H., WILSON R.J.M.;
"A circular DNA in malaria parasites encodes an RNA polymerase like that of prokaryotes and chloroplasts.";
MOL. Blochem. Parasitol. 44:115-124(1991).
-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION DNA-DEPENDENT RNA POLYMERASE CATALYZES TRIPHOSPHATES AS OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATT 513
            MISCELLANEOUS: THIS RNA POLYMERASE IS ENCODED ON A CIRCULAR DNA. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                         SUBSTRATES. CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N
                                                                                                                                                                                                          Biochem. Parasitol. 66:221-231(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                       Apicomplexa; Haemosporida; Plasmodium
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                                                                    PYROPHOSPHATE
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1159 236	1208 GTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGT 1 : : :
1209 219	1258 TACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAG 1
1259 204	1308 CATTTCGTTTCATCCATTATTTGTTACCAAAGTTGÅTCGTGCATATCGAG 1 :: :: :::::::: 191 euPheIleTyrAsnAsnIleIleAsnLysLysIleLeuIle 2
1309 191	1358 CGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGT::::::::::
1359 179 .	1408 GACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCG
1409 162	1458 TTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTG ::: :: ::: :::::::: 152 rgilellePheLysileSerLysLeuAsnile
1459 152	1499 ACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGT :::::: :::::::
1500 135	1543GTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA ::: ::::: ::: 119 IleGlnLeuPheLysLysAsnAsnLysIlePheIleIleLysPheLysAs
118 .	yLeuTyrLysThrCys
1544	1544
1544 102	1583 ACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATG :::: ::::::::::::::::::::::::::
1584 86	1633 AATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACT ::: 70 ASNIleASnASnLeuLeuLySIleIleLeuThrLeuLySLeuASnPheIl
	Align seg 1/1 to: RPOB_PLAFA from: 1 to: 1024
	alignment_block: US-09-323-427-2/rev x RPOB_PLAFA :.
	alignment_scores: Quality: 112.00 Length: 665 Ratio: 0.373 Gaps: 28 Percent Similarity: 45.113 Percent Identity: 17.594
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ed through a collaboration and the EMBL outstation - e no restrictions on its content is in no way ge by and for commercial //www.isb-sib.ch/announce/	ppyright. It is producte of Bioinformatics Institute. There are tutnions as long as it tis not removed. Usas agreement (See http: elisb-sib.ch).

404	AAGCAATAATAAAACTGCCATATA	4
454 489	503 GCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGC :::: :: :: :::::::::::::::::::	A C
473	67 PheAsnTyrLeuLeuSer	4
0	CCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATT	(n
554 466	GCA	4 0
604 457	38 TIGCCAGTTGATTTACGTCACCGTGCACTCTGCA :::: ::::: 40 eAsnLysThrThrIleLeuThrIleAsnLysAsnThrPheLysIleCysA	
440	24 PheTyrAsnIleSerPheAsnA	
639	TACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGC	_
689 423	07 heTyrAsnArgTyrAsnPheLysLeuLeuI	
0	TlePheLeuAsnLeuLysTyrLeuPheValIleTyrTyrLysHis1	
728	28	
	luGlyLeuThrCysGlyLeuValAsnTyrLeuThrThrA	
7	AGCTGCGCAACT	
746 373	795 ACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTG :: ::::::::::::::::::::::::::::	
in t	ysīleAsnMetIleThrThrGlyLeuAsnSerLysPheIleLeuAsn	
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806 340	847 TTACCATTANAGAACCAAATAGCGAATGTGTTCGACCACAAT :::::::::::::::::::::::::::::	
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848	97 ATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGT	
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ρι	ATAATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCAC	
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866	TTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGA::::::::::	1.1
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260	### ##################################	
10	TGCTATCATTGGTCAGCCAGTTTATC	
243	236 snileTyrlleAsnLeuLeuAsn	

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Seq_documentation_block:
ID YQH3_CAEEL STANDARD;
AC Q09276;
AC Q09276;
DT 01-NOV-1997 (Rel. 35, Last
DC C Enkaryota; Metazoa; Nemato
OC Rhabditina; Rhabditoidea;
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RN SULSTON J.;
SULSTON J.;
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CC This SWISS-PROT entry is C
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CC EMBL; 247067; CAA87330.1;
DR WORMPEP; C43C3.3; CE01525;
KW Hypothetical protein; Trar
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 55.1 KD PROTEIN C43C3.3 IN CHROMOSOME
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Caenorhabditia; Rhabditida; Bukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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        EMBL; Z47067; CAA87330.1; ..

WORKPEP; C43C3.3; CE01525.

Hypothetical protein; Transmembrane; ATP-binding.

TRANSMEM 11 31 POTENTIAL.
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luGlyIleValIleTyrValSerCysIleLysIleIleIleArgAsp... 546
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euTyrThrSerLeuHisLeuAsnIleTyrGluIleSerLeuAsnIleIle 646
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Quality:
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NP_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                 1340 CCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCAT...CC 1294
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141 hrIleProTyrGlySerGluCysAspValThrLeuThrAspLeu...... 155
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                                                                                                                                                                                                                                                                ATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACA 1244
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|ProLysHisArgTyrAlaGluThrThrValValLeuGluAspAsnAlaAs 172
                                                                                                                                    ACTGCTTTTCAA.....ACTCAAATTGTCCCGATGCCAGTATG 1156
                                                                                                                                                                                                                                   pLeuSerPheGlyLysThrThrArgLeuAsnHisValPheCysLeuTyrT 189
                                                                  CCGTTATGAAATTTTG.....GATGGTGGACCAACCGGTCAAC 1118
                                                                                                    AsnGlyHisGluValIleAlaSerThrGlyGlyLysProLysPro..... 216
                                                                                                                                                                    hrArgAsnValLysThr.....lleArgPheSerAspValSer
        CA..
                                     .LysValGluMetLeuPheArgSerThrAspSerGlyLysThrLeuGlnA 233
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0.559
47.229
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Gaps: 24
Percent Identity: 21.446
          .GTTCAATTTGCTATCATTGGTCAGCCA...
ATP (POTENTIAL).
09C77468 CRC32;
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ROSENBERG

L.C.,

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seq_documentation_block:
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   NEAME P.J., CHOI H.U., ROSENBERG L.C.;
"The primary structure of the core protein of the small, leucine-rich proteoglycan (PG I) from bovine articular cartilage.";
J. Biol. Chem. 264:8653-8661(1989).
                                                                                                                                                        XU J.H., RADHAKRISHNAMURTHY B., "Primary structure of bovine aor cloned CDNA.";
                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1030 ATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAAT
                                                                             MEDLINE; 89255324.
                                                                                              SEQUENCE OF 38-369. TISSUE=CARTILAGE;
                                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (Rel. 18, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BI
                                                                                                                                                                                                     MEDLINE; 96113563.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt ArgArgThrThrArgSerAlaProThrAspAspAsnGlySerLeu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTG 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rgPheArgHisLysArgSer......IleThrAspLeuGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt lnSerThrValPheValHisCysGlnValGlnValCysLeuLysLys...}
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                                                                                                                                        Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                        Int.
                                                                                                                                   37:263-272(1995)
                                                                                                                                                                  B., SRINIVASAN S.R., aorta biglycan core
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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US-09-323-427-2/rev
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CARBOHYD
DISULFID
DISULFID
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SEQUENCE
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CARBOHYD
CARBOHYD
                              775 AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA
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REPEAT
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REPEAT
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PIR; A33701; A33701.
PFAM; PF00560; LRR; 8.
PFAM; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DS-PGII, from bovine articular cartilage and skin isolated by octyl-
sepharose chromatography.",
J. Biol. Chem. 264:2876-2884(1989).

-i- TISSUE SPECIFICITY: FOUND IN THE EXTRACELLULAR MATRICES OF SEVERAL
CONNECTIVE TISSUES, SPECIALLY IN ARTICULAR CARTILAGES.

-i- PTM: THE TWO GLYCOSAMINOGLYCAN CHAINS ATTACHED TO BIGLYCAN CAN BE
EITHER CHONDROITIN SULFATE OR DERMATAN SULFATE.

-i- SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, from bovine articular cartilage and skin isolated by octyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEAME P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHOI H.U., JOHNSON T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=CARTILAGE;
MEDLINE; 89123388.
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SEQUENCE OF 38-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 10\,\cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY.
                                                                                                                                                                            Quality:
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                                                                                                                                                            Ratio:
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38
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93
117
141
162
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                                                                PGS1_BOVIN
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0.873
40.803
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                                                                                                                                          Percent Identity:
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C -> E (IN REF.
A -> R (IN REF.
KK -> Y (IN REF.
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Gaps:
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Bovinae; Bos.

Biochem. Mol.

299 13 20.736

2).

PGS1_BOVIN P21809; P792 01-MAY-1991

(PG-S1).

364

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seq_documentation_block:
ID KM65_YEAST STAN
                                          seq_name: SwissProt_38:KM65_YEAST
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sAsnHisLeuCysGluIleProProAsn......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC 308
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                                                                                                                                                                                                LeuArgGluLeuHisLeuAspAsnAsnLysLeuSerArgValProAlaGl 296
                                                                                                                                                                                                                                                                                                                                                      TTCAGTAATCTTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                               ATCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                             lyIle......ProLysAspLeuProGluThrLeuAsnGluLeuHis 236
                                                                                                     TCACAAATTATACCTTG.....TATTGCCCAATTTTTATGGGCATC 89
                                                                                                                                                                  ......ATTTTATTCTAACAGTTTATCATTTGTGATAATA 130
                                                                                                                                                                                                                                                               ATGAATAGTTTCGTTTGTTATTATCA...TCATTATCAACTTGTCCT... 164
                                                                                                                                                                                                                                                                                                                     STANDARD;
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           742
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alignment_scores:
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE SERINE/THEEONINE-PROTEIN KINASE YMR216C (EC 2.7.1.~).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. SIMILAR TO S.POMBE DSK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetaceae; Saccharomyces.
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DEDMAN K., BROWN D., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.,
                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ACT_SITE
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z49809; CAA89931.1;
HSSP; P24941; 1AQ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                              419 SerGlyAsnArgAsnIleProSerSerIleAsnAsnAsnAsnSerIleAsnAs
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                                                                                                                               TACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCG 1538
                                                                                                                                                                                              ATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTG 1588
                                                                                                                                                                                                                               \verb|nGlyIleGlyIleLysAsnSerAsnAsnSerPheLeuAsnSerValProH|\\
AATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGA 1438
                                                                                                                                                                .....AsnAsnAspAsnSerLysAsnLysAsnAsnAsn.AsnAsn
                                                                                               .....AspAsnAsn.....
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Ratio:
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Gaps: 13
Percent Identity: 20.462
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                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Crar
Eukaryota; Metazoa; Chordata; Crar
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                                                                    MEDLINE;
ECKHARDT
                                                                                                                                                                                                                                                                                    01-OCT-1989 (Rel. 12, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
APOMUCIN (MUCIN CORE PROTEIN) (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          637
                                                                                         TISSUE=SUBMAXILLARY GLAND;
MEDLINE; 91236743.
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              carboxyl-terminal
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                                            Porcine
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        A.E., TIMPTE C.S., submaxillary mucin terminal domain in
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  ABERNETHY J.L., ZHAO Y., HILL R.L.; contains a cystine-rich, addition to a highly repetitive,
                                                                                                                                                                                                                                 Craniata; Vertebrata;
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"Determination of the site-specific O-glycosylation pattern of the porcine submaxillary mucin tandem repeat glycopeptide. Model proposed for the polypeptide:galnac transferase peptide binding site.";

J. Biol. Chem. 272:9709-9719(1997).

-i- FUNCTION: APOMUCIN IS PART OF MUCIN, THE MAJOR GLYCOPROTEIN SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE THE ORAL CAVITY AND TO PROTECT IT FROM THE EXTERNAL
                                                                                                                                                                                                                                                      Glycoprotein;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M61883; AAA30998.1; -. EMBL; M21174; AAA30990.1; -. PIR; A40009; A40009.
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ECKHARDT A.E., TIMPTE C.S., ABERNETHY J.L., TOUMADJE JOHNSON W.C. JR., HILL R.L.;
"Structural properties of porcine submaxillary gland J., Biol. Chem. 262:11339-11344(1987).
                                                                                                                                              REPEAT
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J. Biol. Chem 266.067
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J. Biol. Chem. 263:1081-1088(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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SIMILARITY: CONTAINS 1 CWFC DOMAIN.
SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
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SUBUNIT: INTERMOLECULAR DISULFIDE BONDS COULD
MULTIMERIC MUCIN STRUCTURE.
SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.
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PS01225; CTCK_2; 1.
PS01208; VWFC; 1.
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1708 785 1658 797 1608 797 1558			

772 CAGGTGGTGCCGC : 1039 nThrTrpCysAla	AGAACCAC ::: .GlnAsnT	AGATCAGTATTA	906 AGCTCACGTATAC	956 TATTTGCTAAATAATTTGG? ::: 999 CysLeuPheAsnAsnThrAs	1006 ACGGTGATACTGTGGAAATTCT 	1038 GGTTGTCCATTCCT	1076 TGGACATGCGP :: 952 CysThrCysThrGl	1126 CCGGTCAACCAGTTCAA ::: 935 euGlyGluGluLysSer	1175 .ATTGTCCCGATGCCAGT :::	1187 TTTCAAACTCAA ::: 908 GlyAlaThrGluAs	1234 ATAAAACAGTTAGTGCACA :: ::::: :: 891 erLysGluIleThrAlas	1281 CAAAGTTGATCGTGCATATCGAG	1331 ATTTTTGTAACAACAGCTGTTGTC	1381 CATTTGATTCATGCAATGTTGCG	1422 TAATGATGAAGGTGGACGT	1472 TTCGAAGGACATGTT ::: 841 PheLysGly	1519 AATGTGGACCAACTTCAA 824 lySerGlyThrThrSerS	
GluGluAspArgValTyrAs	AAGGATTCGGAGCTGTTAA hrGlyPheThrAlaValVal0	ATTAAAGAACCAAATAGC	AAATATGCGGATCGATCACAGC	ATATCCAACAG :: spTyr	AAATGCTGA	ATTCCTGCTTTGTCGATGAT ::: ::: roThrCysLysThrGlyGluArgLeuIle	GATTCTGAAACCGTTGAT :::::::: phrGluAlaLysThrValAspCysLysP	TTTGCTATCATTGGTCAGCC ::: proGlyAspValTrpThrAl	ATGCCGTTATGAAATTTTG ::: 1CysHis	pGlnGluAsnGluAsnLysThrG	\GATTGAGGTATCTGAA :: : ::: srProLysValSerSerPr	TACAATGCTTTT :::::: leSerAlaThrGlyS	ATTTCGTTTCATC	GTTGCGCGTACACGATCTCT ::: valThrSerSerGlnGluGl	ACGTCAAGTTGCCGGAATTTCA.	: :	AATAACAATCAATTITATIA 	erThr
AGCAAAACCTGCTGC. 743 pSerLysGlnCysCysT 1056	/sProLysGl 10	GAATGTGTTCGACCACAA 807 	TTTTCTATCAATGCC 85/ 1007	TGGCCAAGA 90	, H D	.GGTA 10 :::1 sAlaA 98	968	TTATCATAAA 107	GACCAA 112 yProL 935	yCysProAlaPr	ATCACAACTGCT 118 GluThrThrAla 907	ACATGGAAGCTG 123 ::::::: erThrSerValS 891	TATTTGTTAC 128	 erArgGlu 872	yAsnSer	60 I	uAlaThrThr	rThrGluThrG 824

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alignment_block:
US-09-323-427-2/rev x NU5M_APILI
                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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                                                                                                                                                                                                                                                                  Align seg 1/1 to: NU5M_APILI from: 1 to: 554
                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
         1228
                                                                                                                                  1265 TATC......GAGTACAATGCTTTTACATGGAAGCTGA 1234
                                                                                                                                                                                                                           1315 CTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCA 1266
                                                                   1233 TAAAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L06178; AAB96805.1; -. PFAM; PF00361; oxidored_q1; 1. PFAM; PF00662; oxidored_q1_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1073 TyrAsnGlyCysThr 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=THORAX;
MEDLINE; 93114603.
CROZIER R.H., CROZIER Y.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .696 TATCATTGATGTACG 682
                                   44 etLysPheAsnPheLeuLeuIleAspTyrLysSerLeuMetPheIle 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 554 AA; 65590 MW; 9E256E2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization."; Genetics 133:97-117(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
                                                                                                            27 rLeuAsnLysGluPhePhePheGluTrpAsnIleTyrThrPheAsnSerM 44
                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apis mellifera ligustica (Common honeybee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        744 ..AGCTGCGCAACTTCGTTTACTCAAGAAAGATCTGCAGAACCGGAGAA 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P34855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NU5M_APILI
                                                                                                                                                                                         LeuPheGluPheSerPheLeuMetMetLeuMetSerLeuTyrLeuLeuTy 27
                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                 103.00
0.396
46.931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
.....CAGTTAGTGCACAGATTGAGGTA 1206
                                                                                                                                                                                                                                                                                                                                                       Length: 554
Gaps: 34
Percent Identity: 21.480
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                                                                           1229
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513 348	TCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATT !	332
331	CALAMA SERVER COLOR MATERITY OF SERVER COLOR MATERIA COL	
604 315	ATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCA ::: MetPheMetCysValGlySerTyrMetH1sTyrMetTyrSerA	0 0
654 300	CGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGC	80 0
704 283	AAC ::: /Ser	753 268
754 268	AAGGATTCGGAGCTGTTAAAACAGGTGGTGCTGCAGCAAA ::: ::: euValAlaAsnPheGluLeuAspLeuLysLysValValAlaTyrSerT	υīω
794 251	TTCAGAACCAC	235
806 234	ATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAAT	N 5
856 220	ACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCA	
203	LysSerAlaGlnIleProPheSerThrTrpLeuProMetAlaMetMetAl	187
186	yrLysMetAsnGluPheMetMetIleTyrIleLeuLeuMetAlaPheThr TAATGGTTGGTGAAGAAGGTT	170 928
929		929
929 170	AAATATTTGCTAAATAATTTGGAATATCC :	959 153
960 153	GTAACGGTGATACTGTGGAAATTCTAAA1 ::::: :: ValThrIleLeuLeuAsnArg	1009 140
139	yrCysLeuValIleTyrTyrMetLysMetLysSerPheThrSerGly	123
1010		1012
1013 123	GTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTV :: Annual control contro	1055
1056 106	CTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG	1105 96
- 4	euMetileLeuphe	91
1106	CCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTT	1155
1156 91	TCTGAAATCAC ::: rMetAsp	1205 77
77	<pre>PheLeuValSerMetIlePheSerMetIleIleIleTyrSerIleSerTy</pre>	61

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seq_name: SwissProt_38:IF2_BACSU
                                                                                                                                                                                                                                   _documentation_block:
	IF2_BACSU STANDARD; PRT; 716 AA.
	P17889; 031757;
	01-NOV-1990 (Rel. 16, Created)
	01-NOV-1990 (Rel. 16, Last sequence update)
	15-DEC-1998 (Rel. 37, Last annotation update)
	TRANSLATION INITIATION FACTOR IF-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482
                                                                                                                                                                                                                                                                                                                                                                                                                                                         498
                           "Isolation and molecular genetic characterization of the Bacillus sene (infB) encoding protein synthesis initiation factor
                                                                             MEDLINE: 90236932.
SHAZAND K., TUCKER J., CHIANG R., STANSMORE K.,
SPERLING-PETERSEN H.U., GRUNBERG-MANAGO M., RABINOWITZ J.C.,
                                                                                                                                                                            Bacillus subtilis.
Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                         46
                                                              LEIGHTON T.;
                                                                                                                            STRAIN=168;
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                         INFB.
                                                                                                                                                                       Bacillus/Staphylococcus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euValGly.....SerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCAAA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt tileAsnLeuIleIleGlyThrIlePheThrValSerTyrSerPheArgM}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGAAGGCATAAAAATAATGTTAGAATCATCGAAG......CAATA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATTCATTATTCAGTAATCTTTTATATGCATACTATTGTAAATGTTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGluAspLysIleMetCysIleSerMetMetMetMetIlePheSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTAGGAA.....ATAATTACTGTAATACAATAAGTGATATTTTC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATCATCCTTCTAATAACTAATTTTAGCTAACAA.....ATATATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt AspLeuIleIleGluMetPhePhePheSerLysMetIleTyrPheSerMe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rLeuIleTyrSerLysLeuIlePheAsnLeuMet.AsnPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.....TCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etIleLeuValLeuThrSerLysPheLeuMetMetAsnValIleTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTAGGCCATGAATAGTTTCGTTTGTTATT.....A 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                    etPheThrTyrGluValTyrIleGluLysSerIleIleGluIleLeuSer 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGTGATAATATCACAAATTATACCTTGTATTGCCCAATTTTTATGGGCA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euIleLeuLeuAsnAsnLysIleGlyTyrPheLysMetSer.PheLeuPh 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATCATTATCAAC.....TTGTCCTATTTATTCTAACAGTTTATCAT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt lpheLysMetIleMetValGlyLeuIleMetGlyPheAsnPheTyrLysL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt AsnLeuLeuGlyIleAsnLeuLeuMetIleTyr.....LysLeuMetVa}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eMet...AsnLeuIleTyrLysIleIleTyrLysLysIleIleMetMetM 498
 Bacteriol. 172:2675-2687(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATTTCCTATTCTGTA.....AACAATTCACTTATTTGCATTATTGCA 47
                                                                                                                                                                                                                                                                                                                                                                                          SerLys 516
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTAAA 41
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US-09-323-427-2/rev x IF2_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                    Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M34836; AAA22673.1; -.
EMBL; Z18631; CAA79234.1; -.
EMBL; Z99112; CAB13536.1; -.
PIR; A35269; A35269.
PIR; B35269; A35269.
PIR; B35269; B35269.
PIR; B35269; B35269.
PIR; S31994; S31994.
HSSP; P02990; 1ETU.
SUBTILIST; BG10268; INFB.
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SHAZAND K., TUCKER J., GRUNBERG-MANAGO M., RABINOWITZ J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Similar organization of the nusA-infB operon in Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 175:2880-2887(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its tuse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/announce/entities.com/a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
NP_BIND
NP_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initiation recommendation. Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; pF00009; GTP_EFTU; 1.
Initiation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli."
nAsnAsnAsnLysAsnGlnHisGlnGlnLysProValLysProLysLysG
                                                                                                                                  PheAsnLysAsnLysLysAsnAsnAsnLysLysAsnLysArgAsnAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93259931
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226
272
326
36
716 l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                102.50
0.418
47.115
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368
233
276
329
56
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INITIATION FACTOR IF-2-BETA (PROBABLE).
G-OOMAIN.
GTP (BY SIMILARITY).
ACB9B730 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity:
                                                                                                                                                                                                                                                                                         ;
0
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Gaps:
                                                                                                                                                                                                                                                                                            716
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                                                                                                                                                                    115
                              132
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G 962	·····GGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTG	1004
e 419	GlyArgGlySerVa	403
	CCATGCTGCTTTGTCGATGATGGTAAC	1033
l u 402	 	386
G 10	TGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT	1083
FA 1084 : 1L 386	GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTT: :::: ::::::::::::::::::::	369
1 369	GlyGluThrIlePheValProLeu.SerAlaLeuThrGlyLys	353
7 11	CTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATG	1183
TC 1184 :	AAATCACAACTGCTTT ::: :: euValProclualatr	1233 336
336	alAsnLysIleAspLysGluSerAlaAsnPro	20
12		1250
319	::::::: ::::::: GluAlaIleAsnHisAlaLysAlaAlaGluV	303
7 1	CCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAA	1300
CGT 1301 :: lvv 303	ACAACTGTTGTCATT	1332 286
G1 286		N
GG 1333	TGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCC	1382
hr 273		26
262	THICOCOMANHOANDCANOCOMOAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ي س
AG 14	CATGTTTATGTGAAAGGTCTTTATGATCA	1463
G1 248	LysThrThrLeuLeuAspSerIleArgLysThrLysValValGluGly	23
1464	AATTTTTAATACACGTAATGCATTCGAAGGA	1493
ly 231	euGluIleArgProProValValThrIleMetGlyHisValAspHi	215
1494	TTGAATGTGGACCAACTTCAATAACAATC	1522
:: pL 215	:::::: uGluGluThrGluLeuGluLysTyrGluGluProAspAsnGluGluA	198
AA 15	· · · · · · · · · · · GAAGGTGAGCCAG	1538
1539 Le 198	CITAITIGCAITIGTCTIATTCGATTCGACAATIGCTGACAATIGCTGCTC	182
	euweusiyvaimetalainrileasnGinGluLeuAspLysAspT	
15	TTATTGCTTTCTGTACTACA	1600
etL 165	AlaGlu.GluLeuGlyLysGluProSerGluLeuIleLysLysL	149
	AAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCGT	1641
Leu 148	<pre>luLeuProGluLysIleThrPheSerGlyThrLeuThrValGlyAla</pre>	132
1642	AGACAGGAAGCAATCTTAGTTTTTCT	T997

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seq_documentation_block:
ID MUCS_BOVIN STANDA
AC P$8091;
DT 01-FEB-1996 (Rel. 33,
DT 01-OT-1996 (Rel. 33,
DT 01-OT-1996 (Rel. 34,
DE SUBMAXILLARY MUCIN-LI
OS BOS taurus (Bovine).
OC Eutheria; Cetartiodac
CC Eutheria; Cetartiodac
CC Eutheria; Cetartiodac
COC Eutheria; Cotartiodac
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SUBMAXILLARY G
RX MEDLINE; 90370871.
RA BHARGAVA A.K., WOITAC
RT PIOCE. Natl. Acad. Sci
CC -:- SUBCELLULAR LOCAT
CC -:- SIMILARITY: CONTA
CC -:- SIMILARITY: CONTA
CC -:- SIMILARITY: CONTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: SwissProt_38:MUCS_BOVIN
TISSUE-SUBMAXILLARY GLAND;

BHARGAVA A.K., WOITACH J.T., DAVIDSON E.A., BHAVANANDAN V.P.;

"Cloning and cDNA sequence of a bovine submaxillary gland mucin-like protein containing two distinct domains.";

Proc. Natl. Acad. Sci. U.S.A. 87:6798-6802(1990).

-!- SUBCELLULAR LOCATION: SECRETED.

-!- TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.

-!- SIMILARITY: TO PORCINE APOMUCIN.

-!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                    MUCS_BOVIN STANDARD; PRT; 563 AA. P98091; O1-FEB-1996 (Rel. 33, Created) O1-FEB-996 (Rel. 34, Last sequence update) O1-OCT-1996 (Rel. 34, Last annotation update) SUBMAXILLARY MUCIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     575 AsnVal 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 TAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 686 GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAATG 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sAspIleAsnLeuIleValLysAlaAspValGlnGlySerAlaGluAlaL 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euThrAlaAlaLeuGlnLysIleGluValGluGlyValLysValLysIle 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACTICGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysLeuSerLeuAspAspLeuPheGluGlnIleLysGlnGlyAspValLy 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pGlnPheLeuValPheLysAspGluLysThrAlaArgSerValGlyGluA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAAT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerThrProValGluIleThrGlyLeuAsnAspValProGlnAlaGlyAs 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATATCCAACAGATTTA.....ATGGCTGGCCA 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ......GCCGCAGCAAAAACCTGCTGCAGCTGCGC 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..ArgAlaMetValAsnAspIleGlyArgArgValLysThrAlaGlyPro 450
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alignment_block:
US-09-323-427-2/rev x MUCS_BOVIN
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: M36192; AAA30657.1; --
HSSP; P00214; 1FTC.
HSSP; P501208; VWFC; 1.
PROSITE; P501185; CTCK_1; 1.
PROSITE; P501225; CTCK_2; 1.
PFAM; PF00007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institutes as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILAR
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Glycoprotein.
DOMAIN 61 15
                                                                                                                                                                                                                                                               1678 GTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAAATCGAATTT 1629
                                                                                                                                                                                                                                                                                                                1698 AGCAATA.....ATAACCCCATCAA 1679
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                                                  1478 AATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGG 1429
                                                                                                                                                                                                                                                                                                                                            221
                                                                                                                                                                                                                                       207
                                                                            CAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGT 1479
                                                                                                                                                          TATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGC 1529
                                                                                                                                                                                    |||||| ::: |||||||
| roGlyGlyPheAsnAlaGluAlaThrThrPhe.....LysGluHis 220
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rGlyIleGlnThrGlyIleThrGlyThrGlySerGlyThrThrSerSerP 207
                                                                                                                                                                                                           ACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACTACACT 1579
TTGCCGTAATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCAT 1379
                                                                                                                               .....LeuSerGlyThrThrArgGlyArgSerGlyThrThrValIleP
                         ThrAla.....valValSerGly.....
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112
148
338
471
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0.602
42.931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 389
Gaps: 19
Percent Identity: 21.594
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BY SIMILARITY
BY SIMILARITY
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POTENTIAL
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                                                                                                                                            243
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AC P14198; DT 01-JAN-1990 (Rel. 13, Created)
doc A#
seq_name: SwissProt_38:AAC4_DICDI
695 ATCATTGATGTACGAAC 679 ::: 1:: 476 alasnValThrValAsn 481
745 CAGCTGCGCAACTTCGTTTACTCAAGAAAAAATCTGCAGAACCGGAAAAT 696 ::: :::
4 -
TTTCGACCAC 8::: IleSerTyrS 4
GAAGCTCACGTATACAAATATGCGGATCGATCACACCACCACCACCACCACCACCACCACCACCACCAC
407 hrCysLeuPheAsnAsnAsnAspTyr
90 AATTUTAAATUUTAH SAHADA SAHA
GTCCATTCCTGCTTGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATG
1078 AATGGACATGCGATTCTGAAACCGTTGATACTITCTGC 1041
TIGCTATCATIGGTCAGCCAGTITATCATA ::: colyaspileTrpThralaAsnCysHisL 360
ATGAAATTTTGGATGGTGGACC 112
TGAAATCACAACTGCTTTTCAAACT 117::: :::: :::: ::::
1278 AGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAA 1229 :::: :::: :::: 302 gileThrThrSerSerArgIleProTyrProGluThrThrValV 317
302
ro 289
luS 273

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alignment_block:
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Ratio: 0.667
Percent Similarity: 43.228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-323-427-2/rev x AAC4_DICDI
                                                                         1487
                                                                                                                                             1537
                                                                                                                                                                                                                1587
                                                                                                                                                                                                                                                                                                                                            1687 CCCCATCAAGTGGAAGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAA 1638
1464 ACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATG 1415
                                                                                                                                                                                                                                                                                  1637
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHAW D.R., RICHTER H., GTORDA R., OHMACHI T., ENNIS H.L.;

"Nucleotide sequences of Dictyostelium discoideum developmentally regulated cDNAs rich in (AAC) imply proteins that contain clusters of asparagine, glutamine, or threonine.";

MOI. Gen. Genet. 218:453-459(1989).

-!- DEVELOPMENTAL STAGE: THE CONCENTRATION OF AAC-RICH MRNAS IS LOW IN DOWNAMY SPORES AND GROWING CELLS, BUT INCREASES DURING SPORE-GERMINATION AND MULTICELLULAR DEVELOPMENT.

-!- MISCELLANBOUS: SEVERAL PROTEINS DERIVE FROM AAC-RICH MRNA, WHICH, DUE TO A FRAMESHIFT ALSO HAVE ACA AND CAA CODONS AND THUS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat.
                                                                                                                                                                              85
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                                                                                                                                                                                                                                                                                                                                                                                         54
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01-FEB-1994 (Rel. 28, Last annotation update)
AAC-RICH MRNA CLONE PLK330 PROTEIN (FRAGMENT).
Dictyostelium discoideum (Slime mold).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Dictyosteliida; Dictyostelium.
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                                                                                                                                    TACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCG 1538
                                                                                                                                                                                                                                         sn.....GlyAspIleAsnAsn......
                                                                                                                                                                                                                                                                                                                                                                                AATACACGTAATGCATTCGAA.....
                                                                                                                                                                                                                                                                           ATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTG 1588
                                                                                                                                                                                                                                                                                                               n.....AsnAsnAsnThrSerIleSerAsnA
                                  ........AsnCysPheGluThrCysAspPheLysAlaThrGluArgGl 108
                                                                                                                                                                     .....CysLeuAlaThrPheGluGln.ValGlnAsn.....
                                                                                                    ASN-, THR- OR GLN-RICH.
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314
317
317
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317
317
35893
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Gaps: 18
Percent Identity: 20.461
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ASN-RICH.
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seq_documentation_block:
ID VGLH_HSVSA STANDA
AC P1649;
DT 01-AUG-1990 (Rel. 15,
DT 01-AUG-1990 (Rel. 15,
DT 01-OCT 1996 (Rel. 34,
DE GLYCOPROTEIN H PRECUR
GN GH OR 22.
OS Herpesvirus saimiri (
OC Viruses; dsDNA viruse
OC Gammaherpesvirinae.
RN [1]
                                                                                                                                                                                                                                                                           seq_name: SwissProt_38:VGLH_HSVSA
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  Herpesvirus saimiri (strain 11).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
[1]
                                                                                                                       P16492;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
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                                                                                      GLYCOPROTEIN H PRECURSOR. GH OR 22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT 828
                                                                                                                                                                                                                                                                                                                     SerGlnCysPheGlnLysAsnCysCysLysProGln
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rgArgAlaHisArgGluValAsnThrPheValGlnValPheAspValCys 183
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US-09-323-427-2/rev x VGLH_HSVSA
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Quality:
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Percent Similarity:
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EMBL; D00400; BAA00302.1; -.
EMBL; D00543; BAA00433.1; -.
PIR; J00010; VGBE11.
PIR; J00010; Transmembrane; S
Glycoprotein; Transmembrane; S
SIGNAL
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MEDLINE; 92333688.

ALBRECHT J.-C., NICHOLAS J., BILLER D., CAMERON K.R., BIESINGER B., NEWMAN C., WITTMANN S., CRAXTON M.A., COLEMAN H., FLECKENSTEIN B., HONESS R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HONESS R.W., CRAXTON M.A., WILLIAMS L., GOMPELS U.A.;
HONESS R.W., CRAXTON M.A., WILLIAMS L., GOMPELS U.A.;
HONESS R.W., CRAXTON M.A., WILLIAMS L., GOMPELS U.A.;
The sequence of the thymidine kinase gene
"A comparative analysis of the sequence of the thymidine kinase gene
"A comparative analysis of the sequence of the thymidine kinase gene
"A comparative That INDUCES NEUTRALIZING AND
I. FUNCTION: GH AND GL FORM A COMPLEX THAT INDUCES NEUTRALIZING AND
SYNCYTIA INHIBITING ANTIBODIES (BY SIMILARITY).

SYNCYTIA INHIBITING ANTIBODIES (BY SIMILARITY).
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"Conservation of glycoprotein H (gH) in herpesviruses: nucleotide sequence of the gH gene from herpesvirus salmiri.";
y. Gen. Virol. 69:2819-2829(1988).
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J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CARBOHYD
                                                                                                                                               1656 AATCTTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGA 1607
                                                                                                                                                                                                                                                             1706 ACAACAACAGCAATAATAACCCCATCAAGTGGAAGGAAGAAGACAGGAAGC
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                1606 TTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTTTTTTTCGATT 1557
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                                                                                            ThrIleSerCysHisIleThrProAsn.....
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42.121
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....ThrLeuLeuPheGlyHisSerHisTyrLeu 214
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Gaps: 39
Percent Identity: 20.000
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POTENTIAL.
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884GATCGATCACAGCTTTTCTATCA 862
95 ACAAATATGCG8
roT 45
rSerGluArgLySmetheuheuhernschraagaAgCTCACGTAT 89
TG
SerHisIleTyrThrAlaTyrSerTyrThrTyrMet 42
394SerLysH1sValberAlavalalullurus
1059 AACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATG LULU
uSerArgHis393
AsnvalproLysHisvallleThrSerLeuSerHisGlnAspLysTnrAs so
CAGT
::: :::: ::::::::::::::::::::
CAGTATGCCGTTATGAAATTTTGGATGGTGC
6 ACAACTGCTTTTCAAACTCAAATTGTCCCGATGC
330 yrMetSerGluLeu
ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTG
1290 ATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTT 1247 ::::::::::::::::::::::::::::::::::::
PheLeuValIl 3
lulleArgAspGlyCysAsnIleAsnAsnIleValAsnPr
ATGCAATGTTGCGCGTACACGATCTCTGAATCCA 13
TCAAGAAGGTT
nLeuGlnAs 2//
57ratgtgaaaggtctttatga 14
 ysHisValGluSerPheLysPh
A CAMPOGAAGGACATGTT
AATTGAATGT :
CGGTTGACAATGGTGTCGAAGGTGAGCCAGA 1

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132 ATATCACAAATTATACCTTGTATTG 108
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                                                                                         ATCATTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATA 133
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pGlyAsnLeuHisIleHisTyrLeuIleLeuMetAsnAsnGlyThrValI 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AATGTTCAGAACCACAAGGATTCGGAGC 781
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ID YAY3_SCHPO STANDA
AC Q10211;
DT Q10211-1996 (Rel. 34,
DT Q1-CT-1996 (Rel. 34,
DT Q1-CT-193 (Rel. 34,
DT
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US-09-323-427-2/rev x YAY3_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                        1362 TGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTG 1313
                                                                                                                                                                                                                                                                                                                     1412 GGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGT 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1462 ATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAA 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1491 TTTTAATACACGTAATGCATTC......GAAGGAC 1463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1541 GTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATCAA 1492
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z69380; CAA93342.1; --
Hypothetical protein; Transmembrane.
TRANSMEM 265 285 POTENTIAL.
TRANSMEM 564 584 POTENTIAL.
TRANSMEM 626 646 POTENTIAL.
SEQUENCE 649 AA; 74488 MW; F04F8763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
99 euLeuAspPhePheHisArgProTrpGluAspTyrGluProLeuTyrPro 115
                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                 isPheSerIleThrProIle...GluGlnThrSerCysLys......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \verb|nPheAspSerProSerIlePheAlaArgIleLeuAspAlaArgAlaGlyH|
                                                                                                                           eLeuHisThrLysPheTyrSerGluArgGlyValLeu.....ArgL
                                                                                                                                                                                                                                                                Quality:
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0.554
43.672
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646 P
74488 MW;
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Gaps: 23
Percent Identity: 22.333
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594 619

662 275

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1283 ACCAAAGTTGATCGTGCA......TATCGAGT 1258
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149 alSerLysIleThrGluAsnTyrTyrGlnAlaGluPheValProAlaSer 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGG 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATCTGAAATCACA...ACTGCTTTTCAAACTCAAATTGTCCCGATGCCA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAA...... 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyAspProLysTyrIleLeuAspCysValProSerGlyAspGlnLeuLy 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA 991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pTyrvalThrProAsn.....LeuValAspLysL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \verb|euGluAspSerThrLysArgTyrTrpArgAlaTrpIleGlnGlnCysVal|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrThrGlyArgTyrArgGluPheValGlnArgAsnAlaLeuThrLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                        CAGAACCACAAGGATTCGGAGCTGTTAAAACA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                       TATTACCATTAAAGAACCAAATAGCGAATGTGTT...CGACCACAATGTT
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erLeuProGluAspLeuGlyGlyValArgAsnTrpAspTyrArgPheThr 302
                                                                                                                                                                                                                                                eArgAlaGluAlaValGluTyrMetSerPheIleTyrHisValLeuLysL
                                                                                                                                                                                                                                                                                                          TrpIleArgAspSerAlaPheThrIleTyrAlaLeuAlaGlnLeuGlyPh
                                                                                                                                                                                                                                                                                                                                           .....GGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT.....
                                                                                                                                                                                                               AAAGATCTGCAGAACCGGAG....AATATCATTGATGTACGAACTGATATC 672
                                                                                                                                                                                                                                                                          719
                                                                                                                    AACACCCTTGAAATTAGCGATGATAATCAAGCTTTG...CCAGTTGATTT 625
                                                                                                                                                                                  ysLysAsnLysAspGlyGlyIleAsnIleVal.....
                                                        uThrHisLeuArgGly.....TyrTyrAsnSerHisProValArgIle.
                                                                                       ACGTCAC...CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTG
                         CTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTT 528
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ATGGG

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Seq_documentation_block:
ID YCF2_MARPO STANDA
AC P09975;
AC D1-MAR-1989 (Rel. 10,
DT 01-MAR-1989 (Rel. 26,
DT 01-MAR-1986 (Rel. 26,
RE CHORPOPHETICAL 259 KD F
RE SEQUENCE FROM N.A.
RA OHYAMA K.;
RA OHYAMA K.;
FUKUZAWA I
R
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US-09-323-427-2/rev x YCF2_MARPO
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pIR; A05037; A05037.
PIR; S01591; S01591.
MENDEL; 5295; MARPO; ycf2:1.
PFAM; PF00004; AAA; 1.
Chloroplast; Hypothetical protein.
SEQUENCE 2136 AA; 259911 MW; A2F
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01-MAR-1989 (Rel. 10, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
HYPOTHETICAL 259 KD PROTEIN (ORF 2136).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Er
Marchantiales; Marchantiaceae; Marchantia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marchantia polymorpha (Liverwort).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its two by non-profit institutions as long as its content is in no way may be another the statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Chloroplast gene organization deduced from complete sequence liverwort Marchantia polymorpha chloroplast DNA."; Nature 322:572-574(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OHYAMA K., FUKUZAWA H., KOHCHI T., SHIRAI H., SANO T., SANO S., UMESONO K., SHIKI Y., TAKEUCHI M., CHANG Z., AOTA S., INOKUCHI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                1652 TTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCG
                                                                                                                                                                                                                                                                                                                                                            709 AsnAsnLysLeuIleThrTrpLysLysIleSerAsnLysLeuValIleSe
                                                      TCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGG
                                                                                                                                                                                                                                                heSerPheSerLysAsnSerValLeuAspThrPhePheAheAsnLysLys
SerPheAsnIleIle.....
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Ratio:
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0.316
46.375
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Percent Identity:
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            ....ThrvalllePheAspLys.L 770
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33
18.278
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1552	TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA :::	1503
770	nPheGlnGluIleGlnLysIleLeuAsnCys	786
1502	CGAAGGACATGTTTATGT	.4
1462	erLeuPhePheAsnSerLysAsnIleLysLysThrLysIlePheLy	803
1452 803	GTAATGATGAAGGTGGACGTC	1403
1402	AGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACA	1353
811	: : : : : : :	15
1352	ATCCACGTGGTATTTTTGTAACAACAACTGTTGT	1309
816	erPheAsnAspLysGluPheAsnTlePhe	826
1308	ATCGTGCATATCGAG	1259
827	GluIleAsnAsnAspPheLeuM	841
1258	ACAATGCTTTTACATGGAAGCTGATA	1221
841	gPhePheLysLysTyrLeuTyr.TyrArgIleTyrLysAs	357
1220	AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGT	1171
857	snProIleGluAsnArgGlnLeuLeuGlnAsnPhePh	374
1170	GATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTC	121
1120	netreacher de la constant de la cons	3
		07
1076	ACAT	.039
907	snLeuLeuTyrLeuArgLeuLeuLysIlePheLe	24
1038	GGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAA 9	89
924	rg9	24
988	CTCTTGATAAATATTTG(39
925	AsnPheLeuLeuII	30
938	CAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATA	889
931	SerPheIleGluLysLysAsnAsnL	942
888	CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTA	839
942	.AsnValLeuLeuVal 9	54
838	AACCAAATAGCGAATGTGTTCGACCAC8	9
955	yrLysPhePheAspAsnIlePheAsnPheHisPheLeuLy	971
808	AATGTTCAGAACCACAAGG 7	90
971	LysAsnIleGluIleIleLeuAsnAsnGlnAsnTyrPheG	88
8	AAACCTGCTGCAGCTG 7	40
988	uLysSerLeuLeuLysLysThrTyrLeuLysAsnLeuAsnLeu	1002

	: SwissProt_38:GALU_PSEAE	seq_name:
	TCATTTGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	33 1232
34 1231	CTATTCTGTAAACAATTCACTTATTTGCATTATTGCAATTAAAAAGTATT :::::::: ::: lulleileGlnTyrLeuThrAspArgSerArgSerLeu	83 1219
84 1219	TTATGGGCATCATTTC	1202
100 1202	TTTGTGATAATATCACAAATTATACCTTGTATTGCCCAATTT: ::: ::: ::: ::: TrpValIlePheSerLeuValIlePheIlePheLeuTyrTyrGlnLysIl	141 1186
142 1185	ATCA uTyr	167 1169
168 1169	GTTTGTTATTATCATCATTATCAACTTG :::	195 1152
196 1152	ATTGTAAATGTTTCATCATTAGGCCATGAATAGTTTC	232 1136
233 1136		281 1119
282 1119	AATACAATAAGTGATATTTTCATCAAAACTTCTTCTATCGCTTTTAT::: ::: :: ::: :: ::: ::: ::	328 1103
329 1102	AATTTTAGCTAACAAATATATAGTAGGTAGGAAATAATTACTGT ::: :: ::: !: erTrpPhePheThrLeuGluTrpTrpGluTyrAsnThrTyrIleLeuLeu	372 1086
373 1086	AATAAAACTGCCATATATATTCGTTTCTTATCATCCTTCTAATAACT:	422 1075
423 1075	TTCGTCCAAATCAGAAGGCATAAAAATAATGTTAGAATCATCGAAGCAAT ::: ::::::::::::::::::::	472 1060
1059		1059
473		522
523 1059	AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGG	. 566 1050
567 1050	GTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAA	616 1041
617 1040	CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACC::: :::::::::::::::::::::::::::	1035
667 1034	AGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACAC ::::::	. 716 1019
717 1019	CGCAACTTCGTTTACTCAAGAAA 	739 1003

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seq_documentation_block:
ID GALU_PSEAE STANDA
AC Q59633;
DT 01-NOV-1997 (Rel. 35,
DE GALU.
OS PSEUDOMORAS ABRUPANTE + (CC PSEUDOMORAS.
RN [1]
CC PSEUDOMORAS.
RN SEQUENCE FROM N.A.
RP SEQUENCE SEQUENCE

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CC This SMISS-PROT entry
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percent Similarity:
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
UTP--GLUCOSE-1-PHOSPHATE URLDYLLTRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE
DYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHATE
PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHORYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN STATIONARY PHASE SURVIVAL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
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-!- CATALYTIC ACTIVITY: UTP + ALPHA-D-GLUCOSE 1-PHOSPHATE
PYROPHOSPHATE + UDP-GLUCOSE.
PYROPHOSPHATE + UDP-GLUCOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U03751; AAB01486.1; -.

PFAM; PF00483; NTP_transferase; 1.

Transferase; Kinase; Nucleotidyltransferase.

Transferase; Kinase; Nucleotidyltransferase.
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                                                                GTATT.....TTTGTAACAACAACTGTTGTCATTTCGTTTCATCCA
                                                                                                                                    {\tt sLeuLeuAspGluCysSerPheSerTyrThrArgGlnThrGlnMetLysG}
                                                                                                                                                                                                         TCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTG
                                                                                                                                                                                                                                                                             AsnGlnIleLysGlyThrAspLysGluLysTyrLeuValGlyIleArgLy
lyLeuGlyHisAlaIleLeuThrGlyArgProLeuIleGlyAspGluPro
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ID CYAA_DICDI STANDA
AC Q03100;
DT 01-JUL-1993 (Rel. 26,
DT 01-JUL-1993 (Rel. 26,
DT 01-JUL-1993 (Rel. 26,
DT 01-JUL-1993 (Rel. 26,
DT 15-DEC-1999 (Rel. 39,
DE ADENVLATE CYCLASE, AC
PYROPHOSPHATE-LYASE)
ACAA OR ACA.
OS DictyOstelium discoid
CC Eukaryota; DictyOstel
RN 2520URNCE FROM N.A.
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PITT G.S., MILONA N.
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CC THUCTION: COORDII
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01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ADENYLATE CYCLASE, AGGREGATION SPECIFIC (EC 4
PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE: 92233467.

PITT G.S., MILONA N., BORLEIS J., LIN K.C., REED R.R., DEVREOTES P.N.;

PITT G.S., MILONA N., BORLEIS J., LIN K.C., REED R.R., DEVREOTES P.N.;

PStructurally distinct and stage-specific adenylyl cyclase genes play

"Structurally distinct and stage-specific adenylyl cyclase genes play
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ysvalile 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold).
Eukaryota; Dictyosteliida; Dictyostelium.
       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheAlaValValLeuAlaAspAspLeu.....CysValAsnLe
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WITHIN A DEVELOPING ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.

CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP; PYROPHOSPHATE.

CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP; THIS REGULATION NEGATIVELY REGULATED BY EXTRACELLULAR CAMP; THIS REGULATION NEGATIVELY REGULATION THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP PART OF THE MECHANISM THAT ESTABLISHES THE MECHANISM THAT ESTABLISHES THE MECHANISM THAT ESTABLISHES THE MECHANISM THAT ESTABLISHES THE MECHANISM THAT ESTABLISH THAT ESTABLISHES THE MECHANISM THAT ESTABLISH THAT ESTAB
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                                                                                                                                                          DEVELOPMENTAL STAGE: CELL AGGREGATION AND LATER STAGES.
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                 DURING AGGREGATION.
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EMBL; L05496; AAA33163.1; JOINED.
EMBL; L05497; AAA33163.1; JOINED.
EMBL; L05498; AAA33163.1; JOINED.
EMBL; L05498; AAA33163.1; JOINED.
PIR; B42239; B42239.
HSSP; P26769; 1AB8.
DICTYDB; DD02024; ACAA.
DICTYDB; DD02024; ACAA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contential
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                                                 CACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGT 1533
                                                                    uMetSerAsnIleLysLysProLysSerArg......PheIleAspA 903
                                                                                         ATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACTA 1583
                                                                                                               luAspPheLysIleLysSerLysSerAsnSerSer.Phe...GluIleG1 889
                                                                                                                                TCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAAATCGA 1633
                                                                                                                                                    nAsnAsnLysAsnGlnAsnAsnIleTyrGlyAsnAsnAsnAsnAsnGluG 874
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576	CTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTG	725
726 1166	b AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGGCAACTTCGTTTA 7	1154
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-	sThrIleSerValAsnLys	1138
326	CAGCTTTTCTATCA	875
876 1138	2 LysLeuAlaMetArgLysAlaTrpValValAsnCysLysIleAsnPheLy 1	1122
ı \mu	TARTGCCTCCCAACAACCTTATCCAACTTATCAACTAACAAC	27.7
N)	ATGTGCTCTTGATAAATATTTTGCTAAATAATTTGGAATATCCAACAGATT	972
1109	4 rileGlyPheValile	1104
973	2 TTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGG	102
1104	8 SerIleLeuIleSerProThrLeuThrAsnHisLeuTyrGluThrAspTy	108
1023	2 CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC	107
1087	::::::::::::::::::::::::::::::::::::	107
1073	3 TCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA	111
1114 1071	3 CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGT	116 105
1056	eu.IleArgPheGlnAsnProLeuAlaArgSerSerLeuThrArgValCy	104
1164	7 TATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG	120
1208 1040	7 ACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGG :	125 102
1023	LeuserPnethrargllePneArgThrProLeuValTyrGlnIl	
N	ATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGT	130
1008	yrLeuValMetGlyIleAlaPheLeuValTyrIleGly	996
1308	7 GTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTC	135
996	9 uAspAspHisIleMetAspSerAlaProTyrPheAsnSerAsnVallleT	97
1358	TTGATTCATGCAAT	138
979		967
1389	GAAGGTGGACGTCAAGTTGCCGGAATT	1415
966	ysTyrValIleIleAsnAs	953
1416	5 GACATGTTTATGTGAAAGGTCTTTATGATCAAGAA	146
ū	::: ::::: :: ThrThrGluLysPhePheHi	9
4	.493AATTTTAATACACGTAATGCATTCGAAG	149
936	920 LysGluIleIleGlnIleAspGluAspPheValLysValThrLysLeuAr	9

sp_organelle:Q33559

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3.1e-116
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.5e-25
.2e-24
.2e-19
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.3e-06
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..4e-57
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.1e-29
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.8e-43
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.2e-49
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                1 Q93115 ascaris lumbricoides (1 Q19707 caenorhabditis elegans 10.18479 meloidogyne artiellia. Q9xvm7 caenorhabditis elegans 1 Q9xvm7 caenorhabditis elegans 1 Q9xvm7 caenorhabditis elegans 1 Q9xvm7 caenorhabditis elegans 1 Q21540 caenorhabditis elegans 1 Q21540 caenorhabditis elegans 1 Q21540 caenorhabditis elegans 1 Q22164 caenorhabditis elegans 1 Q22164 caenorhabditis elegans 1 Q22167 caenorhabditis elegans 1 Q22167 caenorhabditis elegans 1 Q23097 caenorhabditis elegans 1 Q22627 caenorhabditis elegans 1 Q22627 caenorhabditis elegans 1 Q21573 caenorhabditis elegans 1 Q19304 caenorhabditis elegans 1 Q23587 caenorhabditis elegans 1 Q2328 drosophila melanogaste 1 Q18298 caenorhabditis elegans 1 Q23724 caenorhabditis elegans 1 Q23724 caenorhabditis elegans 1 Q23724 caenorhabditis elegans 1 Q2368 dictyostelium discoid 1 Q37298 plasmodium falciparum 1 Q27288 plasmodium falciparum 1 Q3580 plasmodium falciparum 1 Q37288 plasmodium falciparum 1 Q36648 plasmodium falciparum 1 Q36648 plasmodium falciparum 1 Q36648 plasmodium falciparum 1 Q36648 plasmodium falciparum 1 Q4648 plasmodium falciparum 1 Q4668 caenorhabditis elegans 1 Q4668 caenorh
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Seq_documentation_block:
ID Q93115
AC Q93115
AC Q93115
DT 01-FEB-1997 (TrEMBLre
DT 01-FEB-1997 (TrEMBLre
DT 01-FEB-1997 (TREMBLRE
DT 01-FEB-1997 (TREMBLRE
DT 01-FVB-1998 (TREMBLRE
DT 01-NOV-1998 (TREMBLRE
OC ASCATIS lumbricoides; Nacarid
RN [1]
OC ASCATIS lumbricoides; Ascarid
RN [1]
OC ASCATISOINE; 9790131.
RA MEDLLNE; 9790131.
RA TIMNOUNI M. BAZZICA
RT Gene 193:81-87(1997).
DR EMBL; U73005; AAB6664
KW Signal.
FT CHAIN
SOUENCE 385 AA; 4
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US-09-323-427-2/rev x Q93115
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sp_invertebrate:077372 -
sp_invertebrate:097230 -
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                                                                                      1310
          1260 AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG
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 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIMINOUNI M., BAZZICALUPO P.;
"cut-1-like genes of Ascaris lumbricoides.";
Gene 193:81-87(1997).
                                                                                                                   83
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                                                    GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
                                                                                                             CAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACAT
gValGlnCysPheTyrMetGluAlaAspLysThrValSerThrGlnIleG
                                                                                                                                                                                                                                                                                                                                                                                                                 MetCysArgAlaValSerPhe...LeuAlaLeuPheGlyLeuAlaAlaAl
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Ratio: 4.593
milarity: 92.784
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17
385
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385
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145.18
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CUT-1-LIKE CUTICLIN PROTEIN.
; BDEB1169 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identity:
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Gaps:
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913 ! 097272 plasmodium falcipar
4981 ! 077372 plasmodium falcipa
1423 ! 097230 plasmodium falcipa
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DT 01-NOV-1996 (TREMBLRE
DT 01-NOV-1996 (TREMBLRE
DT 01-JAN-1999 (TREMBLRE
DE F22B5.3 PROTEIN.
                                                                      seq_name:
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uhspileSeraspargaspGluhlaLeuproMetAspLeuArgHisArgA
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                                                                                                                                                             TCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCT 664
                                                                                                                                                                                                                                                                                                                         ..GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA 714
                                                                                                                            la.....ArgHisAlaArgGlyGlnGlnValIleLeuSerProAlaAsn
                                                                                                                                                                                                                  CACTTCTGCAACAT...AATGGACAACCTGTAATACTTGCTGCAGTACAA
                                                                                                                                            CATTGCATTGATTGCCGCCGTCATTATTACCATTTCGTTTAAATTTCGTC
                                                                                                           CAAATCAGAAGGCA 453
                                                                                        roGlnGlnLysAla 385
                                                                      sp_invertebrate:Q19707
          6 (TrEMBLrel. 01, 6 (TrEMBLrel. 01, 9 (TrEMBLrel. 09,
                                               PRELIMINARY;
             Created)
Last sequence update)
Last annotation update)
                                                  PRT;
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BUTTON J., CONNELL M., COPSTY T., COOPER J., COULSON A
BONFIELD J., BUTTON J., CONNELL M., COPSTY T., COOPER J., COULSON A
CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LIOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
LIGHTNING J., LOYD C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
PARSON N., SMITH A., SONNHAMMER E., STADEN R., WILSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
ROOPRA A., WEINSTON S., WEINSTON S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Caenorhabditis elegans.
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EMBL; Z50044; CAA90355.1;
SEOUENCE 389 AA; 42983
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13 LeuValAlaSerValSerAlaIleProValAspAsnAsnValGluGlyGl 29
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                                  CTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGA
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seq_documentation_block:
ID 018479
AC 018479;
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-NOV-1998 (TREMBLrel. 05
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DT 01-NOV-1998 (TREMBLREL. 05
DE CUTICLIN-1.
GN MTCUT-1.
OS Meloidogyne artiellia.
OC Eukaryota; Metazoa; Nematc
                                                                                                                          seq_name:
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                                                                                                                        sp_invertebrate:018479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGC
   Nematoda;
                                                                                                                                                                                                                                                                           .SerPheArgGlnGluLeuCysIleSerSerPhe
                                               05,05
                                             Created)
Last sequence update)
Last annotation updat
Secernentea; Diplogasteria; Tylenchida;
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                                             update)
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alignment_scores:
Quality:
Ratio:
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Ratio: 4.042
Percent Similarity: 77.751
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1025 TGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGA
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EMBL; X96677; CAA65452.1; -. 
Cuticle.
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                                                                                                                                                                          GGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCC
                                                                                                                        TGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAG 1226
                                                                                                                                                                                                                                                                          ATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT 1326
                       lyThrCysAspSerGluThrIleAspThrPheCysAlaValValHisSer
                                                                                       CGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAAT
                                                                                                                                                                                                                           lAspArgAlaTyrArgValGlnCysPheTyrMetGluAlaAspLysThrV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTG
                                                                         uGlyGlnProIleGlnPheAlaThrIleAlaGlnGlnValTyrThrSerG
                                                                                                                                                                                                                                                                                                                               spSerCysAsnValAlaArgThr...AspAlaGluProLysGlyValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                              ProPheGluGlyHisValTyrValLysGlyLeuPheAspGlnAlaGlyCy 67
                                                                                                                                                                                                                                                                                                                                                                                sArgSerAspGluHisGlyArgGlnValAlaGlyIleGluLeuProPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ePheThrValArgAlaIleProValAspAsnGlyValGluGlyGluProG
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seq_documentation_block:
ID Q9XVM7 PRELIMINA
AC Q9XVM7;
AC Q9XVM7;
DT 01-NOV-1999 (TrEMBLre
DT 01-NOV-1999 (TrEMBLre
DT 01-NOV-1999 (TrEMBLre
DT 01-NOV-1999 (TrEMBLre
DE F35F1.1 PROTEIN.
GN F35F1.1.
GN F33F1.1.
GN F33F1.1,
GN F53F1.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: sp_invertebrate:Q9XVM7
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
F53F1.1 PROTEIN.
                                                                                                                                        Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaAlaThrProProProAlaAlaAlaProProAlaProTleAlaProAl 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAACAGGT......GGTGCCGCAGCAAAACCTGCTGCAGCTGCG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTA 776
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|ysvalGlyAlaGlyGlyAlaGlyAlaProProProAlaAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alleProAlaArgValGlnArgLeuArgThrArgGlnLeuArgLeuLeuA 333
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          of contiguous nucleotide
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RP SEQUENCE FROM N.A.

RX MEDLINE; 94150718.

RA MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CAAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA CARTON R., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAITREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUDIN M., VAUGHAN R.;

THERRY MEIG J., THOMAS K., VAUGHAN R.
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Quality:
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US-09-323-427-2/rev x Q9XVM7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1559 ATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACC
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EMBL; Z81088; CABO3124.1; -.
SEQUENCE 364 AA; 40843 MW;
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82 lePhevalLysAspPheAlaSerGluGluValCysThrSerArgGlyThr 98
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                                                                                                                                                                                                                                                                                                                                                                                                           GTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGA 1210
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LeuLeuCysLeuTyrArgGluSerGlnValThrValAlaAsnAsnIleSe
                                                                                                                                          TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA 1110
                                                                                                                                                                                                                                              {\tt rValAspGluIleSerThrIleSerTyrAsnValAsnLeuThrMetProT}
                                                                                                                                                                                                                                                                                                    GGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAG
                                   TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA 1060
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.ACCGTTGATACTTTCTGCGCGGTTGTCC 103:
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alignment_scores:
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US-09-323-427-2/rev x Q9XYU9
                                                                                                                                                                                                                                                                                                                     seq_name: sp_invertebrate:Q9XYU9
                                                                                                                                                                                   Align seg 1/1 to: Q9XYU9 from: 1 to: 206
                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                               1008 TAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATA 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
Q9XYU9 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           O9XYU9;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CUTICULIN-1 (FRAGMENT).
                 806
                                                              958
                                                                                                                                                                                                                                                                                                                                      RAMZY R., HELMY H., ADELY M., CURTIS K., WEIL G.;
"Wuchereria bancrofti L3 cuticulin-1 cDNA partial sequence.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125580; AAD28743.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           Wuchereria bancrofti.
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Wuchereria.
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GAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATG
                                 y \texttt{AsnGlyAspLysValGluLeuLeuAsnAlaAspGlyCysAlaLeuAspL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTAAAACAGGT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspGlnGluCysValArgProIleCysGluAspValGluGlyGlyGlyAl
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pLysGlyMetIleIleLeuIleLysGluAspSerPheCysMetValValH
                                                                                                                                                                                                                                                                                                                     206 AA;
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4.064
86.364
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alignment_scores:
    Quality:
    Ratio:
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                                                                                                                                                   alignment_block:
US-09-323-427-2/rev x 096775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: sp_invertebrate:096775
                                                                                                Align seg 1/1
1310 GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCAFATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _documentation_block:
096775 PRELIMI
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cut-1-like genes are present in the filarial nematodes Brugia pahangi and Brugia malayi and, as in other nematodes, code for components of the cuticle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O96775;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ012617; CAA10074.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
LEWIS E.K., HUNTER S.J., TETLEY L.,
DEVANEY E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Filarioidea; Onchocercidae; Brugia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brugia malayi.
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184 lePheValIleValSerValAlaThrIleValAlaIleThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 spileAsnGluGluPheThrSerLeuProAsnAlaLeuArgHisArgSer
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|InCysThrGluProGlnGlyPheGlyAlaIleLysThrArgAsnglyVal
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ValīleSerPheHisProLeuSerValThrLysValAspArgAlaTyrAr

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seq_name: sp_invertebrate:Q21808
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                  WILSON R., ANNECOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONRIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONRIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN A., MORTIMORE B., O'CALLAGHAN M.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
WATERSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
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Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Phahditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COTTAGE A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAATATTTGCTAAATAATTTGGAATATCCA 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z49207; CAA89068.1;
                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                      290 AA; 33215
                                                              654.50
3.306
69.965
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Last sequence update)
Last annotation update)
                                                                    Percent Identity:
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                                                                                                                               Length:
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Align seg 1/1 to: Q21808 from: 1
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seq_name: sp_invertebrate:Q21540
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4 SerProArgGlyLeuPheLeuSerThrAsnValValAalAlaPheAsnPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGT 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATATGCGGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC
                                                                                                                                                                                                                                                                                                                       CATTAAAGAACCAAATAGCGAA...TGTGTTCGACCACAATGTTCAGAAC 797
                                                                                                                                                                                                                                                                                                                                                                                           ATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC
                                                                                                                                                                                   AG...GTGGTGCCGCAGCAAAACCTGCTGCAGCTG.......CGC 737
                                                                                                                                                                                                           CA.....
                                                                                                                                                                                                                                                                                                   spTyrIleIleProAsnAspAspIleIleSerLeuAsnTrpLeuGlnArg
                                                                                                                                                                                                                                CAAGGATTCGGAGCTGTTAAAAC
                                                                                                                                                                                                                                                      roproArgArgArgSerAsnThrLeuProAlaProAspAspAsnIle
                                                                                                                                        AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT 687
                           snAlaPheLeuPheIleIleSerLeuValSerIleValHisValCys
                                                                      ....GluLeuCysMetThrAlaIleGlyThrThrLeuLeuValPheLeuA
                                                                                             GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 637
                                                                                                                    AsnPhe....
                                                GCCAGTTGATTTACGTC.....ACCGTGCACTTCTGC 605
                                                                                                                      .....AspMetArgIleSer....
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Sequence of the control of the contr
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                                                                                                                                                                                                                                                           1443 TTATGATCAAGAAGGTTGCCGT.....AATGATGAAGGTGGAC 1406
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA R., SAUNDERS D., SHOWNKEEN I
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
                                                                                                                                                                                                                                                                                                                                          242
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Q21540;
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Q21540 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 273428; CAA97806.1; -. PFAM; PF00092; vwa; 1. PFINTS; PRO0453; VWFADOMAIN. SEQUENCE 550 AA; 61445 MW;
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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                                                                                                                        GTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGT 1356
                                                                                                                                                                                      sTyrH1sAspGluGluCysArgAlaGlyProGluLysPheProAspSerA
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LysalaSerThrLysGlnProPheGluGlyAsnValPheValMetAspHi 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                         heArgProGlyThrProGluIleIleCysGlyProAspArgIleGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATC 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValArgValPheThrValGluSerPheGluGlnLeuAspArgAlaLeuAl 213
ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT 1306
                                                          rgSerIle...GlyLeuThrValProPheSerAlaCysAsnValHisArg
                                                                                                                                                                                                                                                                                                                                                                                       AATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCT 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a.....AspSerLeuThrTrpSerMetCysLysThrGluP
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Gaps: 8
Percent Identity: 40.533
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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seq_documentation_block:
ID Q19053
AC Q19053
AC Q19053
DT Q1-NOV-1996 (TrEMBLre
DT Q1-JAN-1998 (TrEMBLre
DE E04D5.3 PROTEIN.
GN E04D5.3 PROTEIN.
GN Caenorhabditis elegan
OC Eukaryota; Metazoa; N
QC Rhabditina; Rhabditoi
                                                                                                                                                                                                                         seq_name: sp_invertebrate:Q19053
                                                                                                019053
019053
01-NOV-1996 (TrEMBLrel. 01,
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1999 (TrEMBLrel. 09,
   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyAlaAspLysAspThrPheGlyMetLeuValHisSerCysTyrValAs
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                                                                                                Created)
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GRADNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER B., O'CALLAGHAN M.,
LIGHTNING J., LLOYD C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D.,
SMALDON N., SMITH A., SONHHAMMER E., STADEN R., SULSTON J.,
WANTSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WARTSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
elegans.";
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[2]
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EMBL; Z66496; CAA91280.1;
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                                                                                                                                                                                                                                                                                                            TTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCT 1236
                                                                                                                                                                                                                                                                                                                                                                                 TGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTG 1286
                                                                                                                                                                                                                                                                                                                                                                                                                   ValArgHisAspSerCysGlyValArgArgGlnArgGluIleAsn.... 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACG 1336
                                                                                                                                                                                                                                          GATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTT 1186
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                                                                                                                                   TCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATG 1136
                                                                                                                                                                                                                                                                                                                                                luAla...GlyGlySerProIleLysTyrAlaArgIleGlyAspGlnVal
                                                                                                   GTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT 1086
Quality:
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seq_name: sp_invertebrate:Q93532
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                                                                                                                                                      alignment_scores:
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US-09-323-427-2/rev x Q93532
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                                                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONTROL R., FAVELLO A., FULTON L.,
GARDONER A., GREEN P., HAMKINS T., HILLIER L. JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LASTEER M., COLLLAGHAN M.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON M., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATENSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATENSTOCK L., WILKINSON-SPROAT J., WOHLDMAN E.]
elegans.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TREMBLIEL.
01-FEB-1997 (TREMBLIEL.
01-JAN-1999 (TREMBLIEL.
F20D1.8 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
         1622 TCTTCTGAAATGATGATTCGTCTTATTGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                    Nature 368:32-38(1994).
EMBL; Z78542; CAB01742.1; -.
SEQUENCE 315 AA; 35785 MW;
                                                                                                                                                                                                                                                                elegans.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG
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ysAspValAsnTyrGlyCysSerAsnThrGlnProGlnCysProThrSer 260
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                                                 Q93532
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114 LysGlyIleMetMetThrAlaThrIleIleIleSerPheHisProMetPh 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1237
                                                                                                                                                                                                                                                                                                                                                                                          214
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                                                                                                                                                                                                                                                                                                              229
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                                      CTCACGTATACAAATATGCGGATCGA 879
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                                                                                                          GGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATA 955
                                                                                                                                                                                                                                                                                                                                                                                ValLeuThrGluSerLysThr...GluGluValAlaPheAlaThrValGl
erGlnValCysSerTrpThrValArg
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296 erGinValCysSerTrpThrValArg 304
seq_name: sp_invertebrate:Q22164
seq_documentation_block:
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alignment_block:
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                                                                                                                                 1316 ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGC 1267
                                                                                                                                                                                                                                                                                 1366 ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA 1317
                                                                                                                                                                                                                                                                                                                                                                                                                              1416 TGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCA 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1451 AAAGGTCTTTATGATCAAGAAGGTTGCCGT......AATGA 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1601 CTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGT 1552
1266 ATATCGAGTACAATGCTTTACATGGAAGCTGATAAAACAGTTAGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1551 TGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAA 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1501 TAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTG 1452
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DUBBIN R., ERVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
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EMBL; 266565; CAA91480.1; -.
SEQUENCE 384 AA; 43964 MW;
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
T04F8.4 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LeuValGluPheThrTyrPheValLeuGlyPheSerAlaAlaIleGlnAs
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                                                            ValLeuIleIleSerPheHisProLeuPheLeuThrArgMetAspLysAl 126
                                                                                                                                                                                                             snMetAspArgGlnArgMetIleAlaProGluGlyMetMetPheSerThr 109
                                                                                                                                                                                                                                                                                                                                                          pGlnPheGlyArgProValGlyGlyIleLysLeuAsnHisGlyAlaCysA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysGlySerTyrAsnArgProGluCysArgValAspTyrSerThrLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leAspMetGlnPheArgThrArgLysGlnPheAsnGlyLysValTyrVal 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pAspAsnGluLeuIleGlyGlnProGluIleGlnCysAsnAlaAspThrI
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Percent Identity:
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seq_name: sp_invertebrate:Q9XVN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 laIleAspValSerAsnLeuProThrGluSerValGlnSerAspLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetProThrCysSerTyrThrIleArgArgAspGlnLeuAspGlyProIl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sThrAspArgLeuLeuLeuGlyAspProThrTyrValGluAlaLeuAsnM
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eLeuLysTyrAlaLysValGlyAspGlnValValHisArgTrpGlnCysA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTA...A 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAAAACAGGTGGTGCCGCAGCAAAAACCTGCTGCAGCTGCGCAACTTCGT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sAspGlyIleThrProProMetCysSer...... 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.....GTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTG 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heLysAspAlaAsnSerAsnGluLysGlnIleValLysArgAsnAlaArg
                                                                                                                                                                                                                                                                                                                                                   TGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTG
                                                                                                                                                                                                                                                                                                                                                                              ThrPheLysProLysAspAlaAsp......MetPheSerGlnThrVa
                                                                                                                                                                                                                                                                                                 ATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAATACTT 579
                                                                                                                                                                                                                                                                                                                           lTyrValMetAspLysGluAsnGlyAspSerThrSerAlaGlnAlaAlaG
                                                                                                                                                                                                                                                                                                                                                                                                           TTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAAC
                                                                                                                                                                                                                                         GCTGCAGTACAAAATGGAATCTGCATGTCACCA......TTTGG
                                                                                                                                                        aValThrPhePheThrPheIlePheValLeuPheValThrThrIleLeuV 365
                                                                                                                                                                                    CTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTA 491
                                                                                                  alvalvalTyrHisArgTyrCysLysAsnGlu
                                                                                                                           TTACCATTTCGTTTAAATTTCGTCCAAATCAG 459
                                                                                                                                                                                                              ...LeuAspProGlnThrIleCysLeuAlaProLysLeuLeuValValAl
        Created)
                                     PRT;
                                                                                                           375
                                        610 AA
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alignment_block:
US-09-323-427-2/rev x Q9XVN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: Q9XVN2 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONDRIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONDIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
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LICHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
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WATSON B., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON B., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATCH STANDER M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATCH STANDER M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATCH STANDER M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
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WATCH STANDER M., WEINSTON R., WILKINSON-SPROAT J., WOHLDMAN P.;
WATCH STANDER M., WEINSTON R., WILKINSON SPROAT J., WOHLDMAN P.;
WATCH STANDER M., WEINSTON R., WILKINSON SPROAT J., WOHLDMAN P.;
WATCH STANDER M., WEINSTON R., WILKINSON SPROAT J., WOHLDMAN P.;
WATCH M., WEINSTON R., WILKINSON SPROAT J., WOHLDMAN P.;
WATCH M., WEINSTON R., WILKINSON SPROAT J., WOHLDMAN P.;
WATCH M., WEINSTON R., WILKINSON SPROAT J., WOHLDMAN P.;
WATCH M., WATCH M.
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Rhabditina; Rhabditoidea; Rhak
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EMBL; Z81086; CABO3116.1;
SEQUENCE 610 AA; 68585
                                                                                                                                                                                                                                                                                                                                                                                                                                      1526 GAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAA 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1570 TGTCTTATTCG.....ATTCCGGTTGACAATGGTGTCGAAGGTGAGCCA 1527
1332 TATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTA 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 uLeuIleTyrAsnArgIlePheLeuGlnSerIleThrIleLeuIleLeuL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| ||| :::::::||| |||:::
34 LeuArgPheGluSerValGlnPhe...LysAsnProProIleLeuLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 euserThrserSerCysPheGluIleGlnAsnGlyValValGlyLysPro
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                                                                                                                                                                                                                                                                                                                                                                              ysValGlnHisSerAlaAspAlaHisSerSerProGlnGluPheThrIie 132
                                                                                                                                                                                                                                                                           sProPheAsnGlyArgIleTyrValAspGlyGluSerAspLysGlnHisC
                                                                                                                                                                                                                                                                                                                              TGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTT 1427
                                                                                                                                                                                                                      GC.....CGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTT 1383
                                                     ProlleGlyAlaCysAsnMetArgArgGlnArgThrLeuHisProArgGl 149
                                                                                                        CCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGG 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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2.593
66.443
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Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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8
35.906
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Seq. ACD DIT OF THE CONTROL OF THE C
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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LICHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPEA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
Q23097 PRELIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1082 CATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGT 1033
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 GluHisGlyAlaIleSerAlaTyrThrAsnAlaHisValPheLysTyrAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  982 ATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTTGGAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAACAGAT...TTAATGGCTGGCCAAGAAGATCCTCACGTATACAAATATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lAspGlnGluTyrSerLeuProValCysAlaTyrHisLeuLysAsp...G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
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                                                                                                                                                                                                                                                                                                            COULSON A.,
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alignment_block:
US-09-323-427-2/rev x Q23097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1282 CCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGAT 1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1479 TAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1529 CCAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACG
                                                                                                                                                                                                                         211 lrystysCysPheValThrAspGlyAspGlyGluAspHisAlaValValA
                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994),
EMBL; Z71267; CAA95850.1;
SEQUENCE 387 AA; 43212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 rLysProPheArgGlyAsnIlePheValLysGlyArgAlaLysAspLysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 ProLysVallleCysAlaGluAsnAspLeuAlaLeuAspIleValThrSe
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                                 GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG
                                                                                                      CCAACAGATTTAATG...GCTGGCCAAGAAGCTCACGTATACAAATATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspAlaSerLeuMetArgAlaHisAlaSerSerGlnValPheLysTyrAl
                                                                                                                                                                        ATGCTGATGGATGTGCTCTTGATAATATTTTGCTAAATAATTTTGGAATAT 933
                                                                                                                                                                                                                                                   CCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAA 983
                                                                                                                                                                                                                                                                                                   HisValTrpGluCys.....ThrProAlaAspMetGlyMetLeuVa
                                                                                                                                                                                                                                                                                                                                        CATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGT 1033
                                                                                                                                                                                                                                                                                                                                                                              lyProAsnGlyProThrLeuThrTyrAlaAsnValGlyAspIleValPhe
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GluIleValThrGlnAsnIleAspValSerMetIleProThrThrGluLe 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTAT 1330
                                                                                                                                                {\tt spPheAspGlyCysAlaThrAspProPheLeuLeuSerGluLeuSerTyr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hr Lys Asn Asp Arg Ala Phe {\tt His Val Lys Cys Phe Tyr Met Glu Pro Asp}
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6
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 278
                                                                                                            886
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                                                                         261
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01-FEB-1997 (TIEMBLIEL 02,
01-NOV-1998 (TIEMBLIEL 08,
01-JAN-1999 (TIEMBLIEL 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILIR; 94150718:

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

BONFIELD J., BURTON J., CONNELL R., FAVELLO A., FULTON L.,

GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., CALLAGHAN M.,

LIGHTNING J., LLOYD C., MCKURRAY A., MORTINGRE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., MCKURRAY A., MORTINGRE D., SHOWNKEEN R.,

SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,

SMALDON N., SMITH A., SONHAMMER E., STADEN R., WATERSTON R.,

THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

WATSON A., WEINSTOCK L., WILKINSON-SPORDER FROM CONTROLSONE III Of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZK265.8 PROTEIN.
   LENNARD N.
Submitted
                                                                                                                                                                  "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBSON R
                                                                                                                                             Nature 368:32-38(1994).
                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCAAAT .....AGCGAATGTGTTCGACCACAATGT ..........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lnMetGlyMetCysGlnGluValThrProProAsnCysGlyValLysLys 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leu.....LeuValLeuAspProAlaAspArgGlyLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuileLeuileThrileValSerLeuThrValVal.SerThrAlaLeuV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..AlaproSerProPheCysValProArgLeuLeuLeuProValLeuPro 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGCATGTCACCATTTGGCTTCTCAATGTTTATG.....GGTTTAAGC 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATCAGAAGG.....CATAAAAATAATGTTAGAATCATCGAAGCA 425
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       (JUL-1996) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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EMBL; Z75713; CAB03520.1;
EMBL; Z75713; CAB00057.1;
EMBL; Z81143; CAB00057.1;
SEQUENCE 440 AA; 49299 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1557 TCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAA 1508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1507 CTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTT 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt TyrAlaLysGlyArgAlaGluLeuGluAspCysTyrLysAspAspPheGlu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lyMetLysSerLeuArgSerValAspProArgGlyMetTyrTyrGlyIle 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yAsnGlnLysThrArgLysProHisPheAspLeuGlnPheGlyAlaCysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG 1167
                                                                                                                                                                                                                      GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA 991
                                                                                                                                                                                                                                                                                             rgValLeuHisGlnTrpHisCysAsnAspGln.....MetTyrGly
                                                                                                                                                                                                                                                                                                                                                                     CAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTGGA...CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC 1091
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pVallleAspAspLysGlyCysProlleAspProlleLeuIleThrGlyI
                                                                           AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
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MW; 3F2BBBA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 33.438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
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Seq_documentation_block:
ID 022680 PRELIMINARY;
AC 022680;
DT 01-NOV-1996 (TrEMBLrel 01
DT 01-NOV-1996 (TrEMBLrel 01
DT 01-NOV-1999 (TrEMBLrel 12
DE 72268.7 PROTEIN
...
OC CHARYOTES METAZOS; NUMBATO
OC Rhabditins; Rhabditoidea;
RN [1]
RP SEQUENCE FROM N.A.
RA THOMAS K.;
RL SUBMITTED (APR-1995) to th
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE; 94150718
RA MILSON R., AINSCOUGH R., A
BONFIELD J., BURTON J., CO
RA GARDNER A., GREEN P., HAWK
RA JONES M., KERSHAW J., KIRS
RA LIGHTNING J., LLOYD C., MC
RA PARSONS J., PERCY C., RIFK
RA SMALDON N., SMITH A., SONN
RA THIERRY-MIEG J., THOMAS K.
RA WATSON A., WEINSTOCK L., W
RT "2.2 Mb of contiguous nucl
RT elegans.";
DR EMBL; 249071; CAA88879.1;
DR HSSP; P03000; 1TIF.
SOUTH A., 50819
HSSP; P03000; 1TIF.
                                             alignment_block:
US-09-323-427-2/rev x Q22680
                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: sp_invertebrate:Q22680
Align seg 1/1 to: Q22680 from: 1 to: 609
                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAYELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RELEGISCO."
                                                                                                                                                                                                                                                                            Nature 368:32-38(1994).
EMBL; Z49071; CAA88879.1; -.
HSSP; P03000; lTIF.
SEQUENCE 609 AA; 68882 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLrel. 01, 01-NOV-1996 (TREMBLrel. 01, 01-NOV-1999 (TREMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 rProLysPro 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      711 TGCAGAACCG 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 GluGluGluLysAlaProSerSerArgArg.....LysThrTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  843 CATTAAAGAACCAAATAGCGAATGT.....GTTCGACCACAATGT. 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 LysPheAlaAspLysProGlyValTrpPhePheCysGlnValGlnMetCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 leArgTyrSerSerAspLeuGlnArgAlaTyrAlaGluSerSerValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt sMetLysLys...HisGlyMetCysAspGlyIleThrProProSerCysG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGAATATCCAACAGATTTAATG...GCTGGCCAAGAAGCTCACGTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCC 762
                                                                                                                                                      Quality:
Ratio:
                                                                                                                           453,50
2.399
65.854
                                                                                                              Gaps: 11
Percent Identity: 37.282
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Last annotation update)
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                                                                                                                                                                                                                                                                                  OBA2EEOC CRC32;
                                                                                                                                                                              Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COULSON A.,
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1611 GATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATT 1562

ProlleLys 287

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1126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1373 TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGT 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                782 GCTGTTAAA 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 sValTyrValArgGlyPhePheProGlnThrValCysHisLeuAsnTyrC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                        {\tt nValMetValHisPheSerCysGlnIleThrThrCysGlnLysGlnGluA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTTAATGGCTGGCCAAGAAGCT...CACGTATACAAATATGCGGATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rCysValValArgAspGluSerGlyLysAspPheGlnPheIleAspGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           snGlyProValValArgPheAlaAsnValGlyAspValValValHisLys 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA 1077
                                                                                           snGlyCysGluGlyIleSerProProIleCysArgProMetAspLeuGly
                                                                                                                                                                                             ATAGC...GAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGA 783
                                                                                                                                                                                                                                                                                                                                                                                                          ATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asp Leu Lys Ser Ala Phe Thr Ala Val Arg Ala Phe Arg Tyr Ala Asp Gluer Control of the Control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgGlyCysValThrAspPheSerLeuPheProGluValSerTyrSerAsp 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACA 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TrpThrCysAspSer.....AspArgPheGlyPheValValHisSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTC 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAA 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnGlnArgIleAsnValSerAspIleProSerThrAlaLeuGlnSerLy 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spLysAlaTyrArgLeuAsnCysIleTyrArgGlnGlnGluSerThrLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGA 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProCysAsnValArgArgArgAsnValAlaProProSerIleSerTy 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGACGT.....CAAGTTGCCGGAATTTCACTTCCATTT...GAT 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerGluGlyIleArgLeuHisIleAsnProThrGlyThrPheGlyGlyHi
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                                                                                                                                                                                                                                                                                                   268
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Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
        5:...
6:...
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49: em_hum5:*
50: gb_pl3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

KEYWORDS		ACCESSION	DEFINITION	LOCUS	CEF22B5	RESULT 1
HTG; Cuticulin; Elongation factor; GTP-binding ADP-ribosylation	Z50044.1 GI:899234	250044	Caenorhabditis elegans cosmid F22B5, complete sequence	CEF22B5 25823 bp DNA INV 02-SEP-1999		

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REFERENCE
AUTHORS
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Exceptions are indicated by an explicit note. It may be shorter because we only sequence the specified clone. It may be shorter because we arrange for a small overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F22B5. IMPORTANT: This sequence is not the entire insert of clone F22B5.

INFORTANT: This sequence is not the entire insert of clone F22B5. In may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
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2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Submitted (13-JUL-1995) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, usir
predictions from Genefinder (P. Green, U. Washington), and other
available information.
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Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R.,
Coulson, A., Craxton, M., Dear, S., Daniel, Da
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The true left end of clone M05D6 is at 25723 in this sequence. The true right end of clone F14E5 is at 4610 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://webace.sanger.ac.uk/cgi-
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                                                                                                                                                                                                                     from this gene;
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                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .25823) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copsey, T., Cooper, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elegans"
                                                                                                                                                                                                                     ing protein; cDNA EST yk390d8.5 EST yk499d6.3 comes from this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from this gene; cDNA EST CEESX90RB comes from this gene; from this gene; cDNA EST CEESX90RB comes from this gene; cDNA EST cDNA EST yk386c7.3 comes from this gene; cDNA EST yk386c7.5 comes from this gene; cDNA EST yk504b12.3 comes from this gene; cDNA EST yk504b12.3 comes from this gene; cDNA EST yk543g2.3 comes from this gene; cDNA EST yk543g2.3 comes from this gene; cDNA EST yk54b12.3 comes from this gene
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4273. .4393))
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/gene="F22B5.3"
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SEELKKLLGEERLAGASLLVLANKSDLPGAIDVNSIAQVIOMSSVYTSEKKCFLVLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F22B5.1"
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/gene="F22B5.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GTP-binding ADP-ribosylation factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(1870.
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ggptgepydfatigooyyhkwtcdsetydtfcavyhsctyddgngdtyoildengcal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9691. .10234
/gene="F22B5.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKFLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITVKEBNEECARPTCSEPQG
FGAVKQANQTAQFFRVLKKRSAPVMENILDVRAELTTLEVLEGNLPSSLTQAQALVAS
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yk304c8.5 comes from this gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(10849. .10984,11033. .11343,11397. .11521, 11578. .11832,11917. .12154))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA90356.1"
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/gene="F22B5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAEIWLDRSNSKAPWDWERLRDTYWKMPTVAFDLDGRTRKRCELMEQLQDEMLEAAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from this gene"
                                                                                          SDSTVLSGTQSITYKSLNRSIPDEQTFGLSYOPDNTYNILPHLMHEMATDFKSVKMNS
GGCVDSKYAAVWRKVLHTKVRGPTYYVSHYKPDEVFNPELEPDDVVKFSDVPVEHVVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F22B5
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AAQAIFQSIIQDLPMKDLKDVLVRCSDKFEDSATWIRPFLRRSHEMTPFAHIKENRVI
PDGLNFSKVFVSSNPSNAPC"
                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:Q19709"
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CDNA
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EST y
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yk594h3.3 comes
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Best Local (
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                              CTGAGCAGTTTGGTTAGCTTGC------
                                                                                                                                                                                                                                              agctgcaggtttttgctgcggcaccacctgtttttaacagctccgaatccttgtggttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acgtaaatcaactggcaaagcttgattatcatcgctaatttcaagggtgttgatatcagt 680
  TTGATAGAAAAGTTGAGAACGATCAGCGTATTTGTAGACGTGAGCCTCTTGTCCAGCCAT
                                                                                                                                   tgaacattgtggtcgaacacattcgctatttggttctttaatggtaatactgatctggca
                                                                                                                                                                                                                                                                                                                     ACGGACATCAAGAATATTCTCCATTACTGGAGCGGATCTCTTCTTCAAAACTCTGAAGAA 3183
                                                                                                                                                                                                                                                                                                                                                     tcgtacatcaatgatattctccggttctgcagatcttttctttgagtaaacgaagttgcgc 740
                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAACACCATTTTGACAACTTACATTTCCTTCCAAAACTTCCAAAGTTGTGAGCTCAGC
                                                                                                       AGAGCACGTTGGGCGAGCACACTCCTCATTTGGTTCCTTAACAGTAATGGAAATCTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 Similarity 63.3
633; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Mote="limited similarity with the elongation factor EF-3 (Swiss Prot accession number P25997); cDNA EST EMBL:C12588 comes from this gene; cDNA EST yk449D7.5 comes from this gene; cDNA EST yk420b2.5 comes from this gene; cDNA EST yk420b2.5 comes from this gene; cDNA EST EMBL:D36040 comes from this gene; cDNA EST yk421d3.3 comes from this gene; cDNA EST yk421d3.5 comes from this gene; cDNA EST yk421d3.5 comes from this gene; cDNA EST yk420b2.5 comes from this gene; cDNA EST yk421d3.5 comes from this gene; cDNA EST yk396b3.5 comes from this gene; cDNA EST yk395b3.3 comes from this gene; cDNA EST yk35965.5 comes from this gene; cDNA EST yk3595.5 comes from this gene; cDNA EST yk351a5.3 comes from this gene; cDNA EST yk351a5.3 comes from this gene; cDNA EST yk351a1.5 comes from this gene; cDNA EST yk348b2.3 comes from this gene; cDNA EST yk348b2.5 comes from this gene; cDNA EST yk351h3.3 comes from this gene; cDNA EST yk351h3.5 comes from this gene; cDNA EST yk351h3.5 comes from this gene; cDNA EST yk351h3.5 comes from this gene; cDNA EST yk251h3.5 c
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15384. 21812
19ene="F2285.7"
19in(15384. 15575,15622. 16479,16527. 17
18794. 18946,18996. 19449,19497. 19843,
20672. 21600,21677. 21812)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSNWDYLDEVDILPKLPPNFDELRESKKWQERKEALEALLKVLT
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LDPKANYGALVERLQKVLEKDANINVAALAANCITGIANGLRTKFQPFAVSVTPIIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KFKEKKPTLRDPLVACIDAVVATTNLEAVGEIVLAALGKPNPSIKTQTDLFLQRCFMK
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complement(join(12240.
13262. .13392,13465. .1
/gene="F22B5.6"
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/db_xref="GI:3876232"
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/db_xref="GI:3876230"
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Pred. No. 5.1e-49;
0; Mismatches 233;
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                                                                                                                                                                                                          TTAACTGCTCCAAATCCTTGTGGCTC
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3772 TAAACCTTCAAGAAGCATTCCTTAAAAATTACAGAAGTTTCATAGTCTTACCGATCAACC
                        acttgacgtccaccttcatcattacggcaaccttcttgatcataaagacctttcacataa
                                                                                                                                                                                        ggattcagagatcgtgtacgcgcaacattgcatgaatcaaatggaagtgaaattccggca
                                                                                                                                                                                                                                                                              ttggtaacaaataatggatgaaacgaaatgacaacagttgttgttgttacaaaaataccacgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATTCAGAGATCTGGTACGAGCAACGTTGCAAGTATCGAATGGAAGTTCGATTCCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tggcatcgggacaatttgagtttgaaaagcagttgtgatttcagatacctcaatctgtgc
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ACGTGTCCCTCGAAGGCATTACGTGTGTTGAAGTTTACTG
                                                                                 ACTTGACGACCTCCTTCGTCATTTCTACATTCTTGTTGATCGAAAAGTCCCTTAACGTAG
                                                                                                                                                                                                                                                          TTGGTGACAAATTGGGGATGGAAAGAGACGACGACAGTTGTGGTAACGAAGACTCCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTGCATTTTTTAACGAGAAGCTTCTAGTTGATATCAAGCTTTATAATTTCGGTATCC
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Z49125.1 GI:790365 HTG; Cuticulin; Fork head. Caenorhabditis elegans. Caenorhabditis elegans Caenorhabditis elegans cosmid Z49125 CEC47G2 34831 bp C47G2, complete sequence. 02-SEP-1999 Caenorhabditis.

Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, M., Latteille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.

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REFERENCE
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Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of important and clone. It may be shorter because we only sequence the specified clone. It may be shorter because we arrange for a small overlap between neighbouring submissions.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-APR-1995) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2 \ \mathrm{Mb} of contiguous nucleotide sequence from chromosome III of C.
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Direct Submission
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The true left end of clone C47G2 is at 1 in this sequence. The true right end of clone C47G2 is at 6388 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence Z49912.

The true left end of clone T24F1 is at 34731 in this sequence. The true right end of clone T05B9 is at 12750 in this sequence. The true right end of clone T05B9 is at 12750 with the end of sequence start of this sequence (1..101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end of this sequence (34731. .34831) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"similar to cuticulin; cDNA EST EMBL:C10444 comes /note-"similar to cuticulin; cDNA EST EMBL:C12078 comes from this gene; cDNA EST yk262c12.3 comes from this gene; cDNA EST yk262c12.5 comes from this gene; cDNA EST yk265h3.5 comes from this gene; cDNA EST yk278g8.3 comes from this gene; cDNA EST yk278g8.3 comes from this gene; cDNA EST yk278g8.5 comes from this gene; cDNA EST yk439g8.3 comes from this gene; cDNA EST yk439g8.3 comes from this gene; cDNA EST yk439g8.3 comes from this gene; cDNA EST yk30a11.3 comes from this gene; cDNA EST yk583c11.3 comes from this gene; cDNA EST yk583c11.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                             /translation="MMWKPIICLAALVUSASAIPVDNNVEGEPEVECGPNSITVNFNT
KNPFEGHYYVKGLYDQAGCRSDEGGRQVAGIELPTOSCUTARTRSLNPKGVFYSTTVV
RNPFEGHYYVKGLYDQAGCRSDEGGRQVAGIELPTOSCUTARTRSLNPKGVFYCKYEILDG
ISPHOQEVTKVDRAYRIQCFYMESDKTWSTQIEVSDLTTAGTQVVPMCKYEILDG
GPSGQPIQFATIGQQVHKWNTCDSETTDTFGAVHSCTVDDGNGDTVQILNEEGCALD
GPSGQPIQFATIGQQVHKWNTCDSETTDTFGAVHSCTVDDGNGDTVQILNEEGCALD
GPSGQPIQFATIGQQVHKWNTCDSETTDTFGAVHSCTVDDGNGDTVQTLNEEGCALD
KFLLNNLEYFTDLMAGCEAHYYKYADRSQLFYQCOISITIKDPGSECARPTCSEPQGF
KRLNNLEYFTDLMAGAAAPQAGVEEVQAAFVAAAAAPVAAAAAAPAVPRATLAQLRL
GAVKQAGAGGAHAAAAPQAGVEEVQAAFVAAAAAPVAAAAAAPAVPRATLAQLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(2562. _2679,2992. .3217,3898. .4636,4687. .4878)
/gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis elegans"
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/chromosome="II"
15433. .17108
/gene="C47G2.2"
join(15433. .15770,16205. .16531,16772. .17108)
                                                                                                               LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGICLTP
IGFASFLGIGTIVATALSATIFYVARPTSHKH"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA88934.1"
/db_xref="GI:3875030"
/db_xref="SWISS-PROT:003755"
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gene CDS

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/note="similar to fork head domain protein; cDNA EST
/note="similar to fork head domain protein; cDNA EST
EMBL:T01618 comes from this gene; cDNA EST EMBL:D66805 comes from this
comes from this gene; cDNA EST yk288f8.3 comes from this gene; cDNA EST
yk268f8.5 comes from this gene; cDNA EST yk474q115 comes
from this gene; cDNA EST yk670a12.3 comes from this gene;
cDNA EST yk670a12.3 comes from this gene
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//gene="C47G2.4"
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FEYYKEKFPARONSIRHNLSLNDCFVKVARGPGNPGKGNYWALDPNCEDMFDNGSFLR
RRKRYKKNSDTYHEMMSHHPMPFPFILPQGMPFPPRMHPMANIPMLGHPMNPRAVPN
MPAFFIPQNIDSQKLLSMMASRIMPMDAPVSSGQKRTSSSSSPNENGSSAVSDKLSA"
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RVVYWSAQLLTWLILPLLQSYVTAGNFTILGKIRAAVINNALYXAIYSLCFLAILIYA
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ELSAAFVTEYASTRFHYKYTQFVAFGIIVYLITSAVFTIFRLQIYKYHLDPNGFFD
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SIKRSNDRSQRTQNWTNSFGSSNAGNGSTTSKFKRSNKNDEERPMLEDDDEEVEESST
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31534. .31653,31701. .31835,31889. .32104,32160. .32570,
32639. .32935,32998. .33215,33263. .33651,33802. .34049)
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CDS gene

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VERSION
KEYWORDS
SOURCE
ORGANISM
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ACCESSION
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     AUTHORS
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                                                                                                                                        C.elegans
M55997
              w55997.1 GI:156271
cuticle protein; cuticlin 1.
C.elegans DNA.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea;
Rhabditina; Rhabditoidea; Rhabditidae; Pelo
1 (bases 1 to 2310)
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   Sebastano,
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MDETLIAKIADNLIVEEGCPAEELVKKSALISASAKILEAFIKUTYSNAPAQOLEEI
ERNLIERHYSYGLMRECMDNUPYEHSIVEGILANKLUPRILQTVLRDIEAU
GSVWQPLLRLIIELCNTWCMSTHEKIAVAFRSLPFINLIKAAKNLPRAKYLHCLLYKV
VILLLHSSFECDELSPAAEYLLTEGGLIQNIYDTATSPNGSSYWACSGLRSENQNLGD
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MADDFSSFFTISFTAANASSSSSDAWPGSDIHLQGEASDWPLNNSHESKASDPVMVG
LAASISHPGDSSEA*
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Pred. No. 2.
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Mismatches 142;
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                                                 Rhabditia;
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                                                  Rhabditida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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567 c 433 g
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75.1%;
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Pred. No. 9e-45;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     899
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DEFINITION
ACCESSION
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AF125580/c
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AUTHORS
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Best Local Similarity
Matches 449; Conser
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Wuchereria b
AF125580
AF125580.1
                                                                                                                                                                                                      ggcagttttattattgcttcgatgattctaacattatttttatgccttctgatttggacg
                                                                                                                                                                                                                                AAGTGTAAAACCGGTTATTGACATACATATACCTTGTGTCATTGTTGCAACAATTACCGG
                                                                                           cattgagaagccaaatggtgacatgcagattccattttgtactgcagcaagtattacagg
                                                                                                                            TAACAATGTAATAGCAACAATTGTAGCAACAGAAACAATAACAAATATTAGCATACCGGC
                                                                                                                                             ATAATACATAGATGTGTAATATCATTTAATAACATTTTAAACTTTGGTAGAATGTGATCG
attatcatcgctaatttcaagggtgttgatatcagttcgtacatcaatgatattctccgg
                          ATGACCATTCTCATGTGCTAACAATGATGATCGATGACGTAGCGCATTTGGTAATGAGGT 420
                                               ttgtccattatgttg-----cagaagtgcacggtgacgtaaatcaactggcaaagcttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wuchereria bancrofti
Eukaryota; Metazoa; Nematoda; Secernentea;
Filarioidea; Onchocercidae; Wuchereria
1 (bases 1 to 724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (03-FEB-1999) Research & Training Center Diseases, Ain Shams University, Abassia Square, Cai Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wuchereria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramzy,R., Helmy,H., Adely,M.,
Wuchereria bancrofti L3 cuticu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ramzy, R., Helmy, H., Adely, M.,
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                                                                                                                                                                                                                                                                                                                                                             248
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                             DLMAGQEAHVYKYADRSOLFYQCQISTTIKEPNSKCQRPQCTEPQGFGAIKTRNGVAA
ASRQAAAFRVLKKRDVRDENIVDVRTDLNALDINEEFTSLPNALRHRSSLLAHENGHP
VIVATMTQGICMSITGFTLAGMLIFVIVSVATIVAITLLRSHSTKV"
1112 c 128 g 236 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                724 bp
bancrofti
                                                                                                                                                                                                                                                                                                                                                                                                              /product="cuticulin-1"
/product="cuticulin-1"
/protein_id="AAD28743.1"
/db_xref="GI:4741875"
/translation="TVDTFCAVVHSCFVDDGNGDKVELLNADGCALDKFLLNNLEYPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /country="Egypt: Nile Delta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Wuchereria bancrofti"
/db_xref="taxon:6293"
/dev_stage="L3 larvae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to Ascaris lumbricoides cuticulin-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=3
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                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                     Score 263.4; DB 3
Pred. No. 6.3e-36;
0; Mismatches 261
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                                                                                                                                                                                                                                                                                                                DB 35;
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A partial
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                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCAGCGTATTTGTATACGTGTGCTTCTTGTCCAGCCATTAAATCTGTTGGATATTCTAA 120
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U73005
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Gene 193 (1), 81-87
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                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 5792)
Timinouni, M. and Bazzicalupo, P.
                                                                                                                                                                                                                                                                                                                2 (bases 1 to 5792)
Timinouni, M. and Bazzicalupo,
                                                                                                                                                                                                                                                                                                                                                                                                   Ascaridoidea; Ascarididae;
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                             Ascaris lumbricoides
                                                                                                                                                                                                                                                                                Submitted (01-OCT-1996) GA3, NA 80125, Italy
                                                                                                                                                                                                                                                                                                       Direct Submission
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lumbricoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:1657624
                                                                                                                                                                                                                                  /organism="Ascaris lumbricoides"
/variety="suum"
                                                                                     882. .929
                                                                                                                                                                                                                    /db_xref="taxon:6252"
                                                                                                                                                                                                                                                                    Location/Qualifiers
                    /note="cuticlin gene; ASCUT-1;
proteins of other nematodes"
                                                                                                                                                                              /gene="ascut-1"
join(766. .954,2851. .3239,3583.
/product="CUT-1-like
                                                            join(882. .954,2851.
                                                                     gene="ascut-1"
                                                                                                /note="site of transplicing
                                                                                                           /gene="ascut-1"
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                                                                                                                                                          product="CUT-1-like
                                                                                                                                                                      /gene="ascut-1
                                                gene="ascut-1"
            codon_start=
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(1997)
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CUT-1-like
Clete cds.
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   cuticlin protein
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                                                                                                     SL1"
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     precursor"
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                                                                  .4693)
                                         cuticlin
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KEYWORDS
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ORIGIN
                                                                                                                                                                  VERSION
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                                                                                                                                                                                                                            FOCUS
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MAMTCUTI 2504 Apricon Martiellia Mtcut-1 gene.

2N x96677. GI:2648040
2S cuticle protein; cuticlin 1; Mtcut-1 gene.

Meloidogyne artiellia.

Meloidogyne artiellia
Eukaryota; Metazoa; Nematoda; Secernentea; Diplogasteria;
Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae;

"Aloidogyninae; Meloidogyne.
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/db_xref="G1:1657625"

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PFEGHAYVKGLYDQEGCRSDEGGRQVAGISLPFDSCNVARTRSLAPRGIFVTTTVVIS

FHPLFITKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFQTQIVMPVCRYEILDGGP

TGQPIGFATIGGQYVHKWTCDSETVDTFCAVVHSCFVDGSGDTIQILNEEGCALDKY

LLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQITITIKEPNSECPRPTCSEPQGFGA

VRPGGSIAPKKORRCQLRLIKKSGGDYDNTLDVATDFSALDISDREALPMDLRHRAR

HARGQQVLISPANGEICMSPFGFSIFMCLAVALAAAVVVVSFKLRPQQKA"

join(930. 954,2851. 3239,3583. 4083,4499. 4690)

/gene="ascut-1"
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5064. .5070
/gene="ascut-1"
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GGCATTGGTAGAAGAGTTGAGAGCGATCCGCGTATTTGTAGACGTGAGCCTCTTGGCCGG
                    ggcattgatagaaaagctgtgatcgatccgcatatttgtatacgtgagcttcttggccag
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De Giorgi.C.
Direct Submission
Submitted (15-MAR-1996) C. De Giorgi, Dipartimento di Biochimica
Submitted (15-MAR-1996) C. De Giorgi, Dipartimento di Biochimica
Submitted (15-MAR-1996) C. De Giorgi, Dipartimento di Biochimica
2 (bases 1 to 2584)
De Giorgi,C., De Luca,F., Di Vito,M. and Lamberti,F.
De Giorgi,C., De Luca,F., Di Vito,M. and Lamberti,F.
Modulation of expression at the level of splicing of cut-1 RNA ir
the infective second-stage juvenile of the plant parasitic nemato
Meloidogyne artiellia
Meloidogyne artiellia
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nilarity 56.8%;
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2518. .2523
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/translation="MRKLLFAIGVFVALNAIFTVRAIPVDNGVEGEPEIECGPTSITV
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ALDKFLLNNLEYPTDLTAGQEAHVYKYADRSQLFYQCQLSTITKEPHSECARFKCAEF
SGFNAVKVGAGGAGAGAPPAAAAATPPPAAAAPPAPIAPAIPARVQRLRTRGULTLKE
KRAAPGEQVLDVRTEENALDISDKPFNLPAHIRHHHLLMENLSAEPQRRFIYOGGGQV
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/gene="Mtcut-1"
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/protein_id="CAA65452.1"
/db_xref="GI:2648041"
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/gene="Mtcut-1"
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/db_xref="taxon:42426"
/clone_lib="lambda7-2(1)"
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/codon_start=1
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                                                                                                             aa
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                         BMA012617 637 bp
Brugla malayi cut-1 gen
AJ012617
AJ012617.1 GI:3858954
cut-1 gene; cuticlin.
Brugia malayi
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Brugia.
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                     Brugia malayi.
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           Spirurida;
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189
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                                                                                                                                             agcaaattgaactggttgaccggttggtccaccatccaaaat---
                                                                                                                                                                                               CAGAATTTCCACCGTATCACCGTTGCCATCATCCACAAAGCAGGAGTGGACAACTGCGCA
                                                                                               cut-1-like genes are present in the filarial nematodes, pahangl and Brugia malayi, and, as in other nematodes, components of the cuticle
TCAAAAAATTCAAAAAGACATGCCTCGTATCGACAAACAGGCATGGGGACAATTTGAGTT 130
                                               1 (bases 1 to 637)
Lewis, E., Hunter, S.J., Tetley, L., Nunes, C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-NOV-1998) Devaney E., Veterinary University of Glasgow, Bearsden Road, Glasgow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Devaney, E.
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                                                                                                                                                                                                                                                                                                                                                                       174
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                     /gene="cut-1"
/number=2
a 136 c 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="cuticlin"
/product="cuticlin"
/protein_id="CAA10074.1"
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/db_xref="SITREMBI:096775"
/db_xref="STTREMBI:096775"
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OIVPMPVCRYEILDGGPTGQPTQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGN
GDTVEILSADGCALDKYLLNNLEYP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(<2. .164,266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brugia malayi"
/db_xref="taxon:6279"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          266. .484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="cut-1"
join(<2. .164,266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="cut-1"
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/number=1
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                                                                                                                                                                                                                                                                                                            10.7%;
                                                                                                                                                                                                                                                                                              Score 190.6; DB 3
Pred. No. 1.6e-23;
0; Mismatches 54
              ttcataacggcatactggcatcgggacaatttgagtt 1182
                                                                                                                                                                                                                                                                                                                                                                         134
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G61 1QH, UK
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Best Local
                                       Matches 171;
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                                                 Local Similarity
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AJ012618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pahangi and Brugia malayi, and, as in other nematodes, components of the cuticle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cut-1-like genes are present in the filarial nematodes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 358)
Lewis,E._ Hunter,S.J., Tetley,L., Nunes,C.P., Bazzicalupo,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99339397
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Eukaryota; Metazoa; Nematoda; Secer
Onchocercidae; Brugia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brugia pahangi.
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                                                                                                             110
                                       Conservative
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pahangi cut-1
                                                                                                                                             /number=1 350. 356
                                                                                                            /number=2
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/db_xref="GI:3970656"
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                                                                                                                                /gene="cut-1"
                                                                                                                                                                                           LNADGCALDKYLLNNLEYPTDL
                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                             /note="unnamed protein product"
                                                                                                                                                                                                                                                                          join(<1. .191,350. .>356)
/gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Brugia pahangi"
/db_xref="taxon:6280"
                                                                                                                                                                    /gene="cut-1"
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                                                                                                                                                                                                                                                                                                                                                                       join(<1.
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                                                 8.8%;
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                                    Score 156.6; DB 3
Pred. No. 1.1e-17;
0; Mismatches 24
                                                                                                            64
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                                                                                                            120
                                                          DB 34;
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Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latteille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                     overlap between neighbouring submissions.

This sequence is the entire insert of clone F53F1. The true right end of clone M04G12 is at 21759 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence Z81103.

The end of this sequence (39379. .39478) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small content of the specific of the specific of the specific of the specific clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-OCT-1996) Louis, MO 63110, U
jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditia; Rhabditida; Rhabditida; Rhabditida; Rhabditina; Rha
                                                                                                                                                                                                      sequence AL021448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predictions from Genefinder (P. Green, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z81088.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bin/display?db=wormace&class=Sequence &object=F53F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   see:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burton, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z81088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 39478)
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/db_xref="taxon:6239"
                                         /organism="Caenorhabditis elegans"
                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    computer analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-1999
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for a small
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                                                    /yere-predicted using Genefinder; similar to cuticlin;
/note-predicted using Genefinder; similar to cuticlin;
/note-predicted using Genefinder; similar to cuticlin;
/note-predicted using Genefinder; cDNA EST EMBL:C1739
EMBL:D74799 comes from this gene; cDNA EST EMBL:C11739
comes from this gene; cDNA EST EMBL:C12451 comes from this
gene; cDNA EST EMBL:C10189 comes from this gene; cDNA EST yk506b3.3 comes
from this gene; cDNA EST yk379e3.5 comes from this gene;
cDNA EST yk437e9.5 comes from this gene; cDNA EST
yk311h10.3 comes from this gene; cDNA EST yk311h10.5 comes
from this gene; cDNA EST yk341f6.3 comes from this gene;
cDNA EST yk341f6.5 comes from this gene; cDNA EST
yk300g2.3 comes from this gene; cDNA EST yk300g2.5 comes
from this gene; cDNA EST yk324b3.3 comes from this gene;
cDNA EST yk324b3.5 comes from this gene; cDNA EST
yk191d9.3 comes from this gene; cDNA EST
yk191d9.3 comes from this gene; cDNA EST
yk191d9.5 comes
from this gene; cDNA EST yk191d9.5 comes
from this gene; cDNA EST yk191d9.5 comes
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/gene-"F53F1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /t-anslation="MONKEIRRILEDYFPKGFLISESSKYDCHLEDMHLVLQLLLATI
AVNPVPIQNSLYGDVQVECDSRTISVQIKTEKPFVGVIFVKDFASEEYCTSRCTGRLS
AVNPVPIQNSLYGDVQVECDSRTISVQIKTEKPFVGVIFVKDRTYNLLCIXRESQYTV
ARLEIEIGLCGALFQRVLNPKGLAVRTTITISFPFYGIAVGCPPVEFGLIGQQVYNQWKCDNDKGM
INISVDEISTISYNVLTIMPFCTYQILSGGPFGEPVEFGLIGQQVYNGWKCDNDKGM
IILIKEDSFCMYVHTCSVDDGRGETSFLIDSNGCSIDKFLLSNLEYPGNLLAGQEAHV
YKFADRDALFFQCQISITYKEEDQGECVRFICEDVEGGGAPVVGPPPYGMISKNLVNIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="predicted using Genefinder; similar to cuticlin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(14923. .16486)
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/db_xref="GI:3877456"
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/protein_d="CAB03128.1"
/db_xref="d1:3877460"
/db_xref="sptrembl:p91998"
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/translation="MSIKLNTGYDCPLIGLGTYKIIGDQVLPVLDAALTAGYRLFDTA
KVYNNEKEIGDALEILPKHNIKKEDIFITTKMHPNIYENVKKLVDESLSLLKTSYID
KVYNNEKEIGDALEILPKHNIKTLAIATWNDLWECKNAGKIRSVGVSSFEIRHLEELKDL
MYLIHYPKSFDYGDQDPMNKTLAIATWNDLWECKNAGKIRSVGVSSFEIRHLEELKDL
KYLPPCCNQVEYHPHFTREELKNYCKSEGIFFQAFSSLARHNETLLSSEIITTALAEK
KYNPKTTYLLSWATSQKVGIIPKSTNPERLAQNLKTVLLEEEEVKKICNLNLDKHYVR
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1839. 18524)
1839. 18524)
/gene="F53F1.2"
/gene="similar to aldehyde reductase; cDNA EST yk473d8.3
/note="similar to aldehyde reductase; cDNA EST yk473d8.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(18714. .18887,18935. .19056,19113.
19919. .20008,20072. .20251)
/gene="F$3F1.3"
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/db_xref="GI:3877459"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F53F1.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21582. .22009
/gene="F53F1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to aldehyde reductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(21582. .21670,21781. .22009)
/gene="F53F1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGWLVL"
/protein_id="CAB03125.1"
                                     'codon_start=1
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MEDLINE
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACACGTGTGAACTACCATGCAGAATGAGTCTTCTG 15350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aagcaggaatggacaaccgcgcagaaagtatcaacgg 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAATTGAGCACCCATTCGAGTCTATGAGAAATGAGGTTTCACCTCGTCCATCGTCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGCTTCTTGCCCCAGCGAGTAAGTTTCCCCGGATACTCAAGGTTCGACAATAGAAACTTA 15253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tgagcttcttggccagccattaaatctgttggatattccaaattatttagcaaatattta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, R., Aliscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Waterston, J. and Wohldman, P.
                                                      Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. INPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-OCT-1995) Louis, MO 63110, USA. E-mail: jes@Sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; Cuticlin-like protein.
Caenorhabditis elegans.
Caenorhabditis elegans
                                overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                             http://webace.sanger.ac.uk/cgi-
bin/display?db=wormace&class=Sequence &object=E04D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McMurray,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 31536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368 (6466), 32-38 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 31536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       a graphical representation of this sequence and its
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   is not the
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entire insert of clone E04D5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neighbouring submissions.
The true left end of clone E04D5 is at 1 in this sequence. The true
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / yene= cDNA EST EMBL:D71941 comes from this gene; cDNA EST EMBL:D74691 comes from this gene; cDNA EST EMBL:D76330 comes from this gene; cDNA EST EMBL:D76330 comes from this gene; cDNA EST EMBL:C11194 comes from this gene; cDNA EST EMBL:C13213 comes from this gene; cDNA EST EMBL:C13213 comes from this gene; cDNA EST Yk412d7.3 comes from this gene; cDNA EST Yk412d7.5 comes from this gene; cDNA EST Yk454d9.3 comes from this gene; cDNA EST Yk454d9.3 comes from this gene; cDNA EST Yk454d9.3 comes from this gene; cDNA EST Yk413f5.3 comes from this gene; cDNA EST Yk413f5.5 comes from this gene; cDNA EST Yk413f5.5 comes from this gene; cDNA EST Yk413f5.5 comes from this gene; cDNA EST Yk30b11.5 comes from this gene; cDNA EST Yk375c1.3 comes from this gene; cDNA EST Yk375c1.3 comes from this gene; cDNA EST Yk375c1.3 comes from this gene; cDNA EST Yk365e8.5 comes from this gene; cDNA EST Yk366612.3 comes from this gene; cDNA EST Yk598a1.3 comes from this gene; cDNA EST SMBL:C13136 comes from this gene; cDNA EST Yk598a6.3 comes from this gene; cDNA E
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                                                                                                                                                                 EQERKAFQLKKKVEEIKVLKQRVANGDQLQPNQMEKIQRENEYLSELSKLTI"
                                                                                                                                                                                                                                          ETHFESPKELWEVRWRPMTGYNKFAIKELTKTDKMAAGLPIRKKDASHPLNNVPAGAV
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02-SEP-1999

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YIVPVFFIAKVVQFAIPFILILITFERYLWTCTERKRFGITFQVLTLSLSFRKAFSAI
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/db_xref="GI:3875454"
/db_xref="SPTREMBL:Q19055"
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RVSCFYVEGTKKVHNHVDISALTTQLLESETQLPVCRYEILMEAGGSBIKYARAIGDQV
RVSCFYVEGTKKVHNHVDISALTTQLLESETQLPVCRYEILMEAGGSBIKYARAIGDQV
YKKWRCVAELENVYCMKVHSCTVYDGOGFPVTVIDANGCSVDGVILONLEYTSDLTA
GKLAPVFKFADKAGLIFNCOIQLFIKDVNYGCSNTQPQCFTSQYVVEPAQKTTETAEP
YPYDSHESGYVETRPANYPVASSRYPIFTTQAPASYPSSPAPPPGADIDNGYPEPQPI
YTAETPENAYDGIVGENDTEQPFTTSAAYTEDGVYSBLIKRNVCESTEQINGKRP
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/codon_start=1
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/tbanslation="MWSINLTVHIILLVTFSVSHVVTTAVTKATGETTVRGAGQDLGD
/translation="MWSINLTVHIILLVTFSVSHVVTTAVTKATGETGRGAGQDLGD
VSSSFFYETTTASTCADDPNTDCTQYTFLCSNAKYTPLLQQFCAKTCGFCGSGSTAAP
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LILLCLLFATTVVVFIVIVQKQRQILAOTAFFKP"
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/db_xref="GI:3875452"
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/gene="E04D5.4"
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/db_xref="GI:3875453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="E04D5.4"
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ore 83.8; DB 34;
ed. No. 1.6e-05;
Mismatches 137;
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                         FEATURES
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MEDLINE
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                                                                                                                                                                                                                                                                    source
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Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
Exceptions are indicated by an explicit note.
Important: This sequence is NOT nocessarily the entire insert of
the specified clone. It may be shorter because we arrange for a small
overlapping sections once, or longer because we arrange for sections
overlap between neighbouring submissions.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Culson, A., Cardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., O'Callaghan, Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Sanden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P., Walkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 32412)
1 (bases 1, Anderson, K., Baynes, C., Berks, M., Berk
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Caenorhabditis elegans
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Caenorhabditis elegans cosmid F53B6, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematcde.wustl.edu Coding sequences below are predicted from computer analysis, predictions from Genefinder (P. Green, U. Washington), and ot available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor associated protein; Thrombospondin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For a graphical representation of this sequence and its analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The true left end of clone F32H2 is at 32306 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The start of this sequence (1. .105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neighbouring submissions.
The true left end of clone F53B6 is at 1 in this sequence. The true right end of clone F53B6 is at 5116 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94150718
                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                          The end of this sequence (32306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence Z81523
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                                                                                                             /clone="F53B6"
                                                                                                                                                      /chromosome≃"I"
                                                                                                                                                                                               /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                      .32412) overlaps with the start of
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other using

BASE COUNT ORIGIN

10458

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VACVDTSTQ" 5592 c

gene

Matches Query Match

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Conservative

Local Similarity

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PFWLTSKYSDCSMSCGSGTARRSVKCAQTVSKTDGADAHIVLRDDRCHFKKPQETETC
NVVACPATWVSSLNKRHNKIKLNKLKTAQWTECSRSCOSGERRRQVWCEIRDSRGKTQ
RRPDUECDANTKPQTVEVEVSFGSCSRPELLSNRVFEQNAEQKKLTLGIGGVATLYQGT
SIKIKCPAKKFDKKIYWKKNGKKIKNDAHIKVSANGNLRVFHARNEDDAVYECFTDR
LQGNVTLNFKYRDFPASRVDLAPKPQIPSTKNRQRVQVSKEDVLREQASVLHKMNVSL
IEALLTAPNDEKAREGLRKYGNELVARNDIGHNSECROKTCHYAGGYQARGIISCKVTFH
                                                                    comes from this gene; cDNA EST yk193h3.5 comes from gene; cDNA EST yk411f5.3 comes from this gene; cDNA yk411f5.5 comes from this gene"
                                                                                                                                                                                                                                 complement(join(20516. .20602,20648.
21609. .21818))
                                                                                                                                                                                                                                                                                             complement(20516. .21818)
/gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                                                        GGYYQSNYWGKRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(19892. .20022,20241.
/gene="F53B6.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCRFTNGTSVDIQHCDITNRPATTMDCPNQNCKAEWRTSDWGSCSSECGTGGVQLRLLSCVWISSGRPAGRNCEQMRRPHSARACVADEPLPPCMPTASALYQRDASCQDQSRFCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTRPAAEENCVSTSCGRWEAGKWSKCTASCGOGVRRRHVACVGGSDCDEGGRPRQE
TTCYAGIPCSIATNSLDWNDRAYLDGNTFGSMDNHNDWQAPRLVAGEWSTCSSTCGTG
VMSRTVECVAVNPISSAPIKLPMSECQDQEQPKLFESCEVRSCPLQEDSKLSEDEAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RQLRRCLTSKCSGESVRFKVCAQKTCESKSRLARDTICGGEEIVSRGQCEVVCRSRLT
GANFLMRVDDGTPCQAATSRA VCSKGSCQIVGCDGLISSSFRFDACGVCGGRGDTCDN
GKFLMKVSEBYTACASNCDDIVDWSGAGRSIASTSQPIVCVVNAITGRVVPEKLCABV
GKFLMKVSEBYTACASNCDDIVDWSGAGRSIASTSQPIVCVVNAITGRVVPEKLCABV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"predicted using Genefinder; similar to thrombospondin like; cDNA EST EMBL.214404 comes from this gene; cDNA EST EMBL.21571 comes from this gene; cDNA EST yk195c9.5 comes from this gene; cDNA EST yk195c9.5 comes from this gene; cDNA EST yk286g7.3 comes from this gene; cDNA EST yk286g7.3 comes from this gene; cDNA EST yk286g7.5 comes from this gene; cDNA EST yk286g7.5 comes from this gene; cDNA EST yk353h1.3 comes from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(19892. .20283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEIRNVDNSICESLASVRPPETRPCHREDCPRWEASQWSECSSQRCVSSMLAQKRRNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRDQLTHYTPLNLKMLTSLRELYGTHDMKGITESWDALQSNFKCCGVNGTDNAQIWKT
SKWIMHQRAPKLLIPESCCIPSEIERCRSNPFDQDAPPPYYTSTCYEPLQNDLLHVMN
VASWLCITNAIVQVIFVSLKTIKLLNFILLKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKSAIGEEGRKKNQLLKRDFSKLANPLSEFSLYREQPDTQFLKNRKIKNVDQQDSRLFSLLEKYIFHSLSINLTIYLKALHFQTRVFPFKSFPHFNTLKFTFQLKMGALGDSAYGARGRLIKFSYIVTALISILFSISCICYGIWLLARRSQYAELVSPS
                                                                                                                                                            /note="predicted using Genefinder; cDNA_EST yk193h3.3
                                                                                                                                                                                                     /gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB54255.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIKLFHSCDSLEVRQKCCSTCTFVERKKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL: P90884"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB03117.1"
                                                                                                                                                                                                                                                                                                                                                                              translation="MDFGILLVFLMAVAGTFAGISVSFSHSHEFPRHGLLGGGGFNPY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F53B6.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB03121.1"
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/gene="F53B6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(4270. .15311)
/gene="F53B6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB03120.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      platelet-endothelial tetraspan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3308,3430. .3649)
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Best Local Similarity
                                                                    29678
                                                                                                                                                                                                                  1174 atttgagtttgaaaagcagttgtgatttcagatacctcaatctgtgcactaactgtttta 1233
                                                                                                                                1234
1294 ggatgaaacgaaatgacaacagttgttgttacaaaaataccacgtggattcagagatcgt 1353
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                                                                                                                    tcagcttccatgtaaaagcattgtactcgatatgcacgatcaactttggtaacaaataat 1293
                                                           ATTGACTCGAGGAAGAACATCGAATACTGAATGCTCGATCCATTCCCGTCACAAAGAAT 29737
                                                                                                                                                                                  AATTGATTTAATACTTCAGAGTTAACATACCCAACATCAATTTCCGCGTTCAATCCTTTA 29677
                                                                                                                                                                                                                                                                                                             127;
                                                                                                                                                                                                                                                                                                             Conservative
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GRIYVDGESDKQHCVQHSADAHSSPQEFTIPIGACNMRRQRTLHPRGISFSFTMITSF
                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(27666. .27862,27919. .27959,28076. .2877
28905. .29001,29330. .29417,29467. .29606,29648. .29915,
30107. .30301,30478. .30589))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(27666. .30589)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="msrespyslaqlverettnlkvrgssplyshaesmglifpnwvr
VCYRRGPMEYHPYDMNMPPKLVPRPPLHYKFDPPLTERGQIVSETYGRGLLNAGIRPF
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GYPINIQYLPSQGFIRAENIEDYNLRIQAFFKKNIAKIEQKQVVVISDNVMVDLTRNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SpTREMBL: P90883"
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ELADEKIPLRLQKSKGLLNLIDKNFATLAFCRCWIDRLGETKYLMALKGKCSYSTASR
                                                                                           PQIEYEHGAISAYTNAHVFKYADKVQLYFTCTVQLCYKHDGGCEGITPPQCSGHSHGI
                                                                                                                     HPFFVTGMDRAFSIRCFFLESIKGLNAEIDVGTLAPQHVDQEYSLPVCAYHLKDGIEG
HVLRFAQVGQKVTHVWRCDQDASHVYGILIHSCYADDGHGNKFELVDDRGCSTDPFLL
                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F53B6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary prediction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F53B6.t1"
/gene="F53B6.t1"
/note="TTT Lys K-tRNA; predicted using tRNAscan-SE-1.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVETVDDILQCIKKPTCQMNFISLKKGEAQIMDSPILPLTKSLYLVKPFYWTDVPLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F53B6.5"
23555. .24160
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VPLTAIVTTSLPMVAAIAFCAKNRKTVHAKNKNKNKSSKSAKSSKSTRGASKSGKSRR
SSKAKHSKRSSKSSKKGTSGKSGKGSSKRGGKSSKSSKSKKVKTATTSGSOVSTVSAA
                                                                                                                                                                                                                                                                                                                                                                           /note="predicted using Genefinder; similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F53B6.tl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26276. .26348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB03118.1"
/db_xref="GI:3877450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26258. .27459
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QVGHSLAEEVNSIKHSKEMNVAPAKLQYQTLGGVNQIELKNTSNERKAYKIKCSDNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F53B6.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMLILTLFTDRWMAMVGACILQSFAGKIIGKRANLLLNLII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB03119.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVVPLVAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(26258. .26342,26501. .26802,26846. .26926,26974. .27107.
77153. .27288,27334. .27459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Similarity to Rat initiation factor 2 associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F53B6.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRVNPVYGFAEPRSSVK IDVLRLNGEQKTDKLVLLTANANGSTNPHEAFANQAEHREM
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4.2%;
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Score 74.8;
Pred. No. 0.
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                                    DB
                                34;
                             Length 32412;
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Mismatches

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AUTHORS
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CEY111B2_0/c
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CEY11182_0
CEY11182_1
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CEY11182_3
CEY11182_4
CEY11182_5
CEY11182_6
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                 121
                                                                                                                                                                                                      Local Similarity
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                                                                                                                                     1 ttttttttttttttttttttttcacaaatgaaatactttttaattgcaataatgcaaa 60
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                                                                                                                   aatttgtgatattatcacaaatgataaactgttagaataaaataggacaagttgataatg
                                                                    taagtgaattgtttacagaataggaaatgatgcccataaaaattgggcaatacaaggtat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission

Direct Submitsion

Submitted (27-OCT-1999) Nematode Sequencing Project, Sanger Centre,

Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics,

Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics,

Washington University, St. Louis, MO 63110, USA. E-mail:

jes@sanger.ac.uk or rw@nematode.wustl.edu

on Oct 19, 1999 this sequence version replaced gi:6016917.

Onder of segments is not known; 800 n's separate segments.

Order of segments is not known; 800 n's separate segments.

IMPORTANT: This sequence is unfinished and does not necessarily

IMPORTANT: This sequence. Work on the sequence is in progress

and the release of this data is based on the understanding that the

sequence may change as work continues. The sequence may be

contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 614429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans chromosome IN PROGRESS ***, in unordered piec
                                                                                                                                                                                         164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z98857.36 GI:6065761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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NOTE: This is a 'working draft' sequence.

This record will be updated with the finished sequence will
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                                                                                                                                                                                                                                                                                                                           /organism="Caenorhabditis
/db_xref="taxon:6239"
/chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                          103068 c 106254 g 187431 t
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Pred. No. 0.0017;
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                                                                                                                                                                                               Mismatches 154;
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MEDLINE
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tataaaagartactgaataatgaataagcttttcagaagcctataaaagcgatagaagaag 300
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Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Bonfield,J., Burton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Cocallaghan,M., Parsons,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
                                                                                                                                                                                                                                                              bin/display?db=wormace&class=Sequence &object=Y18D10A
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
Exceptions are indicated by an explicit note of the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a smal
overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL034393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-DEC-1998) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, predictions from Genefinder (P. Green, U. Washington), and ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL034393.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368 (6466), 32-38 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.2 Mb of contiguous nucleotide sequence from chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans
                                                                                  neighbouring submissions. The true left end of clone F08A8 is at 152766 in this sequence. The true left end of clone B0019 is at 105 in this sequence. The start true right end of clone B0019 is at 105 in this sequence of this sequence (1...105) overlaps with the end of sequence
                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone Y18D10A. It may be shorter because we only sequence overlapping sections
The end of this sequence (152766 of sequence 299710.
                                                                            of this sequence (1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://webace.sanger.ac.uk/cgi-
                                                     AL008866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 152878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 152878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a graphical representation of this sequence and its analysis
                                                                                                                                                                                     or longer because we arrange for a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152878 bp
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                                    .152878) overlaps with the start
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FEATURES
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KWPEGIHKPEKDSFGLLNSTKIHRNOPPTSDETIAQATAEKKKALGAQGAAGASE
PGSSSSIHGKKGKTVRELQTEMMKGESVEKEKARMRABASAGRSQAPGPAPAASEL
QDPPQDEGLSNSDBGSDSETEEHQKQEKHIPANVTRRSARLSALPVTPKKASSSKMP
PPPSPSPSTPGRRGRPRTLSTMSMEPAAAAVTPAPRGRPRSRSAAKVSENTEPLSEA
PSAPVRGGGRERSRSTMSITEDSEPSTSSTAAKRSKARSDEEEEQDLKITINKSPEK
PKKPSKTTEETVGDULKKRLADTAKTTATVIHTPGPPILTALATALPTVSFTALEP
KKPSKTTEETVGDULKKRLADTAKTTATVIHTPGPPILTALATALPTVSFTALEP
PKAQENPTAELPTTSEISGRAPQALPTSGSAAPPVDDLLSEILSGAKTTKTTKTKT
RKAAPPAVQKSISSTTQOAPPTSVAAPTSGSAAPPVDDLLSEILSGAKTTKTTKTKT
RKAAPPAVQKSISSTTOOAPPTSVAAPTSGSAAPPVDLLSEILSGAKTTKTTKTKT
RKAAPPAVQKSISSTOOAPPTSVHOOTPKSPKOILNSKYGLDISDSEDEEEEERG
METUBEEEEAPPISDSAPTSVHOOTPKSPKOILNSKYGLDISDSEDEEEEERG
METUBEEEAPPISDSAPTSVAOTTRTKNLAQKRKASPPTAGGTTAPKROYIKKSIDS
DILAGAKTTKTTKPKAPPTRVAOTTRTKALAJAKRASPPTAGGTTAPKROYIKKSIDS
ULPPSSSSSTEPPSAPDSASTTSSMKKGGGATMIEAVPCRPGGKAIKREOKPIGMEN
VLPPSSSSSSTEPPSAPDSASTTSSMKKGGGATMIEAVPCRPGGKAIKREOKPIGMEN
VLPPSTERVEN
VLPPSSSSSSTEPPSAPDSASTTSSMKKGGGATMIEAVPCRPGGKAIKREOKPIGMEN
VLPPSTERVEN
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VLPPSSSSTEPPSAPDSASTTSSMKKGGGATMIEAVPCRPGGKAIKREOKPIGMEN
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/gene="Y1
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/gene="Y18D10A.3"
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MEFLRETSAADMWAUMRQRIDANLKPLMNKEEENFLQVSVTLMEHDQOLLEVFISRI
IFELCARESIGSNEGGRLIRLPCHAVEFESAENPDDYTSPVYGKKSTWIRRLFOIL
LNHPNQIGKSTCYILMSDVAKYCRFLVVEEMDKDHMGSEFHLAFRVLMHKDSEQASAV
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                                                                                                                                                             /protein_id="CAA22319.1"
/protein_id="CAA22319.1"
/db_xref="GI:3979940"
/translation="MDGSGEKAIGFLIQFSLNARFWTDKQLLATDEPESSENYQMVRR
/translation="MDGSGEKAIGFLIQFSLNARFWTDKQLLATDEPESSENYQMVRR
/translation="MDGSGEKAIGFLIQFSLNARFWTDKQLLATDEPESSENYQMVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(26502. .26573,27346. .27405,27490. .27580,
27624. .27788,28732. .29006))
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ECEVLRMKLVSTDAAYRESVQREAEAINAKEIAEASLKQGQYDSEFYKKKSASLQEQA
DDAEKHKDQANYWRNKYDSVCALTERLEANNIDIKSKYESTVKLLETAGKRMTSLDNQ
    GWDVELGAPSGNDDDVIHPHSVISLTLPKLCMKNWTGPHFLGGRFVPKSLVDEHELLM
                                                  {	t TSSIPITATLPTNLQAFPLIVDALFGFSFHPPTREPFTEMLKTVRASGIHVFSIDVPS
                                                                                   QFYMKNGKKSTMVHIISKKTVSFIGQKLAAQIDEQLFTKYGFKVEQLMELAGLAAAQA
LAAHYPKSNVAVLCGPGNNGGDGFVCARHLQQFGFTPSIVYPKESRNELMKSLVVQCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(29879. .30346,31220. .31296,31346. .31522,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNDENSYRYNVAPHSAWLPWIQVNGERNRNAEFKLKDFSSVFRLFFEVFLQKCLKRSI
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ALNKLQMCSKKHIKQDWLVTAGCIQGKTAYSAGLKCLPDTEEGKIVQNCAESEEGEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA22309
/db_xref="GI:3979930"
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NVAFDFLRQKMDLIEEQFLKPKEMEKEPKRITAFSVPTVVTKMTKSEAEMLKKESKWQ
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LFFNSQPWKNSLSTSDPSISATEAEASEDPEHLDDVITEPAPPIGEQTLSDDEEEEEEE
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/db_xref="GI:3979929"
                                                                                                                                                                                                                                                                                                                                                               /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MQMNPNKSPPISINFPLFTMSKFLLFISISAVATASDLVEVFGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:6239"
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18D10A.3"
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..16655,17748. .18104,

..20807,22205. .23127,

..26130,26236. .26256))
Query Match
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//protein_id="CAA22320.1"
//db_xref="GI:3979941"
//db_xref="GI:3979941"
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geaidanatsleqhgaaivgnvseekkrslaiffilfvimlatlvyhmlivskihmmp
ESLAIVALGALIGSILSYSRRDWSEIEALSPUFFLVLLPDIIFENAVILNKGYFFSN
EVPILIFBAIFGTTISAMVIGAGLYILGAIGLIEEFTFEEGFAFAMAISAUDPVGTLAI
FVPILIFBAIFGTTISAMVIGAGLYILGAIGLIEEFTFEEGFAFAMISAUDPVGTLAI
FQAVKVESLLYMLVFGESMLNDAVSIVLAATALRHAKPSFNSLPASEIITSAFVTFTE
MFFFSACLGVGIGLLSALLFKHVDLRKTPSLFFALLLIESTIPAYIGMAFFTIKLNFAPMLI
LFGGISMSQFTRHNVSPIAQITFRHTERTISFVAFTSFAYIGMAFFTIKLNFAPMLI
FWSVVLCLLGRACNVFPLAYLVNGCKDVGISMKNQIIMFSGMMGAVCFALULYNDL
DKEKKSILLTTYLELLIFTTIFLGGSALPFISFINGCVBRORRRRFDRNKESTGN
DKEKKSILLTTYLELLIFTTIFLGGSALPFISFINGCVBRORRRRFDRNKESTGN
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/db_xref="GI:3979932"
/db_xref="GI:3979932"
/translation="MNKQLLSCSLKSGKQVTMVVASVATDGVDQQVEISYYDQKVIGN
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GSFGVVFLAKLSTINENVAIKKVLQDKRFKNRELQIMEKLNHPNIVKLKYFFYSSGEK
KDELYLNLILEYVPETVYRVARHYSKQRQQIPMIYVKLYMYQLLRSLAYIHSIGICHR
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58630 . 58895,58941 . 59066,59124 . 59210,59257 . 59373,
59630 . 59775,61492 . 61610,61724 . 61783,61846 . 61939,
62188 . 62409,62843 . 62943)
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                                                                                   DYDGHVENASAWLTLYQLKNEKWQLSRDFEDGLAEKTQSGEAPSELLNLYYFHSATFD
                                                                                                                                                             /translation="MSQNHIILLPDSFKNSMIISKIRAAPLEQPWANIVAKYCLFVAK
YPWPFIIIPLIITICLSMGIILNFKIVRGVNYLYAPLNATWKTEEAVFGENWAKDDDH
FYPGKDILRRQGIYLIVNAKGGGNYLRQEYAQDFLKILDWILMVKLLSSAGRIFTYKD
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50501. .50818,51553. .51971,52106. .52364,52847. .53224)
/gene="X18D10A.6"
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DVWSAGTVMAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIQSMNPNYKEFKFPQI
KAHPWNKVFRVHTPAEAIDLISKIIEYTPTSRPTPQAACQHAFFDELRNPDARLPSGR
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HIDGSIGYHFFSLDCLSLSLTLSTAAVVATATSSSSSPKAFGVSVSLFLWSLLVAWYV
VGVLLVTGGWDREKIVVWQFFHRLPTKRKIENSFAFSSFFFCFLKPMIIGFWTLSF"
                                                                                                                            VCLHFQNDCFSNPHAKLLANIYSKNHQNSMFNITYPIYRSTYATEPIDISKVLGNVSL
                                                                                                                                                                                                                                                                                                            /protein_id="CAA22312.1"
/db_xref="GI:3979933"
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/gene="Y18D10A.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="predicted using Genefinder"
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/db_xref="GI:3979931"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttttttttcacaaatgaaatactttttaattgcaataatgcaaataagtgaattgtttac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acttattgtattacagtaattatttcctacatactatatatttgttagctaaaattagtt 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ataatgaataagcttttcagaagctataaaagcgatagaagtagttttgatgaaaatatc 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaactattcatggcctaatgatgaaacatttacaatagtatgcatataaaagattactga 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acaaatgataaactgttagaataaaataggacaagttgataatgatgataataacaaacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAATATTAATT 2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              attagaaggatgataagaagaaacgaatatatatggcagttttattattgcttcgatgat 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTAATTAAATAAATAATAATTAATTAAATAAATAAACAAATATTAATTAAATAAATGAA 2582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tctaacattatt 448
                                                                                                                                                                               Submitted (07-SEP-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
On Nov 21, 1998 this sequence version replaced gi:3873430.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate
                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans chromosome I clone PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEY18D10
                                                                                                                                                                                                                                                                                                                                                                                            Harris, B.
                                                                                                                                                                                                                                                                                                                                                                                                          Rhabditina; Rhabditoidea; Rhabditidae; 1 (bases 1 to 247332)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL008871.1 GI:3900862
                                                                                                                 NOTE: This is a 'working draft' sequence.
This record will be updated with the finished sequence as soon as it is available and the accession number wi
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                                                                                                   preserved
                                                                                                                                                                                                                                                                                                                                                                              Submission
               /db_xref="taxon:6239"
/chromosome="I"
                                                                                    Location/Qualifiers
/clone="Y18D10"
                                                 /organism="Caenorhabditis elegans"
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ches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Peloderinae;
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*** SEQUENC
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SOURCE
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CEY111B2D/c
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Best Local S
Matches 205
                         AUTHORS
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              JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAAATATTAATTAAATAAACAAATAAATATTAATTAAATAAATAAATAAATAAATTAATTA 77279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agaataggaaatgatgcccataaaaattgggcaatacaaggtataatttgtgatattatc 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttttttttcacaaatgaaatactttttaattgcaataatgcaaataagtgaattgtttac 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTAATTAAATAAATAATAATTAATTAAATAAATAAACAAATATTAATTAAATAAATGAA 77579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acttattgtattacagtaattatttcctacatactatatttgttagctaaaattagtt 376
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                                                                                                                 Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Copper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, M.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
Callaghan, M., Persons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Wateon, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.
Wilkinson-Sproat, J. and Wohldman, P.
Submitted (12-NOV-1999) Louis, MO 63110, USA. jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
Caenorhabditis elegans
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                           Sulston, J.
Direct Submission
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                                                                         94150718
                                                                                         Nature
                                                                                                         elegans
                                                                                                                                                                                                                                                                                                                           Rhabditina;
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                                                           (bases 1
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                                                                                         (6466), 32-38
                                                                                                                                                                                                                                                                                                                             Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                            Secernentea; Rhabditia; Rhabditida;
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                   E-mail:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
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IMPORTANT: This sequence is not the entire insert of clone Y111B2D.
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bin/display?db=wormace&class=Sequence &object=Y111B2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QARKKLKTLLTKLGFPLKIGKFTRKSNSFTQFFAPGKIGRKSVGKVQTGKQTGANSRE
IFKFRKYKKTFYWTKSRNSESGGNLDFDIINTLPDSSEXKNGGGGQDANDLICEKSEN
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LAVEEPMKSRLKEANEQIMKHQVVQIPKYQLKWPDGQAEPSLKGLNRELYEFDKSILS
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QNPRQQPQNQIVQNFQSAPQRHPHQNPQIATSSSSGGVNQFYNNGGAAPPVVEQQAAN
                                                                                                                                                                                                                                    TOKTONKOCLTONDYOLLFDYFGKFEKALEORKAKKËEAERLKKLEEKLKKEKEKOAE
KORIEAKKFEERMKKOOEKOEKERKEREKKEKKEEKE IE LHERKKREEDDRIAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(12998..13081,13735..14229,15626..15715,16386...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTASTPKKEEIGTLETFLKNIFANLDAKGKLYQEKKLKTFDTETLKEITTFIDVMKHH
KTEKVNMEPLIYSLAKSFGMTTQEVMKQVEQEISSKKATTPKPSTNAVLSTISSQKSL
EKNAADMKLTQTDLFTMGEKDIQMLTTIVRSWKSKKEISNSMYTGWLKDVNQLKMNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKVKIRKIKEKSGEKSSKSSDSSSSSSSSDSEDAAGPPRMTGAPPSIRMVSSSSSLKKL
PAPRKPSPPPAVEPTRSVEIIEKPEKTEKPAEKKTAATTSALEPAEKKKKPDSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Y11182D.a"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVAAKPSAPATPKASSSTALRPSTSSTPSQQQSTSTAKAMTSSSTSAEDAKRLLAMNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITPRPISDSLRPLFNQSDEVGGARRWFTRENICSRPAIQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Y111B2D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59651. .59820))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKIKKKKIVPKKVSKLDNPDHLLVASAGQDTYVRLMAIEPETDEKSENIREDSSTTP PDELTSANLESINYTEYRCSSHAVMGHDDWYHSTWSNDRFYLLTASSDKTCIIWK EIDMLWADDVRLGIVGQOAAGFFAAVESSELDLKDSGEKNAEMVVLSSSYFGGLHGW KSTDEQKTFWTALPMTGGHVGEVRDVDWHRSDDGDSGFLMSVGQDQTTRVFAKNGRQQ SYVELARPQVHGHDMQCLSFVNPSIFVSGAEEKVFAFARAFSVKSLEAISGVDTEK SFGDSDLAEFGACVPALGLSNNFMVEGETVDCEHWEEDAFRAAPVVLTSPTEDTDQN UTLWPEQHYLLYGHGYEVYANTANPTGNVLATACKSSHVEHSVVNLMSTSNWSKKSEII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(58932. .59820)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUMLUDEHFYTASRDQKYIVMAESAGQTAPKATYKLDEPYTAIAAVSKDYIVAGLQTG
ELTYLREDSBELHVLEKIGANRIPIDSAVLRLRFSKNGRKLAVATTDAKLRIFNYSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(45598. .45726,45775. .46085,46422. .46521,46742. .4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(58932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHQLTVTQIAWNPSGTRLLTVSRDRTAKLYTEKNGEVDGFDYDCVWTSGKQHTRIIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVARLRLFFCAALRFAIKNLVSETSNGFHAWWTSSIGDLLNSTEIKLDHKAFALCLDA
ISIQNSVLLAVGTSKRFVELYGESADKKSFSRLISVAGHTDWIHSIAFNEKKSVKMAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLTGCDGSVGSVCGCVEDGRKVVAAAWVRFRIAKKAAASHLHSACRKKTTKNQEKPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKIEEEFISASYNPRSHCLTACKTAPLVAYASSLQIAVQTIPKD
DSEVGVIKSTSERRHQKPITVLKRLKSSEIVADEFVTGGVDSRVVLWKLRGEHVEYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(43452. .45329)
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HHGH″
                                                                                                                                                                                                                                    SRSRSASRSPSRSPSPQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="predicted using Genefinder; preliminary prediction"
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Search completed: April 16, 2000, 04:52:00 Job time: 10929 sec
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ORIGIN
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Best Local Similarity 52.3%;
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51879 AAAAAAATGAAAAAATGAGAAAAAAAATGAGAAAAAATTGAAAAA 51833
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/codon_start=1
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/protein_id="Cab60892.1"
/protein_id="Cab60892.1"
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/translation="MRMEIEEGSGLDVASRLAGEYLGDRYNRKMLMITGICIWILA
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VGSGLGFISGSSISQATDSWOMGVRESPIGIACIGLMLMLLDEPVRGACDGARQNGD
RADLIGDIKYLMSIKTFYLASAASIASFFSIGTNSWWTPQYVGFSYAVIHNVPKVPET
ELTQINLIFGIITCMAGLLGVARGSILSRAWRDGSSIFNNHATEKADDVICALSWEVA
LPFLFFAIFIAEYSTNGCLILIYFAIMSMCLNGVNUDVLWANRRATALAVGTM
VAHLFGJBASPYLIGVLSDMLRGDDASAVGHFFALQKALYVPTEMLVVAGAFYLAATF
FVEDDRKREALVQNDEDFWFWYFTELKDADWSESGRGESLIGRRVLSDFTTPDDIETLASV
DEDGINLEEDACTIKFDSIRRKNDDNSVENGQNAADLSDETDEMDVQRPDSGDDDP"
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tcaga	gcctaatgatgaaacat TTTTAATTATAAAATAT	tagaataaaatag AATTATAAAATAT	tgcccataaaaa GTAATTATAAAA	tgaaatactt ATATGTAATT	; DB 1 . 3.1e- tches	35	ents. EPO in	Ω,	n apoB		(T3)	ש ל ד	r ger	mmalian						t; apo	clone				STN						
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Crhis sequence corresponds to the genomic sequence encoding a Plasmodium crhis sequence corresponds to the genomic sequence encoding a Plasmodium craim (W24790). The gene sequence was isolated by screening a CP. falciparum strain T9/96 library with the serum from a missionary created by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones cisolated, clone 729s was used to screen a library generated from Thai created by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones cisolated, clone 729s was used to screen a library generated from Thai created here. The gene contained a 6.85 kb insert including the sequence created here. The gene organisation comprises a first exon, a short created here. The gene organisation comprises a first exon, a short created here. The gene organisation comprises a first exon, a short created here. The gene organisation comprises a first exon, a short created from the containing a 1.8 kb region encoding created from the second exon containing a 1.8 kb region encoding created from the lisation membrane anchoring created from the lisation of the second exon polypeptides of at least 10 created was vaccines for immunotherapy of malaria.

So sequence fisc BP; 2725 A; 463 C; 1215 G; 1749 T;
                                                                                                        Query Match
Best Local :
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Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum; prophylaxis; Thai strain; gene organisation; exon; intron; hydrophob glycosyl-phosphatidylinositol membrane anchoring sequence; antibody;
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derived from the liver stage antigen-3, useful for malaria vacc
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        Duffy antigen binding protein (DABP) and stalic acid binding protein (SABP) conserved regions (see T72889 and T72888 respectively). The var family of genes modulate cytoadherence and antigenic variation of plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte surface. This sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and
                                                                                                                                                                                                                                                      Chitnis C,
Wellems TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium var-7 gene.

Plasmodium var-7 gene.

DBL gene family; SABP; sialic acid binding protein; vaccine;

Duffy binding like gene; Duffy antigen binding protein; eryth

NARP: merozoite; malaria; var-1; var-2; var-3; var-7; immune
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                                                                                                                                           Claim 4; Page 56-61; 96pp; English.
This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to the Duffy binding like (DBL) family of genes which have homology to the
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RESULT
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Best Local
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WO9641877-A2.
27-DEC-1996; F00894.
12-JUN-1995; FR-007007
13-JUN-1995; FR-007007
(INSP) INST PASTEUR.
Daubersies P. Druilhe
WPI; 97-065464/06.
                                                                                                                                                                                                                                                                          prophylaxis; Thai strain; gene organisation; exon; intron; hydrophob glycosyl-phosphatidylinositol membrane anchoring sequence; antibody; vaccine; immunotherapy; malaria; ds.
                                                                                                                                                                                                                                                                                                                08-OCT-1997 (first entry)

P. falciparum liver stage antigen-3 genomic sequence.

Plasmodium falciparum; pre-erythrocyte; liver stage antigen;
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08-OCT-1997
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Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
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                                                                                                                                                                                                                                                                    Plasmodium
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Similarity 47.1%;
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                                      FR-007007.
             Druilhe
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/*tag= c
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/number= ]
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RESULT 5
Q11710/c
ID Q11710 standard; D
AC Q11710;
DT 30-JUL-1991 (firs
DE Dictyostelium plass;
KW slime mould; repli
OS Dictyostelium disc
FH f Key
FT cds
FT cds
FT cds
FT by W09106644-A.
PD 16-MAY-1991.
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Best Local Similarity
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Claim 20; Fig 1A-E; 69pp;
                                                                                                                                                                                        6020 TATGCAAATAAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum poly:peptide(s) and related nucleic acids - derived from the liver stage antigen-3, useful for malaria vaccine
                                                                                                                                                                                                           461 gatttggacgaaattt
                                                                                                                                                                                                                                                                                                                                                                                                       221
                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
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                                                                                                                                                                                                                                                    gaatatatatggcagttttattattgcttcgatgattctaacattatttttatgccttct
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m plasmid Ddp2 containi
replication; Rep gene;
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                        /product=
                                                        Location/Qualifiers
                                                                                                                              DNA;
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47.0%;
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                        involved in
                                                                                             containing
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Pred. No. 0.012;
D; Mismatches 228;
                        extrachromosomal replication
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RESULT 6
Q62924/C
ID 262924;
AC Q62924;
DT 06-DEC-1994 (firs DE Carbamoy1-phosphat KW Carbamoy1-phosphat KW Tarbamoy1-phosphat KW Tarbamodium falcipa FH Key Plasmodium falcipa FT cds
FT Cds P12043-A.
PD 09-JUN-1994.
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Best Local 9
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The sequence of Ddp2 has been found to contain the putative open reading frame indicated in the Features Table. The possible ORF is flanked by regions with similarity to promoter and poly adenylation signals of known Dictyostelium genes. The RNA and polypeptide product of the Rep gene have not, however, been detected. It is believed that the product is produced in low amounts to positively regulate initiation of plasmid replication. The polypeptide may also contain regions that act as negative regulators of plasmid copy number. See also Q11711 and Q11712.

Sequence S852 BP; 2298 A; 651 C; 708 G; 2195 T;
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Slade MB, Chang ACM, Williams
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Carbamoyl-phosphate-synthetase
Carbamoyl-phosphate-synthetase
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                                    /*tag= >
                               /EC_number= 6.3.5.5
                                                                       Jocation/Qualifiers
                                                                                                                                                                          cDNA;
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                                                                                                                    CPSII;
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 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The CDNA sequence encoding the carbamoyl-phosphate-transferase II (CPSII) of Plasmodium falciparum was determined. The CDNA encodes a protein that includes 2 insert sequences not found in other CPSII proteins. The first separates the putative structural subdomain and the glutaminase subdomain of the glutamine-amidotransferase subunit of CPSII, while the second separates 2 ATP binding subdomains of the CPSII subunit, CPSA and CPSb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIX ) UNISEARCH LTD. Flores MV, Osullivan WJ, WPI; 94-200271/24. P-PSDB; R55694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-1993; AU0617.
03-DEC-1992; AU-006206.
16-DEC-1992; AU-006380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPSII subunit, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated from Plasmodium fall
the treatment of malaria.
Disclosure; Page 6-16; 31pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding
                                                                                                           Malaria-specific DNA insert of clone DNA; malaria; clone 41-2; Plasmodium Plasmodium falciparum Ep-322712-A.
                             (BEHW) Behringwerke.
Knapp B, Hundt E, Enders
WPI; 89-194071/27.
P-PSDB; P90417.
acid sequences
Claim 1; Table
                                                                                        05-JUL-1989.
20-DEC-1988;
                                                                                                                                                        1-NOV-1989
                                                                                                                                                                               N90224 standard;
                     New antigenic proteins from Plasmodium
                                                                              30-DEC-1987;
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DE-831351.
 and derived antibodies, 17; 25pp; German.
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47.6%;
25pp;
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ium falciparum, used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding Plasmodium raiciparum calciparum; erythrocyte membrane protein; malaria Plasmodium falciparum; erythrocyte membrane protein; parasite;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T41852 standard;
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e 1052 BP; 394 A; 93 C; 88 G; 477 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                         3461.
                                                5546. .5548
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                                                                      /transl_except=
                                                                                                                                                                                           transl_except=
2909. .2911
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                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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461. .3463
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    CCT
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                                                                                                                                            AAC
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                                                                        Glutamine
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Best Local
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane protein 1 (PFEMP1) or active fragments or analogues of that protein can be used in the treatment or prevention of symptoms of a malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaria. Nucleic acids derived from the PfEMP1 gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different p. falciparum strains. Antibodies specifically immunoreactive with the PfEMP1 polypeptide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the PfEMP1 protein of the MC type of Plasmodium falciparum. An other contents of the most of the mo
                                                                                                                                                                                                                                                                                   7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                               alternative, truncated version of the coding sequence is given in T41853.

Sequence 9789 BP; 4061 A; 1393 C; 1837 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Plasmodium falciparum erythrocyte membrane proteins develop products for the diagnosis, treatment or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-1996.
26-APR-1996; U05798.
27-APR-1995; US-430908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Figure 12; 149pp; English. A polypeptide comprising a Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   develop products for the diagnosis, malaria parasite infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 96-497376/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AFFY-) AFFYMAX TECHNOLOGIES
Baruch DI, Howard RJ, Pask
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                                                                                                                                                                                                                                                                                                       tttttttcacaaatgaaatactttttaattgcaataatgcaaataagtgaattgtttaca
taatgaataagcttttcagaagctataaaagcgatagaagaagttttgatgaaaatatca
                                                                            aactattcatggcctaatgatgaaacatttacaatagtatgcatataaaagattactgaa
                                                                                                                        caaatga taaactgttagaa taaaa taggacaagttga taatga taa taacaaacga
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                                                                                                                                                                                                                                                                                 Conservative
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/transl_except=
6257. .6259
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7754. .8478
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PS Claim 7; Page 59-60; 84pp; English.

CC element and polipoprotein B (apoB) scaffold attachment region (SAR)

CC element clones Rh32 (791530) and Rh10 (731531) respectively carry

CC the 3' human apoB SAR element and the distal 1212 bp 5' human apoB

CC SAR element and 1317 bp proximal sequence. These SAR elements

CC o-map with the boundaries of the human apoB gene chromatin

CC domain. A novel recombinant DNA molecule adapted for transfection

CC domain. A novel recombinant DNA molecule adapted for transfection

CC genomic clone (731532) operably linked to an expression control

CC sequence and to the 5' and 3' SAR elements. The SAR elements

CC increase expression of the recombinant EPO in stable, long-term

CC mammalian cell cultures.

SC Sequence 605 BP; 278 A; 18 C; 35 G; 274 T;
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Human 3' apolipoprotein B SAR element clone Rh32.
Erythropoletin; EPO; anaemia; gene therapy; vector
scaffold attachment region; SAR element; apolipop
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27-JUN-1996.
18-DEC-1995; CA0696.
19-DEC-1994; US-358918.
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                                                  PT New malaria vaccines - contains cysteine-rich DBL family protein pr binding domains homologous domains of the Duffy and sialic acid proteins sequence represents the var-7 gene of plasmodium. Var-7 belongs to CC this sequence represents the var-7 gene of plasmodium. Var-7 belongs to CC the Duffy binding protein (DABP) and sialic acid binding protein (CC Duffy antigen binding protein (DABP) and sialic acid binding protein (SABP) conserved regions (see T72889 and T72888 respectively). The var (SABP) conserved regions (see T72889 and T72888 respectively). The var (CC genes modulate cytoadherence and antigenic variation of CC family of genes modulate cytoadherence and antigenic variation of CC grotein (DABP) are soluble proteins that appear in the culture and the protein (DABP) are soluble proteins that appear in the culture and comparation. The binding of merozoites and schizonts to the erythrocyte composition. This sequence can be used in the compositions of the invention. CC The compositions are for the treatment and prevention of malaria, and CC var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP. The CC compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective inmune response in a mammal to plasmodium merozoites (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium var-7 gene.
DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;
Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response
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Plasmodium var-7 gene.
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07-JUN-1996; U09508.
07-JUN-1995; US-487826.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Chitnis C, Miller LH, Peterson DS, Si
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P-PSDB; W22475.
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Query Match Best Local Similarity Matches 180; Conserv

Conservative

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Score 51; DB Pred. No. 0.1; Mismatches

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Length 19124; Indels

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RESULT 11
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Continuation (3 of 10) o
WP Sequence split into 1
WP Fragment Name
WP X20248_01
WP X20248_01
WP X20248_03
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WP X20248_04
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Best Local Similarity
Matches 203; Conserv
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11-SEP-1984; AU-007066.

11-SEP-1984; AU-007066.

10-SEP-1985; AU-047336.

(HALL-) HALL INST MED RES.
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The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (M60472) or FIRA (M60473). RESA and FIRA antigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.

Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
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DNA coding for Plasmodium falciparum poly;peptide(s) having antigenicity c
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FIRA antigens

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Best Local Similarity
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Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
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11-SEP-1984; AU-007066.
10-SEP-1985; AU-007086.
(HALL-) HALL INST MED RES.
Kemp DJ, Anders R, Coppel RL,
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Claim 4; Fig 1; 55pp; English.
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11-SEP-1985; 006960
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                                                                                              gatgataataacaaacgaaactattcatggcctaatgatgaaacatttacaatagtatgc
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de(s) having antigenicity of RESA or E
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1199. .42
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                       New DNA sequences isolated from endogenous human retroviral element pr new DNA sequences isolated from endogenous human retroviral element pr - and related vectors, transformed cells, proteins and antibodies, pr useful for diagnosis, treatment and prevention of breast cancer pr claim 1; Page 127; 173pp; English.

CC Laim 1; Page 127; 173pp; English.

CC breast tumour specific polypeptides sequences which encode human cc breast tumour specific polypeptides. Detection or measurement of CC human breast tumour specific polypeptides and nucleotide sequences, cor the corresponding RNA in a sample, is used for diagnosis and CC and nucleotide sequences, and the vectors containing the DNAs, are also CC useful in vaccines for inhibiting development (for prevention or CC useful in vaccines for inhibiting development (for prevention or CC craise monoclonal antibodies, used as immunoassay reagents.

SQ Sequence 715 BP; 183 A; 131 C; 86 G; 294 T;
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                 Matches
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09-APR-1997; US-838762.
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                                                                         ACATTTTAAGCAAAAACCTCCCATATACTATTATGTCTTTAAAACATATATAAAGGAAAA
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                                               AATATGACANACATAGGATGGAAGGGAGAAATGGAAATATATGGTGGTAGATTCTTACAT
                                                                                                                                                                       ATTTGAGAATAAACAGANATTTATTTTGAATTTTTACGTTTCNTTGAAGGAATATTGATC
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lecule encoding a breast tumour specific polypeptide #169.
breast cancer; breast tumour tissue; diagnosis; treatment
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Pred. No. 0.
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standard; DNA; 6124 BP

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Q03568;
Q2-AUG-1990
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241. .245
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/label=Regulatory sequence
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                                                                                                                                                                                        /label=Complementary
/note="Alelle I."
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Search completed: April 16, 2000, 04:43:17 Job time: 9896 sec

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Best Local Similarity
Matches 173; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding SERA antigen of Plasmodium falciparum - also DNA encoding signal and regulatory sequences of SERA gene, for diagnosis, prevention and treatment of malaria.

Disclosure; p: English.

Sequence allows for production of antigenic malarial proteins, useful in diagnosis, prevention and treatment of the disease. The sequence may be used in an expression vector, and signal and regulatory sequences may be used to stimulate production of other products.

Sequence 6124 BP; 2567 A; 602 C; 801 G; 2137 T; 17 Others;
 2389
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(DART-) Dartmouth College.
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                                                                                             tgataataacaaacgaaactattcatggcctaatgatgaaacatttacaatagtatgcat
                                                                                                                                                                                                                                      ta
                                               AAAAATTAAATCAAACATATTCAAAAAAATTAAAGTTCTTAAAATTATATAACT
                                                                                                                                           363
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                    Score 49.2; DB 1;
Pred. No. 0.19;
0; Mismatches 188
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
6: /cgn2_6/ptodata/
7: /cgn2_6/ptodata/
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/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
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US-08-484-105-15
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Activator	Patent No. 5340934 Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 41, Appl Sequence 11, Appli Sequence 1, Appli Sequence 1, Appli Sequence 8, Appli Sequence 2, Appli Sequence 2, Appli Sequence 32, Appli

Query Match
Best Local Similarity
Matches 217; Conserv

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Score 64; DB 4; Le Pred. No. 4.5e-06; n. mismatches 235;

Length 665; Indels

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                                                                                                                                                                                                                                                                             COUNTRAL
ZIP: 53701-2115
COMPUTER READABLE FORM:
COMPUTER: FLOPPY disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TANGET FOR PC-DOS/MS-DOS
TANGET FOR PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                    TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Expression System for Clostridium TITLE OF INVENTION: Species
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                                                                                                                                                                                                                CLASSIFICATION:
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STRANDEDNESS:
                               LENGTH:
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                    nucleic acid
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; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT); OTHER INFORMATION: plasmid RP4" US-09-056-075-1
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US-08-487-826B-13/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1465 ATATAAAAATGAGCCTTTATAAAAGCCCCATTTTTTTCATATACGTAATATGACGT 1521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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LOCATION:
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                                                                                                                                                                                                                 COUNTRY: UZIP: 92660
                                                                                                                                                                                                                                              CITY: Newport Beach
STATE: California
                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                STREET:
REFERENCE/DOCKET NUMBER:
               REGISTRATION NUMBER:
                                                                                   FILING DATE:
                                                                                                 APPLICATION NUMBER: US/08/487,826E
                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08487826B
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Wellems, Thoma
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PE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                               Thomas E.
                 29,655
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US-07-867-106-2/c
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Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/07867106 Patent No. 5389526
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO
              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1471
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                        TITLE OF INVENTION: Improved Plasmid Vectors for Cellular TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium NUMBER OF SEQUENCES: 19
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                    COUNTRY:
APPLICATION NUMBER:
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Pred. No. 0.001;
0; Mismatches 191;
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Best Local Similarity
Matches 214; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
1619 AAAGTAATTATAACTAGGTTAGTTTTTATAATTTTT 1583
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: RITELECOMMUNICATION INFORMATION: 215-568-3100
                                                  1979 ATAGAAAAAGTTGGTTAAACTACATTAGTTTTTATAGTTTTTGCATATTTAAAAATAA 1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19920625 PRIOR APPLICATION DATA:
                                                                                                      412 gcagttttattattgcttcgatgattctaacattatt 448
                                                                 121 aattt-----gtgatattatcacaaatgataaactgttagaataaaataggacaag 171
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LOCATION:
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                                                                                                                       tagaagaagttttgatgaaaatatcacttattgtattacagtaattatttcctacatact
                                                                                                                                                             NUCLEIC ACID
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US-08-446-855A-1/c

Sequence 1, Application US/08446855A Patent No. 5849573
GENERAL INFORMATION:

APPLICANT:

Stewart, Thomas Flores, Maria

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RESULT 6
US-08-883-795A-36
; Sequence 36, Application US/08883795A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: genomic
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 No. CITY: Arlington STATE: Virginia
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OPERATING SYSTEM:
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Local Similarity 47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22201-4714
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                                                                                        ttttgatgaaaatatcacttattgtattacagtaattatttcctacatactatatttg
                                                                                                                                                                                                                        TATTAATTGGAAATATATTAATAAGTTTTATATTTCAAGTAATTTTATAAACAAATGAAC
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Best Local
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Matches 222; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 364-73
TELEFAX: (416) 361-1398
INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NERAL INFORMATION: Delcuve, Genevieve
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
TITLE OF GROMENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: Rh 32
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ORIGINAL SOURCE:
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APPLICATION NUMBER: US,
FILING DATE: 27-JUN-199
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Gravelle, Michelin
   367
                                      316 TACATATTTATAATTAAAATGTTTATAATTACATATTTATAATTAAAATGTTTATAAT
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CITY: Toronto
STATE: Ontario
                                                                 307 tgaaaatatcacttattgtattacagtaattatttcctacatactatatatttgttagct
                                                                                                         256 TAAATATTTTATAATTAAAATGTTTATAATTAAATATTTTATAAATTAAAATGTTTATAAT 315
                                                                                                                                       247 agattactgaataatgaataagcttttcagaagctataaaagcgatagaagaagttttga 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                    77 agaataggaaatgatgcccataaaaattgggcaatacaaggta-----taatttgtg 128
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gravelle, Micheline REGISTRATION NUMBER: 40,261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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aaaattagttattagaaggatgataagaagaaacgaatatata--tggcagttttattat 424
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Pred. No. 0.0028;
0; Mismatches 214;
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US-08-487-826B-13
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Best Local Similarity
Matches 180; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO:
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                                                                                                                                      MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                    178
                                                                                         118 tataatttgtgatattatcacaaatgataaactgttagaataaaataggacaagttgata 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Israelsen, Ned REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 92660
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                              atgatgataataacaaacgaaactattcatggcctaatgatgaaacatttacaatagtat 237
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T: 620 Newport Center Drive 16th Floor
Newport Beach: California
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Wellems, Thomas E.
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Miller, Louis H.
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                                                                                                                                                                                                          Score 51; DB 4; Length 19124; Pred. No. 0.01; 0; Mismatches 215; Indels
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US-08-232-463-14
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US-08-232-463-14/c
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   Matches
                              Query Match
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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y Match
2.8%; Score 49.6; DB 1;
Local Similarity 4.3%; Pred. No. 0.016;
hes 16; Conservative 204; Mismatches 148;
                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                                                       TOPOLOGY:
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                              Length 7218;
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Query Match
Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                              * TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stewar, APPLICANT: Flores, Maria V
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
ATTILE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
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                                                                          MOLECULE TYPE:
                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 8920 base pairs
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MEDIUM TYPE: Floppy disk
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                                                                                   TYPE: STRANDEDNESS: SI
                                                                                                                                                                                                                                            NAME: Mitchard, Leonard REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Virginia
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                                                                                                                       nucleic acid
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2.78;
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Score 48.6; DB Pred. No. 0.028;
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             Length 8920;
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US-07-638-431-1/c
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                                                                                                                                                                                                                                          TELEFAX: (301) 295-403
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                      NAME: Spevack, Avrom D. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                         ANTI-SENSE: N
ORIGINAL SOURCE:
                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Spevack, Avrom D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rogers IV, William O. TITLE OF INVENTION: Protective m TITLE OF INVENTION: immunogen an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hoffman, Stephen | APPLICANT: Charoenvit, Yupin APPLICANT: Hedstrom, Richard APPLICANT: Khusmith, Srisin
                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                    TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 19910110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: NMRDC Building STREET: Medical Center
   CELL TYPE:
                 TISSUE TYPE:
                   DEVELOPMENTAL STAGE: erythrocytic stage TISSUE TYPE: Blood
                                                        STRAIN: 17X(NL)
                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Bethesda
                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                     TELEPHONE:
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NMRDC Building 1 T-12 National Naval
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                                                                       Plasmodium yoelii
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erythrocytic stage
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; NAME/KEY: CDS
; LOCATION: 718..3195
; OTHER INFORMATION:
US-07-638-431-1
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PCT-US92-00018-1/c
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Best Local Similarity 48.1%;
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NAME: SPEVACK, AVTAM D.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEFAX: (301) 295-4033
                                                  ATTORNEY/AGENT INFORMATION: NAME: Spevack, Avram D.
                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19920103
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LIBRARY: Py-lar
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                                                                                    CLASSIFICATION:
                                                                                                                                                      SOFTWARE:
                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20814-5044
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Rogers IV, William O.
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Hedstrom, Richard
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                                                                                                                                                      PatentIn Release #1.24
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Sequence 15, App...
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Best Local Similarity 48.1%;
Matches 165; Conservative
                                                                                                                                                                          GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                APPLICANT:
                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                      3321
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ORIGINAL SOURCE:
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 CORRESPONDENCE
            NUMBER OF SEQUENCES:
                         APPLICANT: GAVIN, Kimberly TITLE OF INVENTION: ORIGIN
                                                                                            APPLICANT:
                                                                                                        APPLICANT:
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                                                    APPLICANT:
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LOCATION:
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STRANDEDNESS: double
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STRAIN: 17X(NL)
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                                                                                          McNALLY, Francis
                                                                                                    RINE, Jasper
FOSS, Margit
                                                    LI, Joachim J
                                                                LAURENSON, Patricia HERSKOWITZ, Ira
                                                                                                                                KOBAYASHI, Ryuji
                                                                                                                                              BELL, Stephen P
                                                                                                                                                            STILLMAN, Bruce
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ADDRESS:
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                          REPLICATION COMPLEX GENES
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ADDRESSEE:

FLEHR, HOHBACH, TEST,

ALBRITTON & HERBERT

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Best Local :
                                                                                                                                                                                                                                                                                                           Patent No.
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                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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LENGTH: 2504 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                  APPLICANT:
APPLICANT:
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APPLICANT:
                                       CORRESPONDENCE ADDRESS
                                                       TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                         2370 RWWWWAWWMGATACTACTTCTATTA 2398
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TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
TELEX: 910 277299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-5903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                               APPLICANT:
                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ttttgatgaaaatatcacttattgtatta 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 2.6%; Score 47; DB 1; Local Similarity 45.5%; Pred. No. 0.044; hes 95; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                       5, Application US/08484106
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                                                                                             GAVIN, Kimberly
                                                                                                                                                                        RINE, Jasper
FOSS, Margit
MCNALLY, Francis J
                                                                                                                                                                                                                              KOBAYASHI, Ryuji
                                                                                                                                   HERSKOWITZ, Ira
                                                                                                                                                  LAURENSON, Patricia
                                                                                                                                                                                                                                                                      STILLMAN, Bruce
FLEHR, HOHBACH, TES
Embarcadero Center,
                                                                                                             Joachim J
                                                                                                                                                                                                                                Ryuji
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                   TEST,
                   ALBRITTON & HERBERT
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REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION: TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
TELEEX: 910 27729
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08323170B Patent No. 5733772
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   STREET: TWO CITY: San Francisco
STATE: California
                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                              APPLICANT: Williamson, Kim C. APPLICANT: Kaslow, David C. TITLE OF INVENTION: Cloning at TITLE OF INVENTION: falicipar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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NAME: Osman Ph.D., Richa
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                                                                                               COUNTRY:
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STRANDEDNESS: double
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                                                                                                                                                                                    ADDRESSEE:
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California
                                                                                                                                                               Two Embarcadero Center, 8th Floor
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ilarity 45.5%;
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                                                                                                                                                                                                                                                Cloning and Expression of Plasmodium faliciparum Transmission-Blocking Target Antigen, Pfs230
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Pred. No. 0.044;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9636 base pair:
                                                                                                                                                                                                                                                                                                                                                          6710 CAAAGAGGATTAATATATTTTTTTTTAGGAAAAATGTATCAGAAAATTCATTTAAATTA 6769
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7008 CTAAAGATGTTATT 7021
                                                                                                                                       6888 TTGCTATATTTCCACAAGCATGTTTTAGTAATGTTTTATTAGAATATTATAAAAGTGATT
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                                                                                                                                                                        435 attotaacatt--atttttatgccttctgatttggacgaaatttaaacgaaatggtaata 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 46.4 hes 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/OFILING DATE: 13-OCT-1994 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Quine, Jonathan A. REGISTRATION NUMBER: P-4 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 9636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/010,409
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                                                                                                                                                                                                                                                                                                                                                                                 atgcagattccatt 566
                                                                                                                                                                                                                                  ttattagaaggatgataagaagaaacgaatatatatggcagttttattattgcttcgatg 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acaaatgataaactgttagaataaaataggacaagttgataatgatgataataacaaacg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGAAAAAATGAAGTATCTATTAGTTTAGCTTTGAAAGGGGTTTATGGAAATCGAATT 6589
                                                                       ATGAAGATAGTGAACATATTAATTATTATATTCATAAAGATAAAAAATATAATTTAAAAC
                                                                                                   atgacggcagcaatcaatgcaatgcttaaacccataaacattgagaagccaaatggtgac
                                                                                                                                                                                                                AAAAGTGCACTGTTAAAATTAAAAAAGGAGATATTTTTGGATTGAAATGTCCTAAAGGTT
                                                                                                                                                                                                                                                                                     T--GTGATTTCACAACAGGTTCGACTTCATTAATGGAATTAAATAGTCAAGTAAAAGAAA 6827
                                                                                                                                                                                                                                                                                                                   tcacttattgtattacagtaattatttcctacatactatatatttgttagctaaaattag
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS: ADDRESS: Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-MAR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-MAR-1992
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PRIOR APPLICATION UNIMBER: US 08/075,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 11-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
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REFERENCE/DOCKET NUMBER: 454310-2570
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Tine, John A.
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Search completed: April 16, 2000, 04:36:19 Job time: 9753 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Result Query No. Score Match Length DB ID	igth DB	esult Query No. Score Match Length DB ID	Description
c 1	391.8 22.0	22.0	665 4	2 AI111196	AII11196 SWOV3MCA1
c 2	373.8 21.0		628 3	628 37 AA701731	AA701731 SWOv3MCA1

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RESULT 1
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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
                                                                                                Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae Unpublished (1997) on Sep 12, 1996 this sequence version Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                             AII11196 665 bp mRNA EST 31-AUG-1998 SWOV3MCA1232SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCA1232 5'
                                                                                                                                                                                                                                                                               mRNA sequence.
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AI111196.1 GI:3510080
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C71078 C71078 VUji
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C67783 C67783 VUji
C70345 C70345 YUji
AW208357 SWOV3MCAM
AA624955 SWOV3MCAM
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AA625021 SWOV3MCA6
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tggtccacattcaatttctggctcaccttcgacaccattgtcaaccggaatcgaataaga 1568
                                                                                                                      aataccacgtggattcagagatcgtgtacgcgcaacattgcatgaatcaaatggaagtga 1388
                                                                                                                                                                                                                                                                                                                                                                                                               acgatcaactttggtaacaataatggatgaaacgaaatgacaacagttgttgttacaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tggctgaccaatgatagcaaattgaactggttgaccggttggtccaccatccaaaatttc 1148
TGGACCACATTCAATTTCTGGTTCACCCTTCTACACCGTTATCAACCGGAATAGCATTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The Library is available from Dr. Sara Lustigman (email: slustigmenybc.org)."

86 a 129 c 136 g 213 t 1 others
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/db_xref="taxon:6282"
/clone="SWOv3MCA1232"
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/lab_host="XL1-Blue
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79.9%;
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Pred. No. 1.1e-
0; Mismatches
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                                                             GTTTCAGAATCACATGTCCATTATGGTAACACTGGGTTGACCAATGGTAGCAAATTGA 563
                                                                                        ggtttcagaatcgcatgtccatttatgata--aactggctgaccaatgatagcaaattga 1113
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWOV3MCA1144SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams, S.A., Lizotte-Waniewski, M., Laney, S. Genes expressed in molting L3 larvae of Onchoo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome@smith.edu
                                                                                                                                                                                                                                                                                     slustigm@nybc.org)."
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/lab_host="XL1-Blue MRF'"
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/clone_lib="Onchocerca volvulus molting L3 larva
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/db_xref="taxon:6282"
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Pred. No. 4.3e-65;
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                                                                                                                                                                                                                                                Smith College Department of Biological Sciences Department of Biological Sciences, Clark Scienc College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
On Jan 14, 1998 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI322117 639 bp mRNA SWOV3MCAM12G08SK Onchocerca volvulus molting L3 larva
                                                                                                                                                                                                                                                                                                                  On Jan 14, 1998 this sequence version replaced Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                   Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Filarioidea; Onchocercidae; Onchocerca.
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                                                                                                                                                                                                    genome@smith.edu
                                                                                                 /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                 /lab_host="XL1-Blue MRF'"
                                 /dev_stage="molting L3"
                                                  (SL96MLW-OvmL3)
                                                                /clone_lib="Onchocerca volvulus molting L3
                                                                                 /clone="SWOv3MCAM12G08"
                                                                                                                                  /organism="Onchocerca volvulus"
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AA618895 672 bp mF
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molting L3 larva cDNA
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                    1231 ttatcagcttccatgtaaaagcattgtactcgatatgcacgatcaacttttggtaacaaat 1290
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                                                                                                ACAATTTGTGTNGCAAATGCAGTTGTCATTTCGGAAATTTCAAGTTGAGCGCTAACTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                       439;
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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Onchocerca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Steven A. Williams Molecular Parasitology
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On Sep 12, 1996 this sequence version replaced
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1 (bases 1 to 672)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

a 132 c 129 g 202 t 11 others
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/db_xref="taxon:6282"
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1 (bases 1 to 610)
Williams, S.A., Lizotte-Waniewski,M., Laney,S. and I Genes expressed in molting L3 larvae of Onchocerca Unpublished (1997)
On Oct 30, 1997 htls sequence version replaced gi:2 contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science Center, College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWOV3MCAM02C015K Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVmL3) Onchocerca volvulus cDNA clone SWOV3MCAM02C01 5',
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primer: pBluescript
(SL96MLW-OVML);
/dev_Stage="molling L3"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of 0. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4135853786
                                                                                                                                                                                                                                                              /clone="SWOv3MCAM02C01"
/clone_lib="Onchocerca volvulus
                                                                                                                                                                                                                                                                                                          /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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                                                                                                                                 AA585626 776 bp mRNA EST SW3D9CA349SK Brugia malayi L3 molting-day 9 larva (SAW97MLW-BmL3d9) Brugia malayi cDNA clone SW3D9C
Brugia malayi.
Brugia malayi
Brugia malayi
Eukaryota, Metazoa, Nematoda, Secen
Filarioidea, Onchocercidae, Brugia
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a 106 c 138 g 178 t 1 others
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                  tgatattctccggttctgcagatcttttcttgagtaaacgaagttgcgcagctgcagcag
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                                                                            CTGGTAGAGCTTGATTATCTTCGCTGATTTCAAGGGCGCTAATATCAGTCCTCACGTCGA
                                                                                                                                                          CTGCGGCGAGTACCACTGGTTGTCCACCGAGATGCAAACGTGCACGATGACGTAAGTCAA
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
Tel: 4135853826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brugia malayi
Unpublished (
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'dev_stage="third stage larvae, nine days after infection"

/lab_host="E coli XLI-Blue MRF'"

/note="vector: LambdaZap II (UniZAP XR); Site_1: Eco RI

(5' end); Site_2: Xho I (3' end); Brugia malayi is a

lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi
isolated from the peritoneal cavity of jirds nine days
after infection. The mRNA was converted to double
stranded cDNA using reverse transcriptase and oligo (dT)
followed by Rnase H and DNApol I. The library was
constructed by Michelle Lizotte-Waniewski. The library is
available from the Filarial Genome Project Resource
Center: contact Dr. S.A. Williams, Clark Science Center,
Center Northeaders Ab 01063 USA house 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Brugia malayi L3 molting-day 9 larva cDNA
(SAW97MLW-BmL3d9)"
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On May 9, 1995 this sequence version replaced Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: pBluescript SK.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith College Department of Biological Sciences Department of Biological Sciences, Clark Scienc College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 537)
Williams, S.A., Lizotte-Waniewski, M.,
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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SWOV3MCAM02A04SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM02A04 5',
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                        157
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                                                            /uev_stage= molting us
/lab_host="XLI-Blue MRF'"
/lab_host="XLI-Blue MRF'"
/lab_host="XLI-Blue MRF'"
Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome@smith.edu
                   slustigm@nybc.org)."
102 c 106 g
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(SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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Query Match

Best Local Similarity

17.7%; 78.9%;

Score 314; DB 37; Pred. No. 3.7e-53;

Length 537;

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SOURCE
ORGANISM
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                                                                                                                                                                                                             COntact. Molecular Parasitology
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
Department of Morthampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI322068 552 bp mRNA EST 22-DEC-1998 SWOV3MCAM12A04SK Onchocerca volvulus molting L3 larva cDNA (SU-6MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM12A04 5',
                                                                                                                                                                                                                                                                                                       Unpublished (1997)
On Jan 14, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                   Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S Genes expressed in molting L3 larvae of Onchocerca volvulus
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                                                                                                                                                                                                                                                                                             Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                  Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
                                                                                                                                                                                                                                                                                                                                                                                                                                Onchocerca volvulus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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                                                                                                                                                                    primer: pBluescript SK.
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                                                                                                                                                                                   genome@smith.edu
                                               /clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
                                                                                           /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                 /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                              /clone="SWOv3MCAM12A04"
                                                                                                                         /organism="Onchocerca volvulus"
                                                                                                                                                    Location/Qualifiers
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                                                           mRNA sequence.
AI317885
AI317885.1 GI:
Onchocerca volvulus.
Onchocerca volvulus
Eukaryota; Metazoa; Nematoda;
                                                                                           AI317885 615 bp mRNA EST 1/-DEL-1770 SMOV3MCAM06H12SK Onchocerca volvulus molting L3 larva cDNA (SL96MLM-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM06H12 5',
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GI:4033152

Secernentea;

Spiruria;

Spirurida;

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Query Match
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attacggcaaccttcttgatcataaagacctttcacataaacatgtccttcgaatgcatt
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                                                                                                    ATTTCGGCATCCTGCCTGATCGTATAAGCCTTTCACGTATACATGTCCTTCAAATGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Steven A. Williams
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124 c 123 g 189 t 7
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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco
Xho I; Filarial nematode parasite of humans. 1
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/clone_1ib="Onchocerca volvulus molting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1998)
On Jan 19, 1998 this sequence version replaced gi:2285237.
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S.A. Williams. The Liboratory are also available from Dr. Sara Lustigman email slustigm@nybc.org When requesting this clone from Dr. Lustignees reference the Williams lab clone id - SWOv3MCAM03B05 please reference the Williams lab clone id - SWOv3MCAM03B05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams,S.A., Lizotte-Waniewski,M., Laney,S., Lustigman,S.,
Hillier,L., Allen,M., Bowles,L., Geisel,S., Jost,S., Kucaba,T.,
Marth,J., Steptoe,M., Thelsing,B., White,Y., Wylie,T.,
Chappell,J., Person,B., Gibbons,M., Harvey,N., Pape,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 531) Williams, S.A., Lizo
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Eukaryota; Metazoa; Nematoda;
Filarioidea; Onchocercidae; Or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome@smith.edu
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                                                                      /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture mRNA was isolated from approximately do molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture.
in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                  /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Onchocerca volvulus molting
                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="onch17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Onchocerca volvulus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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                                       Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                         1 (bases 1 to 363)
1 (bases 1 to 363)
Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S. Williams,S.A. Lizotte-Waniewski,M., Laney,S. and Lustigman,S. Williams,S.A. Lizotte-Waniewski,M., Laney,S. and Lustigman,S. Williams,S.A. Lizotte-Waniewski,M., Laney,S. and Lustigman,S.
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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                                                                                                                                   On May 9, 1995 this sequence Contact: Steven A. Williams
                                                                                                                                                                     Genes expressed in molting L3 Unpublished (1997)
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                                                                                                                                                                                                                                                   Filarioidea;
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                   4135853786
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genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
                                                                                                                                                 1995 this sequence version replaced gi:802401
                                                                                                                                                                                                                                                                                                         volvulus.
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a 71 c 77 g 110 t 1 others
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/lab_host="XL1-Blue MRF'"
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                                                                                                                 tgacaacagttgttgttgttacaaaaataccacgtggattcagagatcgtgtacgcgcaacat 1366
  ATCCTGCCTGATCGTATAAGCCTTTCACGTANANATGTCCTTCAAATGGATTACGAGTAT
                                                                                         TACAGGAATCAANCGGAAGGTCAATTCCGGCNACCTGACGTCCACCTTCATCATTTCGGC
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
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On May 9, 1995 this sequence version replaced gi:802407
Contact: Steven A. Williams
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Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
Genes expressed in molting L3 larvae of Onchocerca volvulus
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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Onchocerca volvulus.
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//lab_host="%11-Blue MRF'"
//lab_host="%11-Blue MRF'"
//note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in INDM+ NOTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 1005 independent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The library is available from Dr. slustigm@nybc.org)."

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/db_xref="taxon:6282"
/clone="SWmL3C0758"
/clone_lib="Onchocerca volvulus molting L3
(SL96MLW-OvmL3)"
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library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams
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75.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mark.blaxter@ed.ac.uk
The ABI trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/3D6/MB3D6AA4G10T3.html
seq primer: T3.
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Institute of Cell, Animal and Population Biology
University of Edinburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jan 19, 1998 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA841200
AA841200.1 GI:2922536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brugia malayi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes expressed in day six
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blaxter, M.L., Waterfall, M., Daub, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brugia malayi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 354)
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         ω
The library was constructed by Michelle Lizotte-Waniewski. The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email genome@smith.edu."

81 c 84 g 84 t
                                                                                                                                        /note="vector: lambdaZapII (UniZap XR); Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. mRNA was prepared from third stage larvae of Brugia malayi isolated from the peritoneal cavity of jirds six days after infection. The mRNA was converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 2 x 10E5 independent recombinants and average insert size was 900 base pairs.
                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="third stage larvae, six days after infection"
/lab_host="E. coli XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Brugia malayi day
larvae SAW96MLW-BmL3d6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="3D6AA4G10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Brugia malayi"
/strain="TRS Labs"
                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:6279"
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DB 39;

Length

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REFERENCE
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VERSION
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Best Local Similarity
Matches 301; Conserv
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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
Morthampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA618952 459 bp mRNA EST 12-NOV SWOV3MCA2020SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3C020
                                                                                                                                                                                                                                                                                                                                                                               College, Northampton, Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Sep 12, 1996 this sequence version replaced gi:1405277. Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
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1 (bases 1 to 459)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                          genome@smith.edu
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by
                                                                                                                                                         /clone="SWmL3CO2020"
/clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
                                                                                                                      /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                    /db_xref="taxon:6282"
                                                                                                                                                                                                                                          /strain="Kumba, Cameroons"
                                                                                                                                                                                                                                                           /organism="Onchocerca volvulus"
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                                                                                    Unpublished (1997)
On May 9, 1995 this sequence version
Contact: Steven A. Williams
Molecular Parasitology
College, Northampton, Tel: 4135853826 Fax: 4135853786
                                 Smith College Department of Biological Sciences Department of Biological Sciences, Clark Scienc College, Northampton, MA, 01063, USA
                                                                                                                                                     1 (bases 1 to 395) Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca
                                                                                                                                                                                                               Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Onchocerca.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
85 c 91 g 150 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     day 5 in culture. mRNA was isolated from approximately
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Pred. No. 2.7e-43;
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                                                                                                                       replaced gi:802391
                                                    Science
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clone SWmL3CO318 5',
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A_Geneseq_36: W50144
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-Q-/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19878/app_query.fasta.1
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-GAPOP=12.000 -QFAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
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B. sphaericus SLP. Host cell e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by sequence
                      BAR1 gene product.
                                                                                                                                                                                                                                                                                                                  PtdIns 3-kinase 110 kD catalyt Human PTP-OB. Protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium difficile toxin
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US-09-323-427-3 x R20112
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ID R20112 standard; Pr
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A_Geneseq_36:R97210
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A_Geneseq_36:R99462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP-465404-A.
08-JAN-1992.
27-MAY-1991;
01-JUN-1990;
10-AUG-1990;
30-NOV-1990;
                                                                                                                                                                     197
                                                                                                                                                                                                                                                                                                   526
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Ratio:
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JP-210535.
JP-329911.
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0.541
47.315
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Align seg 1/1 to: R20112 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel DNA encoding peptidyl hydroxy:glycine N-C lyase (PHL) - used to prepare PHL which can be used in the amidation of peptide(s) e.g. human calcitonin.

Claim 4; Page 18; 28pp; English.

The sequence was deduced from a cDNA insert from pAE-III-202-4 (FERM BP-3172). The vector serves as source for a DNA fragment encoding PHL for the construction of an expression vector for the prepn. of recombinant PHL. The protein may be truncated to comprise only residues 383-706 or 383-713. The PHL catalyses the reaction: R-GlyOH -> R-NH2. It can be used to produce peptides with amidated C-termini, e.g. calcitonin, growth hormone, LH-RH. Sequence 935 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CIBA ) CIBA GEIGY AG.
Iwasaki Y, Shimoi H, Suzuki
Kawahara T, Kangawa K;
WPI; 92-010570/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE-III (peptidylhydroxyglycine N-C lyase precursor).
                                                                                                                                                                                                                        147 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-1992 (first entry)
                                         AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                  ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                            lAlaAspGlyTyr.....
                                                                                                                                                                                                                                                                  CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                               TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
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/note= "including PAM
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Gaps: 18
Percent Identity: 19.437
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1077 CTCAATGTTTATGGGTTTAAGCATTGCATTGATT...GCTGCCGTCATTA 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     854 CAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        652 alGlnGlyPheMetLeuAsnPheSerAsnGlyAsp.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        581 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT
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                                                                                                                          GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT
                                                                         ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVa
                                                                                                                                                                                                                                                                        aGlyValProThrGlnGluLysGlnAsnValValGlnGluSerSerAlaG
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                                                                                                                                                                        lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGly
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                                                                                                                                                                                                                                                                                                                                                                    {\tt AlaGlyValSerThrGlnGluLysGlnAsnValValGlnGluIleAsnAl}
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alignment_block:
US-09-323-427-3 x P94856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: P94856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence encodes a derivative of the mature C-terminal alpha-
amidating enzyme from plasmid pXA799.
The plasmid was screened from an E.coll library using plasmid pXA457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression plasmid pUCP1CI799 BglII gene product. alpha-amidating; pAX799; alpha amide; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to screen a larger library.

Although pXA799 is similar to pXA457 at the N-terminus, hydrophobic elements suggesting a membrane function. See also N93060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka S, Matsuo H, Mizuno
WPI; 89-017279/03.
N-PSDB; N94527
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17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-1990 (first entry)
Expression plasmid pucplcI799
                                                 545 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                                        491 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
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              334 AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                        97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
                                                                                                                                                                                                                     AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                                                        lAlaAspGlyTyr.....
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                                                                                ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 333
                                                                                                                 nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI
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US-09-323-427-3 x P94854
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                                                                          Align seg 1/1 to: P94854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               documentation_block:
                                                                                                                                                                                                                                                                                                                Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.

Plasmid pXA799 contains a sequence derived from Xenopus laevis.

Plasmid was screened from an E.coli library using plasmid pXA457
The plasmid was screened from an E.coli library using plasmid pXA457
to screen a larger library.

Although the gene product is similar to that of pXA457 at the N-terminus, lithas an area of hydrophobic elements suggesting a membrane function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka S, Matsuo H, Mizuno
WPI; 89-017279/03.
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15-JUL-1988; 306508.
17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
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Sequence 875 AA;
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CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 546
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seq_documentation_block:
ID R73053 standard; Prot
AC R73053;
DT 06-NOV-1995 (first e
DE Peptidyl C-terminal a
KW Peptidyl C-terminal a
KW Peptidyl C-terminal a
KW trichostatin; CHO.
OS Not specified. Locat
FH Key
FH Key
FH CAPPR-1995
PD 26-APR-1995
PD 26-APR-1995
PD 26-APR-1995
PD 07-SEP-1994; 306587
PR (SUNR) SUNTORY LTD.
PA (SUNR) SUNTORY LTD.
PI FURUKAWA K, Ohsuye P
                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: A_Geneseq_36:R73053
                   26-APR-1995.
26-APR-1995.
27-SEP-1994; 306587.
08-SEP-1993; JP-257881.
(FURU/) FURUKAWA K.
(SURR) SUNTORY LTD.
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Peptidyl C-terminal alpha-amidating
Peptidyl C-terminal alpha-amidating
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Disclosure; Page 10-15; 19pp; English.
3mu-1S cells (i.e. CHO cells expressing a peptidyl C-terminal alpha-amidase enzyme (AE)) were suspended in F-12 medium to which aliquots of trichostatin were added. Cells were cultured for 3 days at 37 deg and then assayed for AE. Without trichostatin, AE productivity was 708 U/ml. At 10, 50, 100 and 200 nM trichostatin, AE productivities were respectively 866, 1897, 1894 and 3359 U/ml.
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                                    TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 630
                                                                                                                    TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
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seq_documentation_block:
ID R88469 standard; Prot
AC R88469:
DT 14-AUG-1996 (first e
DE Feline infectious per
KW Feline infectious per
KW Feline infectious per
KW Feline infectious per
KW Feline infectious per
PN J07327683-A.
19-DEC-1995:
19-DEC-1995:
19-DEC-1995:
PF 10-JUN-1994; J29300.
PR 10-JUN-1994; J29300.
PR 10-JUN-1994; JP-12930
PR (KITA) KITASATO KENK
DR WPI; 96-072341/08.
DR N-PSDB: T10166.
DR N-PSDB: T10166.
DR N-PSDB: T10166.
DR N-SDB: T0166
CG Tipt - Page 14-17;
CC This sequence represe
CC (FIPV-I) splke protest
CC infection. The splke
CC cell with the splke
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US-09-323-427-3 x R88469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding feline infectious peritonitis I virus spike protein used in a vaccine for prevention and treatment of FIPV-I infection Claim 1; Page 14-17; 23pp; Japanese.

This sequence represents the feline infectious peritonitis 1 virus (FIPV-I) spike protein. The FIPV-I spike protein may be used in the production of a vaccine for the prevention and treatment of FIPV-I infection. The spike protein may be produced by transforming a host that the spike protein DNA and expressing the sequence such sequence 1464 AA;
                                                                                                                                                                                                                                                                               789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feline infectious peritonitis 1 virus spike protein. Feline infectious peritonitis 1 virus; FIPV-I; spike protein; vaccine; prevention; treatment.
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(KITA) KITASATO KENKYUSHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAA 223
                                                 oGlnPheTyr.....TyrIleThrLysTrpAsnAsnAspThrSerSerA
                                                                                                                                                                                                                                                                                                                                      ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT
                                                                                                                                                                                                                                                                                                                                                                                           alAsnGlnThrAspLeuPheGluPheValAsnAsnThrGlnAlaArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCACTTCCA.....TTTGATTCATGCAAT.....GTTGCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysAsnSerThrThrGlyGluIlePheThrValValProCysAspLeuTh
TCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG 458
                                                                                                                                                                                                                        TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTAC
                                                                                                                                                                                                                                                                          serArgSerSerThrProAsn.....PheValThrSerTyrThrMetPr
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                                                                                                           AATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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WO9850531-A1. 12-NOV-1998. 01-MAY-1998; AU0315. 22-JUL-1997; AU-00810 01-MAY-1997; AU-0065

O antigen; Olll antigen; wbdM gene; colitose transferase; glucose transferase; diarrhoea; haemorrhagic colitis; diagnosis Escherichia coli.

(UNSY) UNIV SYDNE Reeves PR, Wang L; WPI; 99-059669/05.

SYDNEY. AU-008162. AU-006545.

N-PSDB; X06748.

faeces or patient samples Disclosure; Fig 7; 165pp; English. Disclosure; Fig 7; 165pp; English. This is the amino acid sequence of the protein encoded by the wbdM gene of a gene cluster (see X06748) involved in the biosynthesis of the Escherichia coli Olll O antigen. The protein shows high

Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. for

in, e.g. food

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seq_documentation_block:

ID W88310 standard; Protein;

AC W88310;

DT 26-APR-1999 (first entry)

DE E. coli colitose or glucos
                                                                                                                                              seq_name:
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  26-APR-1999 (first entry)
E. coli colitose or glucos
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coli colitose or glucose transferase
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||GlyAlaArgLeuGluSerLeuMetLeuAsnAspMet......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT.....GTACGA
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                                                                                                                                                                                              heAlaMetGlnValGlnAlaArgLeuAsnTyrValAlaLeuGln
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                                                                                                                                                                                                                                                                                             IleGlyGlyMetAlaLeuGlySerIleThrSerAlaValAlaVal.ProP
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alignment_block:
US-09-323-427-3 x w88310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology with TrsE of Yersinia enterocholitica, and is predicted to be a colitose or glucose transferase. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wold (transferase), wzx (flippase) and wzy (polymerase) genes, within 0 antigen gene clusters improves the specificity of methods for the detection and identification of 0 antigens, e.g. in testing food- or faecal-derived samples, or samples from patients. The 0 antigen is a major virulence factor of enteropathogenic E. sequence 374 AA;
                                                                                                                                                                               303
                                                                                                                                                                                                                                                                                                                                                                                                153 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG 202
                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 LeuThrGlyIleSerGluValLysProThrGlnAsnIleAsn.....
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                                                                                                                                                                                                                                                                                                                          GTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTT 252
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gLeu....
                                                                   ThrAlaHisAsnLysAsnGluGlyGlyAsnAlaArgMetPheCysTyrAr
                                                                                                                                                                           TGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTG...ATCGTGCAT
                                 ATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGAT 449
                                                                                                       ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAG 399
                                                                                                                                         lePheSerArgPheIleArgMetLeuIleProAlaValProLeuIleCys
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Ratio:
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.SerAspPheLeuAlaSerIleThrThrAsnValS 138
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18
21.763
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Seq. ID AC AC DT DE DE KW KW KW OS PN PD PR PR PR PR PR
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                     Ub-MAR-1997.

28-AUG-1996; U14192.

31-AUG-1995; US-521872.

11-CCT-1995; US-540804.

26-JAN-1996; US-590399.
                                                                                                                                                                                                                                                                                                                     _documentation_block:
                                                                                                                              Yeast transcription regulatory factor SRB8. Transcription regulatory factor; suppressor of SRB8; RNA polymerase II; holoenzyme; SWI/SNF. Saccharomyces cerevisiae.
(WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                              04-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                             W13825 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAAT 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AACACCCTTGAAATTAGCGATGATAATCAAGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaCysGluArgProValValAlaThrAspSerGlyGlyValLysGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euLeuIleAlaGlyAspGlyAlaLeuArgAsnLysLeuLeuAsp.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spSerThrAlaValLeuLeuAlaVal......GlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGAT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pPheAspIleAsnValArgLysLysThrArgAspAlaPheAsnLeuLysA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysAsnLysIleValGluIleProAsnPheIleAsnThrAsnLysPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....TCAGAACCACAAGGATTCGGA...GCTGTTAAAACAGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .GAACCAAATAGCGAATGTGTTCGACCACAATGT.........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....LeuValCysGlnLeuAsnLeuValAspLysValPhePheLe
                                                                                                                                                                                                                                                                                             Protein; 1226 AA
                                                                                                                                                                                                    RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     849
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alignment_block:
US-09-323-427-3 x W13825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purified RNA polymerase II holo:enzyme - comprises RNA polymerase II and one or more regulatory proteins, pref. suppressor of RNA polymerase B proteins or SWI/SNF proteins?

Claim 11; Fig 10a-b; 154pp; English.

Novel yeast SRB (suppressor of RNA polymerase B) proteins SRB4, SRB5, SRB9, SRB9 and SRB11 (W13821-28) are transcription regulatory factors that act as positive and negative regulators of RNA polymerase II activity, and are components of the RNA polymerase II activity, and are components of the RNA polymerase II clentify transcription factors involved in RNA polymerase II

C-terminal domain (CTD) function. SRB8 and SRB9 appear to repress CTD activity. Genomic clones (T59904-11) for the SRB appear to repress CTD activity. Genomic clones (T59904-11) for the SRBs have been obtd. SRBs can be used to treat diseases resulting from alteration or deletion of the SRB gene, pref. by gene transfer technology. They copds. that modify gene transcription of DNA and to identify Sequence 1226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: W13825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 AACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 eIleLysValProThrTyrIleArgLysLeuIle......
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GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA 503
                                                                                                                                                                                                                                                           nLeuSerLysThrProLeuSerIleLysIleMetValAlaGluTrpTyrL
                                                                                               CTGAAATCACAACTGCTTTTC....AAACTCAAATTGTCCCGATGCCA
                                                                                                                                                                                                                                                                                                             GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yrAspValLysPheTyrGluIlePheAsnPheAspGlnValValGluIle
                                                                                                                                                      euSerHisLeuCysSerGlyIleLeuSerSerValAsnArgThrValLeu
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                                              LeuLysIlePheLysIlePheCysIleAspLeuGluValPheHisHisPh
                                                                                                                                                                                                       TG.....ATAAAACAGTTAGTGCACAGATTGAGGTAT 409
                                                                                                                                                                                                                                                                                                                                                                   ThrGluGlnIleLysMetArgIleLeuSerAsnAspIleThrAsnLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                        ....TTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGATCTCTGAATCCACGTGGTATTT.............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....SerGlnTyrAsnMetValLeuArgAsnValMetGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGTCTTTATGATCAAG...AAGGTTGCCGTAATGATGAAGGTGGACGT
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0.468
48.338
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16
20.716
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seq_name: A_Geneseq_36:R06400
          26-JUL-1990.
17-JAN-1990; J00042.
17-JAN-1989; JP-005878.
(SUNR ) SUNTORY LTD.
(SUNR ) KITANO K, Tanaka S
WPI; 90-254034/33.
                                                                                                                                                                                                                                 R06400 standard; pr
                                                                                                               Homo sapiens.
WO9008190-A.
                                                                                                                                                                C-terminal alpha amidating
                                                                                                                                                                             17-DEC-1990 (first entry)
Lambda gt10ch2 encoded C-t
                                                                                                                                                                                                                                                                                                                     726
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                                                                                                                                                  lambda gt10ch2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyLeuGluTyrIleIleArgLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTT.....TACTCAAGAAAAGATCTGCAGAACCGGAGAATA....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                    .....TCATTGATGTACGAACTGATATCAACACCCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AACCTGCTGCAGCTGCGCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \verb|nSerGluIleIleAspThrAsnThrSerLysGlnPheGlnLysAlaArgA| \\
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                                                                                                                                                                                                                                   protein;
                                                                                                                                                             terminal alpha amidating enzyme.
ng enzyme; human thyroid gland;
                                                                                                                                                                                                                                   776
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alignment_block:
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Percent Similarity:
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Disclosure; pp; English.

CDNA libraries were prepared from human thyroid gland poly(A) RNA cDNA libraries were prepared from human thyroid gland poly(A) RNA in lambda gtll and gtl0. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gtl0 library, including gtl0chr2.

Restriction analysis indicated that gtl0chr2 encoded a different type of enzyme to one of the other two clones. The DNA can be inserted into vectors for expression in E.coli or (more efficient.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The enzyme is useful for prodn. of physiologically active alpha-amidated peptides from their C-glycyl precursors. See also Q05630 and Q05632.

Sequence 776 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 nTrpGlyGluGluSerSerGlySerSerProLeuProGlyGlnPheThrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
                                                                                                                                                                                                                                                                                                                                                                                           AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alProHisSerLeuAlaLeuValProLeuLeuGlyGlnLeuCysValAla
CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT 636
                                                                                                                                                                                                                                                                                          AAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATCGTGCATAT...CGAGTACAATGCTTTTACATGGAAGCTGATAAAAC
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                                                                                                                                                                                            ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA
                                                                                                                                                                                                                                                                                                                                          eValArgGluIleLysHisSerSerPheGlyArgAsnValPheAlaIleS
                                                                                         ATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.....ACTG
                                             ........AspGlnGluProValGlnGlyPhe......
                                                                                                                                         .....GlyLeuLeuPheAlaValAsnGlyLysProHisPheGly..
                                                                                                                                                                                                                                          erTyrIlePro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt AspArgGluAsnGlyArgIleGlnCysPheLysThrAspThrLysGluPh}
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seq_name: A_Geneseq_36:R06379
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17-JAN-1989; JP-00587
(SUNR) SUNTORY LTD.
Ohsuye K, Kitano K, T
WPI; 90-254034/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _documentation_block:
amidated
See also
Sequence
                                                                                                             Disclosure; pp; English.

CDNA libraries were prepared from human thyroid gland poly(A) RNA in labraries were prepared from human thyroid gland poly(A) RNA in lambda gt11 and gt10. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gt10 library, including gt10chT101.

Restriction analysis indicated that gt10chT101 encodes a different type of enzyme to one of the other two clones. The DNA can be type of enzyme to one of the other two clones.
                                                             The
                                                                                                                                                                                                                                                       coding sequences.
                                                                                                                                                                                                                                                                   C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9008190-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lambda gt10ch101 encoded C-terminal alpha amidating enz
C-terminal alpha amidating enzyme; human thyroid gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670
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                                                                           in animal cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lambda gt10ch101.
                                                                                             nserted into vectors for expression in
                   enzymes are useful for prodn. of physiologically active alphadated peptides from their C-glycyl precursors. also Q05630 and Q05631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTTGATTTACGTC 994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lValGluThrLysMetGluAsnLysProThrSerSerGluLeuGlnLysM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGAT 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....ValMetAsnPheSerAsnGlyGluIleIleAspIlePhe.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ValLeuIleThrThrLeuLeuValIleProValValValLeuLeuAlaI 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..........LysProValArgLysHisPheAspMetProHi
                                                                                                                                                                                                                                                                                                                                              Kitano K, Tanaka
                                                                                                                                                                                                                                                                                                                                                                                          JP-005878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
     AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-terminal alpha amidating enzyme
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                                                                                               E.coli or
                                                                                               (more efficiently)
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alignment_scores

Quality:

87.00

Length:

322

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alignment_block:
US-09-323-427-3 x R06379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561 nTrpGlyGluGluSerSerGlySerSerProLeuProGlyGlnPheThrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eValArgGluIleLysHisSerSerPheGlyArgAsnValPheAlaIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGACATGTTTATGTGAAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
TANAACAGGTGGCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
                                        ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
                                                                                 AGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT
                                                                                                                         hrAsnThrValTrpLysPheThrLeuThrGluLysLeuGluHisArgSer
                                                                                                                                                                  CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT
                                                                                                                                                                                                        sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT
                                                                                                                                                                                                                                                 AGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGAT
                                                                                                                                                                                                                                                                                         .....LysProValArgLysHisPheAspMetProHi
                                                                                                                                                                                                                                                                                                                                  GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....AspGlnGluProValGlnGlyPhe......
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45.652
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Percent Identity: 18.944
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alignment_block:
US-09-323-427-3 x R06399
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                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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CDNA libraries were prepared from human thyroid gland poly(A) RNA ibraries were prepared from human thyroid gland poly(A) RNA in lambda gtll and gtll. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gtll library, including gtllothT201. Restriction analysis indicated that gtllothT201 encodes a different type of enzyme to the other two clones. The DNA can be inserted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This enzyme is useful for prodn. of physiologically amidated peptides from their C-glycyl precursors. See also Q05631 and Q05632.
Sequence 974 AA;
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Lambda gtlOch201 encoded C-terminal alpha amidating enzyme.
C-terminal alpha amidating enzyme; human thyroid gland;
lambda gtlOch201.
                                                   197
                                                                                                                                                                                           631 CysGlnProThrAspValAlaValAspProGlyThr.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-1989; JP-005878.
(SUNR ) SUNTORY LTD.
Ohsuye K, Kitano K, Tanaka
WPI; 90-254034/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 into vectors for expression in E.coli or (more efficiently) in
                                                                                                                                                                                                                                                    97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACTCAAGAAAAGATCT.....GCAGAACCGGAGAATATCATTGATGTA 930
                                                                                                                                          AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
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                                                                                                                                                                                                                                            TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leAlaIlePheIle 780
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                                                                                            .GlyAlaIleTyrValSerAspGlyTyr.
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0.592
45.652
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Percent Identity: 18.944
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                                                                                                                                                                     CGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCC 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
                                                                                                                                                                                                                                                                               TACTCAAGAAAAGATCT.....GCAGAACCGGAGAATATCATTGATGTA
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                                                     AGTTGATTTACGTC 994
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                                                                                                             .ValLeuIleThrThrLeuLeuValIleProValValValLeuLeuAlaI 883
                                                                                                                                                                                                                                                                                                                                    lValGluThrLysMetGluAsnLysProThrSerSerGluLeuGlnLysM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC 436
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seq_documentation_block:
ID R74171 standard; Pr
AC R74171;

Protein;

3038

seq_name: A_Geneseq_36:R74171

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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PT Novel DNA encoding triol poly-ketide synthase - used to isolate and pridentify homologues of triol poly-ketide synthase, and in the treatment of hyper-cholesterolaemia of hyper-cholesterolaemia prof hyper-cholesterolaemia prof hyper-cholesterolaemia prof hyper-cholesterolaemia prof station of the plasmid ploA was claim 12; Figure 2; 107pp; English.

CC designated pTPKS100. Splicing of the introns from the DNA sequence and translation of the 9114 nt ORF results in a protein of 3038 AAs (R74171) with a mol. wt. of 269,090 cd altons. Inspection of the TPKS AA sequence for active claim of 3038 AAs (R74171) with a mol. wt. of 269,090 cd altons. Inspection of the TPKS AA sequence for active contraction of site synthases and fatty acid synthase (FAS) activities polyketide synthases and fatty acid synthase (FAS) activities cresulted in the identification of candidates for expected sites (see FT). Except for the presence of a methyl transferase, not present in FAS, the succession of activities on the TPKS protein is the same as that observed for the rat FAS
                                                                                                                                                                                                                            Align seg 1/1
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     1188
                                                                                                        1175 ValalapheGlnThrValIleGlyAla.....TyrSerSerPro.....
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Sequence
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/label=_misc_feature
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Aspergillus terreus triol polyketide synthase.
Triol polyketide synthase; TPKS; HMG-COA reductase inhibitor;
hypercholesterolaemia; LDL- cholesterol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 95-193816/25.
N-PSDB; Q92323.
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Conder MJ, Davis CR,
Reeves CD, Vinci VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1995.
28-OCT-1994; U12423.
02-NOV-1993; US-1481
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                                                 CAATGGTGTCGAAGGTGAGCCAGAAATTGAATGT......GGACCAACTT 109
                                                                                                                                                                     ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGA 65
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/label= misc feature
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38.347
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282. .288
/label= misc feature
.GlyAspArgArgLeuArgCysLeuTyrValProThrH 1200
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/label= misc
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Gaps: 24
Percent Identity: 19.703
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832	TTCGACCACAATGTTCAGAACCACAAGGATTCGC	783
1445	<pre>!!!!! IleLeuGluIle</pre>	1442
782	CGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC	733
732 1441	CAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGAT ::: ::: ::: laargGluLeuValalaGlnIleAlaHisArgTyrGlnSerMetAsp	683 1426
682 1426	TGATAAATATTTGCTAAATAATTTGGAATATC	1409
650 1409	GGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	604 1394
1393	${\tt roHisValArgLeuValGlnArgValGlyGlnHisLeuLeuProThrVal}$	1377
603		603
603 1377	TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT ::: ::: ::::::::: naspThrGluAlaGlnIleGluHisLeuCysThrAlaAsnSerTyrHisP	561 1360
560 1360	ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT	511 1351
1350	:::::: ::::::: ::::::: ::::::::	1341
سند	aAlaPheHisLeuGlnLysGlnTleGluTrpLeuGlu	1326
460	TTTTCAAACTCAAATTGTCCCGAT	420
419 1326	ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC::::::::::	370 1313
369 1312	AAGTTGATCGTGCATATCGAGTACAATGCTTTTAC :::	335 1296
334 1296	GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCA :::: ::::: yProLeuThrProAspSerLeuLeuAspAsnProGluTyrTrpAlaThrA	289 1279
288 1279	TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT::::::::::::::::::::::::::	241 1263
240 1262	ATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGAT:::	194 1247
193 1246	TGTTTATGTGAAAAGGTCTTTATGATCAAGAAGGTTGCCGTA :::::	153 1233
152 1233	ACAATCAATTTTAATACACGTAATGCATTCGAAGGACA ::: :::::::: SerGlyCysGluLysValAlaPheAsnThrIleAsnThrTyrAspLysGl	115 1217
1216	;;; isValAspArgIleThrLeuValProSerLeuCysLeuAlaThrAlaGlu	1200
114	CAATA	110

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alignment_block:
                                                                                             alignment_scores:
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                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1990; 301034.

06-FEB-1989; US-307366.

(UNIG-) UNIGENE LAB INC.

Betelsen AH, Mehta NM, Beaudry GA;

WPI; 90-248308/33.
                                                                                                                                                  expression vector. The AEE encoded is used as a catalyst in the conversion of a peptidyl substrate to a corresp. peptidyl amide. This can be used for making a protein biologically active, e.g. calcitonin or growth hormone releasing factor. See also Q05637. Sequence 944 AA;
                                                                                                                                                                                                                          The corrsp. DNA sequence hybridises, under stringent conditions, with a DNA sequence (I) which encodes an alpha amidating enzyme (AEE) and is foreign to the host cell into which it is transformed. (I) is connected to a promoter and is contained in an expression vector. The AEE encoded is used as a catalyst in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha amidating enzyme. Alpha amidating enzyme; peptidyl amide EP-382403-A.
                                                                                                                                                                                                                                                                                                                           Prodn. of alpha amidating enzyme - using prokaryotic eukaryotic expression vectors having transcriptional Claim 3; page 19; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q05636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1990 (first entry) Protein encoded by sequence which hybridises with DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ....LeuGluLysThrMetAlaHisAlaArgSerLeuLeuLysProGlyG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTTTGCCAGTTGATTTACGTCAC...CGTGCACTTCTGCAACATAATG 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euAspIleArgArgSerProAlaGluGlnGlyPheGluPro...HisAla 1511
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                                                                         Quality:
                                                         Ratio:
                                  86.50
0.588
43.363
                                  Length:
Gaps:
Percent Identity:
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17.994
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Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
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                                               836 lGluProLysValGluAsnLysProThrSerSerGluLeuGln.....
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GAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAA
                                                                                                                                               ValLysLysAlaGlyIleGluValGlnGluIleLysAlaGluAlaValVa
                                                                                                                                                                                               ....CAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTT..
                                                                                                                                                                                                                                                 hrAsnThrValTrpLysPheThrLeuThrGluLysMetGluHisArgSer
                                                                                                                                                                                                                                                                                                 .....AAATATGCGGATCGATCACAGCTTTTCTATCAATGC
                                                                                                                                                                                                                                                                                                                                                      sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT
                                                                                                                                                                                                                                                                                                                                                                                                    AGATTTAATGGCTGGCCAAGAAGCTCACGTATAC.........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....ValMetAsnPheSerSerGlyGluIleIleAspValPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....AspGlnGluProValGlnGlyPhe.....
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Align seg 1/1 to: R10323 from: 1 to: 944 97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
alignment_block: US-09-323-427-3 x R10323
alignment_scores: Quality: 86.50 Ratio: 0.588 Percent Similarity: 43.363 Percent Identity: 17.994
CC sequences of Type A and Type B are substantially identical with the CC exception of an intron region from bases 1178-1492 (CDS) of the CC Type B cDNA. SQ Sequence 944 AA;
CC pref. between posns. 2340 and 2690 (counting from the CDS). This CC results in the expression of an 87 rather than a 105 kD prod. The
CC includes a membrane spanning domain which may be undesirable in a CC recombinant DNA expression system, possibly inactivating the enzyme. CC A stop codon can be placed unstream of the domain-encoding sequence.
CC of other recombinant polypeptides such as calcitonin. The sequence
CC be divided into distinct types, the sequence below being encoded by CC Type B. (Type A is given in R10322). The sequence can be inserted to the correction when the correction of the correction with the correction of the correction with the correction of the correction with the correction of the correction of the correction with the correction of the
CC derived cell lines such as TVT 10028. The church form this control of the country of the country the c
PT Expression systems for antiating enzyme - comprises proxaryotic PT or entraryotic hosts contg. a recombinant expression vector contg. PT the corresp. DNA sequence.
PI HETEISEN AH, MENTA NM, HEAUGTY GA; DR WPI, 91-022433/04. DR N-PSDB; Q10278.
PF 01-FEB-1990; 049043. PR 06-FEB-1989; US-307336. PA (UNIG-) UNIGENE LAB INC.
PD 29-NOV-1990.
DT 08-APR-1991 (first entry) DE Type B alpha-amidating enzyme. Amidation; post-translational modification; AE.
umen 0323 0323
seq_name: A_Geneseq_36:R10323
980 CAGTTGATTTACGTC 994 :::::::::::::::::::::::::::::::::::
930 ACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGC 979 ::: ::: ::::::::: :::
880 CTTCGTTTACTCAAGAAAGATCTGCAGAACCGGAGAATATCATTGATGT 929 :::::: :::: ::: ::: 852 MetGlnGluLysGlnLysLeuSerThrGluProGlySerGlyValSerVa 868
851Lys 851

	CAGTTGATTTACGTC 994	980
979 884) ACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGC	930 868
9	:::::: MetGlnGluLysGlnLysLeuSerThrGluProGlySerGlyValS	Úπ
929	CTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGA	088 T C 8
7	GAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCC	ت ۱
850	 	836
829	GACCACAATGTTCAGAACCAC	799
w	ValLysLysAlaGlyIleGluValGlnGluIleLysAlaGluAlaValV	820
ا ف	CAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTT	757
819	The sent to the se	803
. 0	sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHis	
72	AGATTTAATGGCTGGCCAAGAAGCTCACGTATAC	
786	5LysProValArgLysHisPheAspMetProHi	776
686	GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGA	637
775	3ValMetAsnPheSerSerGlyGluIleIleAspValPhe	763
636	CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC	587
762	5AspGlnGluProValGlnGlyPhe	755
586	ATGGACATGCGATTCTGAAACCGTTGATAC	537
754	::: 	742
536	ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCA	487
741	:: ::: ::: ::: ::: ::: ::: ::: ::: ::	738
486	AAATTGTCCC	437
w	 	721
436	AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGG	387
386) GATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAAC 	340 705
704	alProHisSerLeuAlaLeuValProHisLe	688
339	ACTGTTGTCATTTCGTTCATTCATTATTTGTTACCAAAGT	298
688	nTrpGlyGluGluSerSerGlySerSerProArg	671
297	:	297
67	AsnSerArgIleValGlnPheSerProSerGlyLysPheValThrG	656
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885 IleValMetPheIle 889

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PT Antibody reactive with part of desmosomal cadherin - exposed on PT surface of epithelial or carcinoma cells, not bound to desmosomes, PT useful for diagnosis and treatment of carcinoma micrometastases PS Claim 7; Page 5; 8pp; German.

CT The present sequence is a segment of the desmosomal cadherin (DC), CC desmoglein Dsg2, which is exposed on the surface of epithelial or Carcinoma cells and not bound to desmosomes. An antibody (Ab) of the carcinoma cells and not bound to desmosomes and the used to CC diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes, to separate, enrich or CC detect living or fixed carcinoma cells by cell sorting methods and CC as a therapeutic to deliver agents, e.g. other Ab or toxins, to CC carget cells. The Ab provides rapid and reliable detection of CC metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-323-427-3 x W13009
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DE19531033-A1.
27-FEB-1997.
23-AUG-1995; DE-031033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WW, Schaefer S;
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                                                                                                                                                                                                                                                                                                                                            299 LeuAspPheSerValIleValAlaAsnLysAlaAlaPheHisAspSerIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; Dsg2; cell; surface; epithelial; carcinoma; desmosome; antibody; epitope; diagnosis; detection; micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W13009 standard; protein; 560 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-1997
                                                                                                                                                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
TTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT......
                                     nIleIleGlyAsnPheGlnAlaPheAspGluAspThrGlyLeuProAlaH
                                                                                                                 SerGluSerMetAsp......
                                                                                                                                                       AAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCA
                                                                                                                                                                                                                               ATGCATTCGAAGGA.....CATGTTTATGTG 162
                                                                                                                                                                                                                                                                    eArgSerLysTyrLysProThrProIleProIleLysValLysValLysA
                                                                                                                                                                                                                                                                                                          T.....GAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTA 136
                                                                                                                                                                                                                                                                                                                                                                                  TTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAAT
                                                                             AGTTGCCGGAATTTCACTTCCATTTGATTCATGCAAT.....
                                                                                                                                                                                             snValLysGluGlyIleHisPheLysSerSerValIleSerIleTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.50
0.822
51.232
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                                                                                                                 .ArgSerSerLysGly.....Gl
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Gaps:
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alignment_block: US-09-323-427-3 x R20026

Align seg 1/1

to: R20026

from: 1

to: 973

alignment_scores:

Quality:

85.00 0.582 43.976

Length: 332
Gaps: 14
Percent Identity: 18.072

Ratio: Percent Similarity:

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seq_documentation_block:
ID R20026 standard; Protein; 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: A_Geneseq_36:R20026
R N-PSDB; Q20198.

R N-PSDB; Q20198.

ToDNA sequence - coding for peptide C terminal amidation enzyme butd. from horse.

Tobtd. from horse.

S Claim 1; Fig 1; 18pp; Japanese.

The sequence was deduced from the DNA sequence determined from a clone isolated from a library prepd. from mRNA extracted from a clone strium tissue. The sequence is one of four similar ones horse atrium tissue. The sequence up to residue 809 at provided which all have the same sequence up to residue 809 at which point they diverge, having different C-termini. The different termini are created by deletions in the last portion of DNA (see feature table).

Sequence 973 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493
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                                                                                                                                                                                                                                          14-MAR-1990; JP-063306.
(SHIS ) SHISEIDO KK.
WPI; 92-012701/02.
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                                                                                                                                                                                                                                                                                               22-NOV-1991.
14-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-terminal amidation enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532 CATAAATGG 540
                                                                                                                                                                                                                                                                                                                                      J03262484-A.
                                                                                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                                                                                                                                                                                                                                                                         Equus caballus.
                                                                                                                                                                                                                                                                                                                                                                                                                              Horse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt spTyrProArgLysThrIleThrGlyThrValLeuIleAsnValGluAsp}
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CT 950	gagaatatcattgatgtacgaactgatatcaacacc	904
903 eu 855	CCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT. ::::: ProAlaSerSerGluLeuGlnLysMetGlnGluLysGlnLysI	857 839
uA 839	 AlaValValGluThrLysMetGl	827
AG 856	GTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCC	807
CACA 806 :: leLy 827	ACCATTAAAGAACCAAATAGCGAATGTGTTCGAC 	757 815
81	:::::::::::::::::::::::::::::::::::	10
GC 75	AAATATGCGGATCGATCACAGCTTTTCTATCAAT	N
sT 799	ATAC TyrValGlyAspAlaHi	782
78	LysProValArgLysHisPheAspMetPr	2 7
83	TGTGCTCTTGATAAATAATTTTGCTAAATAATTTTGGAATATCC	ω
771	AsnPheSerSerGlyGluIleIleAspValPhe	759
CT 636	GCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAAI	587
758	AspGlnLysProValGlnGlyPhe	
ATT 586	GGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCC	537
750	<pre>!:: ::: lyLeuLeuPheAlaValAsnGlyLysProTyrPheGly</pre>	738
AA 536	FCAATTTGCTATCATTGGTCAGCCAGTTTATCAT	487
737		734
CA 486	AATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGAC	437
TC 436 : es 734	TATCTGAAATCACAACTGCTTTTCAAAC :: :aSerPheGlyArgAsnValPheAlaIl	387 717
AC 386 Ph 717	\AGCTGATAA <i>F</i> :::::: spThrLysGlu	340 701
la 700	ValProHisLeuGlyGlnLeuC	684
TT 339	TTGTCATTTCGTTTCATCCATTATTTGTT	298
gV 684	rpGlyGluGluSerSerGluSerAsnProLysProGlyGl	667
297		297
AAC 296 rGl 667	ACGATCTCTGAATCCACGTGGTATTTTI ::::::: eValGlnPheSerProThrGlyArgPhe	247 652
ys 651		651
GC 246	TGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATT	197
. 65		642
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641		630

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Marie Committee and the second

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Search information block: Ouery: US-09-323-427-3
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Database length: 13297546
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:US-08-477-459-20 + 78.50
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-Q-/cgn21/USPTO_spool/US09323427/runat_14042000_170513_19887/app_query.fasta.1
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-XAAPEXT-0.500 -DELEVE-6.000 -DELEXT-7.000 -START-1
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Quality:
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                                                                                                                                    Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                          TELEFAX: (919)541-868 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compa
OPERATING SYSTEM: PC-D
SOFTWARE: PATENTIN Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                 97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: U: FILING DATE: 19910530 CLASSIFICATION: 530
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STATE: New York
                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                         : 935 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                           Villamizar, JoAnn
7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                          linear
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0.541
47.315
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alignment_block:
US-09-323-427-3 x US-07-707-367-2
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 Align seg 1/1 to: US-07-707-367-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 14
FILING DATE: 01-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 329911/90 FILING DATE: 30-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 2: FILING DATE: 10-AUG-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/07707367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kangawa, Kenji
VENTION: No. 5196316el Enzyme and DNA Coding
EQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimoi, Hiroko
Suzuki, Kenji
Ghisalba, Oreste
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Kawahara, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         (914)785-7120
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                                                                                       Length: 391
Gaps: 18
Percent Identity: 19.437
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from: 1
 to: 935
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612
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                                    GCA.....GAACCGGAGAATATCATT...GATGTACGAAC
HisArgSerValLysLysAlaGlyIleGluValGluGluIleThrGluTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alGlnGlyPheMetLeuAsnPheSerAsnGlyAsp......
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                                                                       alGluLysGlnThrGlnGluLysGlnGlnLys.....GlnLysAsnSer
                                                                                                                                              rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV
                                                                                                                                                                                                                                                                                              lyAspAlaHisAlaAsnAlaValTrpLysPheSerProSerLysAlaGlu
                                                                                                                                                                                                                                                                                                                                                                     eAspMetProHisAspIleAlaAlaAlaAspAspGlyThrValTyrValG
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                                                                                                                                                                                                                                                         ...ATTACCATTAAAGAACCAAAT.....AGCGAATGTGTTCGACC
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seq_documentation_block:
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                                                                                                                                                                   PRILING DATE: 15-AUG-1307

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 1-181933

FILING DATE: 31-OCT-1989

PRIOR APPLICATION NUMBER: JP 2-76331

APPLICATION NUMBER: JP 2-76331

TTING DATE: 26-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                       APPLICATION NUMBER: JP 2-205475 FILING DATE: 02-AUG-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/070,30. FILING DATE: 24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    840 leAlaIleAlaIlePheIleArg 847
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                                                                                                                            APPLICATION NUMBER: JP 2: FILING DATE: 24-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lSerPheValLeuIleIleThrLeuLeuIleIleProIleAlaValLeuI 840
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5. 5871995
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Player, Willic
RATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Wegner, Cantor, Mueller & Player, P.C. 1233 20th Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAJIMA, Masahiro
YANAGI, Mitsuo
OKAMOTO, Hiroshi
KISHIMOTO, Jiro
IFUKU, Ohji
KATO, Ichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIDA, Toshio
KAMINUMA, Toshihiko
                     William
                                                                                                                                                  JP 2-106412
                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/070,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version
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alignment_block:
US-09-323-427-3 x US-08-070-301-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 440706
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 989 amino acids
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ORGANISM: Frog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 658
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEPAN: (202) 835-0605
                   581 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 630
                                                                                                               531 TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG 580
                                                                                                                                                                                                         481 GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 530
                                                                                                                                                                                                                                                        384 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 430
                                                                                                                                                                                                                                                                                                                                                                                                                                              713 AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                      AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA.... 291
                                                                                                                                                                                                                                                                                                                                                       uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 696
                                                                 rGly......AspSerThrProValGlnGlyPhe.....
                                                                                                                                                           Gly......ValLeuTyrAlaValAsnGlyLysProTyrTy 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....Суз 663
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0.965
43.103
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21.552
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-477-451-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-477-451-8
                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-477-451-8 from: 1 to: 3200
                                                                                                                                                                                                                                                                                                         US-09-323-427-3/rev x US-08-477-451-8
                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5928865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/477,451
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 510-655-3542 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                 1050 ATTTTGTACTGCAGCAAGTAT......TACAGGTTGTCCATTATGTT 1010
                                                                                                                                   1009 GCAGAAGTGCACGGTGACGTAAATCAACTGGCAAAGCTTGATTATCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 510-601-2708
                                            959 CTAATTTCAAGGGTGTTGATATC.....AGTTCGTACATCAATGATATT 916
                                                                                      761 sLysThrCys......PheSerPheTyrArgLeuIleGluIleV 774
                                                                                                                                                                             745 IleValPheCysArgIlePheGluLeuValTyrArgLeuLeuIleAlaLy 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        791 eGluMetProHisAspIleAlaAlaGlyAspAspGlyThrValTyr 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675 GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  631 AATGCTGATGGATGTGCTCTTGATAAATATTTG.....CTAAATAATTT 674
774 alAsnPheLeuSerGlnPheLeuIleProLysProTyrLeuThrGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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ZIP: 94608-2916
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0.603
43.360
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Gaps: 20
Percent Identity: 22.764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      844 eIleAsnPhe.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 ATAATGGATGAAACGAAATGACAACAGTTGTTACAAAAATACCACGT
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                                                                                                                                                          CATAAAGACCTTTCACATAAACATGTCCTTCGAATGCATTACGTGTATTA 126
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                                                                                                           eIleGln..
                                                                                                                                                                                                      .....LeuIlePheAlaIlePheGluPh 989
                                                                                                                                                                                                                                                                AATTCCGGCAACTTGACGTCCACCTTCATCATTACGGCAACCTTCTTGAT 176
                                                                                                                                                                                                                                                                                                                  heLysValAlaPheCysLeuArgTyrLeuAlaGluIle......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCCATGTAAAAGCATTGTACTCGATATGCACGATCAACTTTGGTAACAA 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGATCTGGCATTGATAGAAAAGCTGTGATCGATCCGCATATTTGTATA 716
                                                                                                                                                                                                                                                                                                                                                                            GGATTCAGAGATCGTGTACGCGCAACATTGCATGAATCAAATGGAAGTGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                              ....TyrLeuLeuIleAspAspHis.....IlePheAsnGlyIleP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....SerIleAsnGlyPheValPheGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....LeuSerLeuLeuGlyGlnLeuLeuGluIlePheG
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SerCysIleL
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alignment_block:
US-09-323-427-3 x US-07-906-349A-6
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Quality:
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                                                                                                                                                                                                                     Align seg 1/1 to: US-07-906-349A-6 from: 1
                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/07906349A Patent No. 5434064
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
'-906-7100'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/643,237
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,349
FILING DATE: 30-JUN-1992
                                                                                   866 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG 915
                                                                                                                                573 ThrThrAlaAlaThrCysAlaCysThrGlyCysThrGlyCysThrCy
                                                                                                                                                                          816 ACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG
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APPLICANT: Skolnik, Edward Y.
APPLICANT: Margolis, Benjamin L.
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES
TITLE OF INVENTION: TARGET PROTEINS
916 AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
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ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
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                                      Ratio:
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3.000
40.260
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                                                                                                                                                                                                                                                                                                                             Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version
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28.571
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                                                                                                                                589
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Percent Similarity:

49.669

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alignment_scores:
    Quality:
    Ratio:
                                                                                                  ; NAME/KEY:
; NAME/KEY:
US-08-415-751-35
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    Sequence 35, Applicati
    Patent No. 5643772
                                                                                                                                                                                                                                                 TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 35
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 03-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: MAY 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Hana Dolezalova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1016 ATGGACAACCTGTAATACTTGCTGCAGTACA 1046
                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                     RECISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GUT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613 rThrThrThrCysAlaThrCysCysThrThr 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    966 TAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATA 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/415,751 FILING DATE: 03-APR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 385 Sher
                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-415-751-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o, Application US/08415751 5643772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 Sherman Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
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NELSON, RICHARD, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PETERSEN,
                                                                                                    Positions coded by nonsense codons are identified as Xaa.
                                                                                                                                                                          Cryptosporidium parvum
                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND RNA ENCODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRYPTOSPORIDIUM ANTIBODIES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLYPEPTIDES BINDING ANTI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAROLYN
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Suite 6
    Length:
Gaps:
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alignment_block:
US-09-323-427-3 x US-08-415-751-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/08325071 Patent No. 5587311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1080 AATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCA 1129
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 n 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 .....TyrGly......CysCysCysCysCys***LeuTrpTyrAs 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 euPheTrpCysCysCysCysCysLeuAsnTrpThrLeuTrpTrp... 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 uCysCysCysGlyCysCysSerLysIleTrpAspAsnCysCysCysSerL 130
                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Ce
TITLE OF INVENTION: Glycoprotein Of A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  808 TGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGC 857
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     978 GCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACA.... 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               928 GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              884 GTTTACTCAAGAAAAGAT.....CTGCAGAACCGGAGAATATCATTGAT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   858 AAAACCTGCTGCAGCTGCGCAAC......883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          761 TCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCAC...AA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 *****LeuGlnPhe.AspLeuCysValLeu*******Trp***ArgLe 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 lnThrIle***HisLeuLysAsnArgCysLysTyrGlnSerThrHisHis 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 yMetArgAsn***ProHisArgGluLeuLeuHisGluLeuValValLysG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 SerAsnLeuLeuGlnHisSerArgArgHisPhePheGluArgLeuGl 36
                                                                                                       STREET: 300.
GTTY: Washington,
                                                                                  ZIP: 20007-5109
                                                                                                    COUNTRY:
                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGluSerGlnIleAspPheLysLeuGlnAsnArgLeu.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....CTGCATGTCACCATTTGGCTTCTC 1079
                                                                                                                                 E: Foley & Lardner 3000 K Street, N.W. ashington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                       COBON, Stewart Gary
MOORE, Joanna Terry
JOHNSON, Law Anthony York
                                                                                                                                                                                                                                                                                                                                                        WILLADSEN, Peter
KEMP, David Harold
SRISKANTHA, Alagacone
                                                                                                                                                                                                                                 CANA Encoding A Cell Membrane Glycoprotein Of A Tick Gut 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 25.828
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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-09-323-427-3 x US-08-325-071-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-325-071-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-325-071-67 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 6004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
                                       294 ......TTCG 312
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                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                        163 sGluLysAsnLeuLeuGlnArgAsp.......serA 173
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APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
ADDITIONATION DATA:
187 ProProAlaAspSer......TyrCysSerProGlySerProLysGl 200
                                                                                                                                                                                                                                 211 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 260
                                                                                                                                                                                                                                                                                                                     161 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 210
                                                                                                                                                                                                                                                                                                                                                               147 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 163
                                                                                                                                                                                                                                                                                                                                                                                                              138 TGCATTCGAAGGACATGT.................TTATG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-JUN-1987 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/242,196 FILING DATE: 06-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/062,109 FILING DATE: 17-MAY-1993
                                                                                                                                                                           rgCysCysGlnGlyTrpAsnThr.....AlaAsnCysSerAlaAla 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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0.612
40.947
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Percent Identity: 21.727
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                                                                                                                                       293
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5112855066666666666666666666666666666666666		CACCCTTGAAATTAGCGA 962 :: .nGluAlaAlaTyrLysGl 451	GAAC ThrGluIleGluC	eGlyGluTrpCysMetM	פ עם	 ATCAGTATTAÇCATTAAAG 778 ::: hrSerIleGlyLysGluV 375	72 36	AATTTGGA ::::: PheThrProAsnIleSe	ATTCTAAATGCTGATGGAT 643 ;; 	serCysTyrCysProT	GCGGTTGTCCATTCCTGC 591	CAGTTTATCATAAATGGA 541	RGGATGGTGGACCAACCGG 491 :: 	26	ACAGTTAGTGCACAGATTG 403 ::: ::: ::: [leThrCysLysSerIleS 250	/SAlaTyrGluCysThrCy 233

seq_documentation_block:
; Sequence 61, Application US/08325071
; Patent No. 5587311

seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-61

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alignment_block:
US-09-323-427-3 x US-08-325-071-61
                                                                                                                                                        alignment_scores:
Quality:
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                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/325,071
FILLING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILLING DATE: 17-MAY-1993
PRIOR APPLICATION NUMBER: US 07/926,368
FILLING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILLING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: 07/242,196
FILLING DATE: 06-JUL-1986
PRIOR APPLICATION NUMBER: PCT/AU87/00401
FILLING DATE: 27-NOV-1987
PRIOR APPLICATION NUMBER: AU P14912
FILLING DATE: 16-OCT-1987
PRIOR APPLICATION NUMBER: AU P12570
FILLING DATE: 19-JUN-1987
PRIOR APPLICATION NUMBER: AU P19196
FILLING DATE: 19-JUN-1987
PRIOR APPLICATION NUMBER: AU P19196
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/111 B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5390
TELEX: 904136
INFORMATION FOR SED ID NO: 61:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SED ID NO: 61:
Align seg 1/1 to: US-08-325-071-61 from: 1 to: 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             TYPE: amino acids
TYPOLOGY: line
WOLDON'S
TYPE AMINO ACID
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOORE, Joanna Terry
JOHNSON, Law Anthony York
WILLADSEN, Peter
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                                                                                                                                                                                                                                                                        protein
                                                                                                              89.00
0.614
40.390
                                                                                                              Length: 359
Gaps: 22
Percent Identity: 22.284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60042/111 BIAU
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320	LysAlaArgLeuIleAla
878	SGTGGTGCCGCAGCAAAACCTGCTGC
305	294 alPheLysValGluIleLeuAsnCysThrGlnAsp
828	TAGCGAATGTGTTCGACCACAATGTTCAGA
778 294	TCTATCAATGC :: euGluAlaIle
728 279	679 TATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC :::
	44 GTGCTCTTGATAAATATTTGCTAAAT
643 253	AAATTCTAA!
239	TGGT SGlyValTyrMetA
591 222	CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTT ::: :::
541 209	TCAACCAGTTCAATTTGCTATCATT:::::::::::::::
491 202	TGGA uCys
450 185	404 AGGTATCTGAAATCACAACTGCTTTTCAAACTGAAATTGTCCCGATG :: ::
403 169	ATGGAAGCTGATAAAACAGTTAGTGC ::: ;:: ValalaGluAspGlyIleThrCysLy
362 152	313 TTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG
312 136	AACTGTTGTCAT ::: spGlyGlnCysIleAsnAlaCysLysMetLysGluAla
296 119	CTCTGAATCCACGTGGTATTTTTGTAACAAC ::::: calaaspSerTyrCysSerProGlySerPro
260 105	TGATTCATGCAATGTT::: ::: AlaAsnCyss
210 92	rga ···
160 82	138 TGCATTCGAAGGACATGTTTATG

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seq_documentation_block:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
                                  APPLICATION NUMBER: AU PH919
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062/109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
ADDITCATTON NUMBER: US 07/026 368
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APPLICATION NUMBER: PCT/
FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07-FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        963 TGATAATCAAGCTTTGCCAGTTGAT 987
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                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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FELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                      APPLICATION NUMBER: AU P. FILING DATE: 19-JUN-1987
                                                                                                                                                                                                                                        APPLICATION NUMBER: AU PFILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-JUL-1988
                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/242,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     etTyrProLysLeuLeuIleLysLysAsnSerAlaThrGluIleGluGlu 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yGlnAsnLysCysValLysValAsp 378
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5587311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOORE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEMP, David Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILLADSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOHNSON, Law Anthony York
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .TTACTCAAGAAAAGATCTGCA.....GAACCG 912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart Gary
                                                                                                                               AU PH9196
                                                                                                                                                                                                                                                                 AU PI4912
                                                                                                                                                                                                                                                                                                                                                                                                                                                           us 07/926,368
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                    60042/111 BIAU
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alignment_block:
US-09-323-427-3 x US-08-325-071-63
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TELERAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 63
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451
                                                                                                                                                             592 TTTGTCGATGATGGT.....
                                                                                                                                                                                                                                                                       542 CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC 591
                                                                                                                                                                                                                                                                                                                            283 nGln.......HisLeuValGlyAsp.....
                                                                                                                                                                                                                                                                                                                                                                                  492 TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                    267 GluAspCysArgValHisLysGlyThrValLeuCysGluCysProTrpAs 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 erHisThrValSerCysThrAlaGluGlnLysGlnThrCysArgProThr 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 sProArgGlyPheThrValAlaGluAspGlyIleThrCysLysSerIleS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGTATGCCGTTATGAA.....ATTTTGGATGGTGGACCAACCGG 491
pLysSerArgLysProGlyProAsnVal.....AsnIleAsnGlyC
                                                                                                       PheMetAspCysGlyValTyrMetAsnArgGlnSerCysTyrCysProTr 320
                                                                                                                                                                                                               hrCysIleSerAspCysValAspLysLysCys......HisGluGlu 303
                                               .....AACGGTGATACTGTGGAAATTCTAAATGCTGATGGAT 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTC...CCGATG
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0.614
40.390
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Gaps: 22
Percent Identity: 22.284
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  334
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5744350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                 ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 190
                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE, P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VINCI, VICTOR A. APPLICANT: CONDER, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        913 GAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 uAspArg.....ValLeuGluAlaIleArgThrSerIleGlyLysGluV 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               729 GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG 778
TELECOMMUNICATION INFORMATION:
                                                                                                               APPLICATION NUMBER: US/08/450,332
FILING DATE: 25-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yGlnAsnLysCysValLysValAsp 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....IleLysAlaArgLeuIleAlaGluLysProLeuSerAsnHisVa 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAMBOSEK, JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONDER, MICHAEL J. MCADA, PHYLLIS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REEVES, CHRISTOPHER D. DAVIS, CHARLES R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA ENCODING TRIOL POLYKETIDE SYNTHASE
                      19076CA
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; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: TPKS Protei
US-08-450-332-2
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US-09-323-427-3 x US-08-450-332-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-450-332-2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 908-594-4720 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1247 ..GlnThrThrLeuPheGlnValGluAsnIleThrPheLysProPheSer 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1233 yAspTyrLeuSerGlyAspIleValValPheAspAlaGlu...... 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1175 ValAlaPheGlnThrValIleGlyAla.....TyrSerSerPro..... 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1217 SerGlyCysGluLysValAlaPheAsnThrIleAsnThrTyrAspLysGl 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1200 isValAspArgIleThrLeuValProSerLeuCysLeuAlaThrAlaGlu 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                      1279 yProLeuThrProAspSerLeuLeuAspAsnProGluTyrTrpAlaThrA 1296
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LENGTH: 3038 amino aci
                                                                                                                                                                                                                                                                          370 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC 419
                                                                                                                                                                                                                                                                                                                                                                                335 AAGTTGATCGT......GCATATCGAGTACAATGCTTTTAC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 CAATA..... 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 CAATGGTGTCGAAGGTGAGCCAGAAATTGAATGT.....GGACCAACTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 ATTGCTTTCTGTACACTATTGCATTGTCTTATTCGATTCCGGTTGA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
.....GlnValLeuAlaSerAlaLysGluGlyArg......
                                                     GTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCT 510
                                                                                                                                                              AACTGCT.....TTTCAAACTCAAATTGTCCCGATGCCAGTATGCC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT.. 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTT...CCATTTGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProProAspAlaSerThrAspHisAlaMetPheAlaArgTrpSerTrpGl 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTTTATGTGAAAAGGT......CTTTATGATCAAGAAGGTTGCCGTA 193
                                                                                                                                                                                                                                                                                                                                laGlnAspLysGluAlaIleProIleIleGluArgIleValTyrPheTyr 1312
                                                                                                                                                                                                                    Ile.....ArgSerPheLeuSerGlnLeuThrLeuGluGluArgGl 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....ACAATCAATTTAATACACGTAATGCATTCGAAGGACA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....GlyAspArgArgLeuArgCysLeuTyrValProThrH 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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linear
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38.347
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Gaps: 24
Percent Identity: 19.703
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seq_documentation_block:
    sequence 2, Application US/08637640
    Patent No. 5849541
                                                                                                                            seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-637-640-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1479 nAlaArgGluGlnPheAlaProPheGluAspArgMetValPheGluProL 1496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            733 CGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAAGAACC 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       683 CAACAGATITAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGAT 732
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                                                                                                                                                                                                                                                         CTGCATGTCACCATTT 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                             lyGlnMetValIleLeuGluIleThrHisLysGluHisThrArgLeuGly 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCA 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleLeuGluIle..... 1445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACAACCTGTAATACTT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCTTTGCCAGTTGATTTACGTCAC...CGTGCACTTCTGCAACATAATG 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT 882
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alignment_block:
US-09-323-427-3 x US-08-637-640-2
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/148,132
FILING DATE: 01.NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REGISTRATION NUMBER: 36,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,640
FILING DATE: 23-AUG-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: VINCI, VICTOR A.
APPLICANT: CONDER, MICHAEL.
APPLICANT: MCADA, PHYLLIS C
APPLICANT: REEVES, CHRISTOP
                                                                                                                                                                                                              1175 ValAlaPheGlnThrValIleGlyAla.....TyrSerSerPro.... 1187
                                                         1200 isValAspArgIleThrLeuValProSerLeuCysLeuAlaThrAlaGlu 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: YOURGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: PIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 908-594-6734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                   66 CAATGGTGTCGAAGGTGAGCCAGAAATTGAATGT.....GGACCAACTT 109
                                                                                                                                                                                                                                                  16 ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGA
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STREET: P.O. BOX 2000; 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: Sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
.....ACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 152
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MCADA, PHYLLIS C.
REEVES, CHRISTOPHER D.
DAVIS, CHARLES R.
HENDRICKSON, LEE E.
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0.481
38.347
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Percent Identity: 19.703
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1479	1463 GlyPheAsnSerTyrThrTyrThrAspIleSerThrGlyPhePheGluGl
882	882
	49ThrGlyGlyAlaThrLysTyrValLeuAlaThrProGlnLeu
1448	Garage Composition of the compos
832	TTCGACCACAATGTTCAGAACCACAAGGATTCGGAG
1445	1442 IleLeuGluIle
782	AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC
732 1441	683 CAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGAT::: :::
1426	STYPA
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1393	OHisValArgLeuValGlnArgValGlyGlnHisLeuLeuProThrVal
603	3
w	
1360 603	TGAT
0	511 ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT
1350	1341GlnValLeuAlaSerAlaLysGluGlyArg
510	AACCAGTTCAATTTGCT
1340	420 AACTGCTTTTCAAACTCAAATTGTCCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGAATTGTCCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGAATTGTCCCGATGCCCGATGCCCGATGCCGATGCCCGATGCCGATGCCCATGCCATGCCCATGCCATGCCATGCCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCATG
) N	
419	AAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC :::::: :::: :::::::: ::::::: Arrgsrphafen:sercintenthrienclininthriencli
1312	Tyr
369	GCATATCGAGTACAATGCTTTAC
334 1296	TCATTTCGTTTCATCCATTATTTGTTACCA::::::::: ::::::::::::: :euLeuAspAsnProGluTyrTrpAlaThrA
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240 1262	TTGAT ::: heSer
1246	::::: IleValValPheAspAlaGlu
193	AAGGTCTTTATGATCAAGAAGGTTGCCGTA
1233	1217 SerGlyCysGluLysValAlaPheAsnThrIleAsnThrTyrAspLysGl

	luIleThrHisLysGluHisThrArgLeuGCTGCAGTACAAAATGG	ADDRESSEE: Hamilt CARRESSEE: Hamilt CARREST: Two Milit CITY: Lexington STATE: Massachuse COUNTRY: USA	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC COM OPERATING SYSTEM: PC SOFTWARE: Patentin F	CURRENT APPLICATION DAT APPLICATION NUMBER: FILING DATE: 11-OCT- CLASSIFICATION: 424	PRIOR APPLICATION DATA PRIOR APPLICATION DATA PRIOR APPLICATION DATA	APPLICATION NUMB FILING DATE: 25 ATTORNEY/AGENT INFO	NAME: Granahan, Patrici REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:	TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240 TELEPAX: 617-861-9540 INFORMATION FOR SED ID NO: 12:	
512 Tvr2soLeuTleTle2laSer2s0ValLueH(s2laTbr0r0rso 152		1019 GACAACCTGTAATACTT	1019 GACAACCTGTAATACTT	1019 GACAACCTGTANTACTT	1019 GACAACCTGTAATACTT	1019 GACAACCTGTAATACTT	1019 GACAACCTGTANTACTT	1019 GACAACCTGTAATACTT	
512 TyrAspLeuileileAlaSerAsnValLeuHisAlaThrProAsp		eq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-540-804-12 eq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Young, Richard A. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. TITLE OF INVENTION: No. 5919666el Factors which Modify Ge TITLE OF INVENTION: Transcription and Methods of Use Ther NUMBER OF SEQUENCES: 39	eq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-540-804-12 eq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Koleske, Anthony J. APPLICANT: Chao, David M. TITLE OF INVENTION: No. 5919666el Factors Which Modify Ge TITLE OF INVENTION: Transcription and Methods of Use Ther NUMBER OF SEQUENCES: 39 CORRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173	eq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-540-804-12 eq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Koleske, Anthony J. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. APPLICANT: Chao, David M. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. APPLICANT: Chao, David M. APPLICANT: WENTION: No. 5919666el Factors Which Modify Ge TITLE OF INVENTION: Transcription and Methods of Use Ther INVENTION: Transcription and Methods of Use Ther OUNBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-POS SOFTWARE: Patentin Release #1.0, Version #1.30	eq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-540-804-12 eq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Koleske, Anthony J. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. APPLICANT: Two Militla Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION: 424 CRACE APPLICATION 1424	eq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-540-804-12 eq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Koleske, Anthony J. APPLICANT: Koleske, Anthony J. APPLICANT: Chao, David M. TITLE OF INVENTION: No. 5919666el Factors Which Modify Ge TITLE OF INVENTION: Transcription and Methods of Use Ther NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: O21/3 ZIP: O21/3 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION NUMBER: US 08/521,872 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION DATA:	eq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-540-804-12 eq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Koleske, Anthony J. APPLICANT: Choo, David M. TITLE OF INVENTION: No. 5919666el Factors Which Modify Ge TITLE OF INVENTION: Transcription and Methods of Use Ther NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION UNMBER: US/08/540,804 PRIOR APPLICATION UNMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 11-OCT-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 12-AUG-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 12-AUG-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 11-OCT-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 17-OCT-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 17-OCT-1995 PRIOR APPLICATION NUMBER: US 08/521,872	eq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-540-804-12 eq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 Patent No. 5919666el Factors which Modify Ge TITLE OF INVENTION: No. 5919666el Factors which Modify Ge TITLE OF INVENTION: No. 5919666el Factors which Modify Ge TITLE OF INVENTION: No. 5919666el Factors which Modify Ge TITLE OF INVENTION: No. 5919666el Factors which Modify Ge TITLE OF INVENTION: No. 5919666el Factors which Modify Ge TITLE OF INVENTION: No. 5919666el Factors which Modify Ge TITLE OF INVENTION: 180. APPLICATION MILITIA DITIVE CORRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER: BIM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION DATA: APPLICATION NUMBER: US/08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION NUMBER: US 08/521,872 PRIOR APPLICATION NUMBER: US 08/521,872 REFERENCE/DOCKET NUMBER: WH194-03A2	
512 TyrAspLeuIleIleAlaSerAsnValLeuHisAlaThrProAsp	056 CTGCATGTCACCATTT 1071 ::: 575 gCysThrGluProPhe 1580	eq_documentation_block: Sequence 12, Application US/08540804 Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Koleske, Anthony J. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. TITLE OF INVENTION: No. 5919666el Factors which modify Ge TITLE OF INVENTION: Transcription and Methods of Use Ther NUMBER OF SEQUENCES: 39	<pre>leq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. APPLICANT: Chao, David M. TITLE OF INVENTION: Transcription and Methods of Use Ther NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173</pre>	leq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Young, Richard A. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, David M. APPLICANT: Thompson, Craig M. APPLICANT: No. 5919666el Factors Which Modify Ge TITLE OF INVENTION: Transcription and Methods of Use Ther NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COMPUTER: Massachusetts COMPUTER READABLE FORN: MEDIUM TYPE: Flappy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30	peq_documentation_block: Sequence 12, Application US/08540804 Patent No. 591966; GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Young, Richard A. APPLICANT: Thompson, Craig M. APPLICANTION: Transcription and Methods of Use Ther CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STATE: Massachusetts COUNTRY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER: Edsachusetts COUNTRY: ISA COMPUTER: ABM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/540,804 FILING DATE: 1-OCT-1995 CLASSIFICATION: 424 CRACKET AND	peq_documentation_block: Sequence 12, Application US/08540804 Patent No. 591966 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Young, Richard A. APPLICANT: Thompson, Craig M. APPLICANT: No. 5919666el Factors Which Modify Ge TITLE OF INVENTION: Transcription and Methods of Use Ther NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US.08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION NUMBER: US.08/521,872 PRIOR APPLICATION NUMBER: US.08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION DATA:	leq_documentation_block: Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Young, Richard A. APPLICANT: Chao, David M. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. APPLICANT: No. 5919666el Factors Which Modify Ge TITLE OF INVENTION: Transcription and Methods of Use Ther NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COUNTRY: USA ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: DBATE: 11-OCT-1995 CURRENT APPLICATION DATA: APPLICATION NUMBER: US 08/521,872 FILING DATE: 11-OCT-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 25-MAR-1994 ATTORNEY/ACENT INFORMATION I	peq_documentation_block: Sequence 12, Application US/08540804 Patent No. 591966 GENERAL INFORMATION: APPLICANT: Young, Richard A. APPLICANT: Chao, David M. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. APPLICANT: Thompson, Craig M. APPLICANT: Chao, David M. APPLICANT: Chao, David M. APPLICANT: USA DISCRES: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militla Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIE: O2173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION DATA: APPLICATION NUMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION UNBER: US 08/521,872 FILING DATE: 25-MAR-1994 ATTORNEY/AGENT INFORMATION: NAME: Granahan, Patricla REGISTRATION NUMBER: 32,227 REFERENCE/DOCKET NUMBER: 33,227 REFERENCE/DOCKET NUMBER: WH194-03A2	to
1512 TyrAspLeuIleIleAlaSerAsnValLeuHisAlaThrProAsp	1056 CTGCATGTCACCATTT 1071 ::: 1575 gCysThrGluProPhe 1580 	CCXXEUTCNUENCE AUUXE	ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. STREET: Two Milita Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173	ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30	ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC POSS/MS-POS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION: 424	ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION LATA: APPLICATION NUMBER: US 08/521,872 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION DATA:	ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION DATA: APPLICATION NUMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION UMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION NUMBER: US 08/218,265 APPLICATION NUMBER: US 08/218,265 FILING DATE: 25-MAR-1994 ATTORNEY/AGENT INFORMATION:	ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION UMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION DATA: APPLICATION UMBER: US 08/521,872 FILING DATE: 25-MAR-1994 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: US 08/218,265 FILING DATE: 25-MAR-1994 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: US 08/218,265	

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; LENGTH: 1226 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-540-804-12
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Quality: 85.50
Ratio: 0.457
Percent Similarity: 47.949
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560 eIleTyrLysLysValLeuLysGluLysAspValProAlaTyrAsnValT 577
                                                                                                         545
                                                                                                                                       521 AGCCAGTTTATCATAAATGGACATGCGATTCTG...AAACCGTTGATA.. 565
                                                                                                                                                                                                          528 luSerLeuGluAlaLeuMetAspIleLeuLeuCysTyrGlnLysLeuPhe 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 AAGGTCTTTATGATCAAG...AAGGTTGCCGTAATGATGATGAAGGTGGACGT 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 AACAATCAATTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 MetMetProSerLeuTyrArgLeuLeuAsnIleLeuIleThrTyrGlyIl 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT 63
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                                                                                                                                                                                                                                                                                                                                                                       GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAAATCACAACTGCTTTTC.....AAACTCAAATTGTCCCGATGCCA 453
                                                   ......CTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGA 602
                                                                                                         SerGlnPhe...IleAsnAspHisIleLeuPheThrLysThrPheIlePh
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Gaps: 13
Percent Identity: 19.744
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ORMATION:	ORNEY/AGENT INFORMAT	
NUMBER: US/08/218,265 25-MAR-1994 ON: 435	CATION NUMBER: G DATE: 25-MAR- TEICATION: 435	
entin Release #1.0, ON DATA:	Patentin	
PC compatible	MEDIUM TYPE: Floppy COMPUTER: IBM PC CO	
LF FORM	OUNTRY: US IP: 02173 PHTER READARLE FORM	
Militia Drive	: Two Militia Lexington MA	
:: 35	UMBER OF SEQUENCES: 3 ORRESPONDENCE ADDRESS:	
n, Craig M No. 5922 Transcri	PLICANT: Thompson, C TLE OF INVENTION: NC	
Richa , Ant	GENERAL INFORMATION: APPLICANT: Young, Ric APPLICANT: Koleske, A	
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otodata/1/1aa/5B_COMB.pep:US-08-218-265-12	ta/1/	S
PAATCAAGCTT 976 ::: elleArgLeu 733	ATCAAGCT ::: leargLe	
TCATTGATGTACGAACTGATATCAACACCCTTGAAAT 956 ::: ::: :::: LysLeuLeuThrPheGluValThrGlnAsnValLeuGlyL 727	TCATTG ysLeuLeu	
PACTCAAGAAAGATCTGCAGAACCGGAGAATA	CAAG :: ysar	
PAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGC 877	8 CGGAGCTGTTAAAAC <i>i</i> :: ::: 7 snValMetLeuLeuI]	
	spThrAs	
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CACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCA 752	CGTATA YSThrG	
GCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC	PASNAS	
<pre>IGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTG 652 :: :: </pre>	ATACTGTG ::: ProPheTr	

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alignment_block:
US-09-323-427-3 x US-08-218-265-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-218-265-12
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TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
FRUGTH: 1226 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-218-265-12 from: 1 to: 1226
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  545
                                        521 AGCCAGTTTATCATAAATGGACATGCGATTCTG...AAACCGTTGATA..
                                                                                                 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 nLeuSerLysThrProLeuSerIleLysIleMetValAlaGluTrpTyrL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 ThrGluGlnIleLysMetArgIleLeuSerAsnAspIleThrAsnLeuGl 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 yrAspValLysPheTyrGluIlePheAsnPheAspGlnLeuValGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 ACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTG......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 ValGlnLeuLeuIleAsnLeuLysIleSerProLeuMetLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 AAGGTCTTTATGATCAAG...AAGGTTGCCGTAATGATGAAGGTGGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 AACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 eIleLysValProThrTyrIleArgLysLeuIle......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 MetMetProSerLeuTyrArgLeuLeuAsnIleLeuIleThrTyrGlyIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAAT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                    CTGAAATCACAACTGCTTTTC.....AAACTCAAATTGTCCCGATGCCA
                                                                                                                                                                                                                                           GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA
                                                                                                                                                                                                                                                                                           lll||
lentysIlePheLysIlePheCysIleAspLeuGluValPheHisHisPh
                                                                                                                                                                                             ePheLysTrpIleGluPheIleValTyrHisGlnLeuLeuSerAspIleG
                                                                                            luSerLeuGluAlaLeuMetAspIleLeuLeuCysTyrGlnLysLeuPhe
                                                                                                                                          ATTTGCTA.....TCATTGGTC
                                                                                                                                                                                                                                                                                                                                                                                          euSerHisLeuCysSerGlyIleLeuSerSerValAsnArgThrValLeu 494
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SerGlnPhe...IleAsnAspHisIleLeuPheThrLysThrPheIlePh
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5736139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,60
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOSITION
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           660 rGluIleIleAspThrAsnThrSerLysGlnPheGlnLysAlaArgAsnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            644 AsnPheProGluValPheGlnValAsnIleArgPheLeuLeuHisAsnSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                594 LeuLysValAspAsnAspLeuArgIleGluLeuGlnSerValTyrAsnAs
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FILING DATE:
                                                                                                                                                                                                 ZIP: 94104
                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                          CITY: SAN FRANCISCO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ysValTyrSerMetIleAsnAsnSerAsnGlnAlaValGlyGlnThrTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6, Application US/08480604A
                                                                                                                                                                                                                                                     CALIFORNIA
                                                                                                                                                                                                                        UNITED STATES OF AMERICA
07-JUN-1995
                       US/08/480,604A
                                                                         Version
                                                                         #
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:

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alignment_block:
US-09-323-427-3 x US-08-480-604A-6
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; MOLECULE TYPE:
US-08-480-604A-6
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-480-604A-6 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/429
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:

NAME: INGOLIA, DIANE E.

REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD
TELECOMMUNICATION INFORMATION:
TELECHENCE: (415) 705-8410
TELECHENCE: (415) 705-8328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/985,321
FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         213
                         829 GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 878
                                                                                    248 GlnGluLeuLeuAsnIleTyrSerGlnGluLeuLeuAsnArgGlyAsnLe
                                                                                                                                                                           232 snSerAsnHisGlyIleAspIleArgAlaAsnSerLeuPhe...ThrGlu
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                                                                                                                                                                                                                                                                                                             679 TATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC 728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 TyrTyrLysSerGlnIleAsnLysProThrValProThrIleAspAspIl 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT 578
264 uAlaAlaAlaSerAspIleVal.....ArgLeuLeuAlaLeuLysA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/329,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/422,711 FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                    AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC
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31-OCT-1989
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0.825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPHD-01763
                                                                                                                                                                                                                                                                  .....Lys.IleA
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                            TELEFAX: (415) 397-83 INFORMATION FOR SEQ ID NO:
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 01
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL, LI
STREET: 220 MONTGOMERY STREET,
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WILLIAMS, TITLE OF INVENTION: V
                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION UNBER: US 08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 AspLeuPheLysThrIleSerArgProSerSerIleGlyLeuAspArgTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879
                      TOPOLOGY:
                                                                                                                                                                                                                         NAME: INGOLIA, DIANI REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10 CLASSIFICATION:
                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \verb|snTyrThrSerGluAsnPheAspLysLeuAspGlnGlnLeuLysAspAsn|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \verb|pGluMetIleLysLeuGluAlaIleMetLysTyrLysLysTyrIleAsnA|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTTC.....GTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCA 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94104
                                           amino acid
                                                                                                                                                                                                                                           INGOLIA, DIANE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                       (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-1995
                                                                                                                                     397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VACCINE FOR CLOSTRIDIUM BOTULINUM NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JAMES A.
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                                                                                                                                                                                                                                                                                                                                                                            US 07/985,321
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seq_documentation_block:
; Sequence 65, Applicati
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   Quality:
                                                                                                                                                                                                                                                                   seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
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                                                                                                                                                                                     Patent No.
                                                                                                                                                                  GENERAL INFORMATION:
                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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      APPLICANT: APPLICANT:
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                                            APPLICANT:
                                                                                                                                                                                                                                                                                                            345 PheLysLeuIleIleGluSerLysSerGluLysSer 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 GlnGluLeuLeuAsnIleTyrSerGlnGluLeuLeuAsnArgGlyAsnLe
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                                                                                                                                                                                                                                                                                                                                                                                     {\tt snTyrThrSerGluAsnPheAspLysLeuAspGlnGlnLeuLysAspAsn}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pGluMetIleLysLeuGluAlaIleMetLysTyrLysLysTyrIleAsnA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGATGTACGAACTGATATCAACACCC............
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....TTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATT.... 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTTC......GTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCA 922
                                                                                                                                                                                                                                                                                                                                                                                                                                ..TACGTCACCGTGCACTTC......TGCAACATAATGGACAAC 1024
                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-65
                                                                                                                                                                                     5, Application US/08325071 5587311
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KEMP, David Harold
SRISKANTHA, Alagacone
RIDING, George Alfred
RAND, Keith No. 5587311man
                                                                                WILLADSEN, Peter
                                                                                            MOORE, Joanna Terry
JOHNSON, Law Anthony York
                                                                                                                                         COBON, Stewart Gary
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0.825
52.551
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Gaps: 9
Percent Identity: 22.449
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alignment_block:
US-09-323-427-3 x US-08-325-071-65
                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-325-071-65
                                                                                                                                 Align seg 1/1 to: US-08-325-071-65
                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                             SEQUENCE CHARACTERISTICS: LENGTH: 620 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-UL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 08/062,109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DN
TITLE OF INVENTION: G1:
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                 138 TGCATTCGAAGGACATGT.....TTATG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
133 sGluLysAsnLeuLeuGlnArgAsp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELL: ZV-
TELEFAX: ZV-
TEX: 904136
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                    Quality:
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                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Foley & Lardner 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                      620 amino acids
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0.575
40.669
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Percent Identity:
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                                                                                                                                   from: 1
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22
21.448
   .SerA 143
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963	GAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTACCCA	2
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912		386
388		371
885	ACTTCGT	379
371	::: }::: :::IleLysAlaArgLeuIleAlaGluLysProLeuSerLysTyrVa	357
878	GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA	829
356	alPheLysValGluIleLeuAsnCysThrGlnAsp	345
828	AACCAAATAGCGAATGTTTCGACCACAATGTTCAGAACCACAAGGATTC	779
778 345	GATCACTACACCTTTCTATCAATGCCAGATCAGTATTACCATTAAAG [330
330	PheAspSerAspHisCysLysArgTyrGl	321
728	TATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC ::: ::	679
320		304
678	GTGCTCTTGATAAATATTTGCTAAATAATTTGGAA	644
304	PLYSSerArgLysProGlyProAsnValAsnIleAsnGluC	290
7 7 7	Fuemerashrizariy.variyimerashariqothashriysiyiriyserori	} ;
606	TTTGTCGATGATGGT	592
273	ysCysIleSerAspCysValAspLysLysCysHisGluGlu	260
591	CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC	542
260	nGln	253
541	TCAACCAGTTCAATTTGCTATCATTAGTCAGCCAGTTTATCATAAATGGA	492
253	GluAspCysArgValGlnLysGlyThrValLeuCysGluCysProTrpAs	237
491	CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGG	451
236	:: ::: erTyrThrValSerCysThrValGluGlnLysGlnThrCysArgProThr	220
450	AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG	404
403 220	163 CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG 40 	363 203
203	alCysLysHisGlyCys.ArgSerThrAspLysAlaTyrGluCysThrCy	187
362	TTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG	313
187	<pre>yProAspGlyGlnCysLysAsnAlaCysArgThrLysGluAlaGlyPheV</pre>	170
312	AACAACTGTTGTCATTTCG	294
170	ProProAlaAspSerTyrCysSerProGlySerProLysGl	157
293	ACGATCTCTGAATCCACGTGGTATTTTTGTAAC	261
156	:::::::::::::::::::::::::::::::::::	143
260	CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC	211

- ||||||::: ||| 405 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 421

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pir2:S42841
pir2:A29959
pir1:D54689
pir2:A37052
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pir2:I57940
pir2:F71606
pir2:I51703
pir1:URHUAP
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pir2:S27799
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pir2:S38673
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pir2:S65074
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-Q=/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19903/app_query.fasta.1
-Q=/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19903/app_query.fasta.1
-DB=PIR_62 -QFMT=fastan -SUFFIX=backtrans.rpr -GAPOP=12.000
-GAPEXT=4.000 -MINATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPOEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MARIX=blosumG2
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
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DNA mismatch repair protein
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                                                                                          dynein gamma heavy chain, oute hypothetical 38.5K protein (fts
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A; Residues: 1-423 <SEB>
A; Cross-references: GB:M55997
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cuticle protein cut-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
C;Accession: A49772
R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P.
Dev. Biol. 146, 519-530, 1991
A;Title: cut-1 a Caenorhabditis elegans gene coding for a dauer-specific nor A:Reference number: A49772; MUID:91323673
A;Accession: A49772
A;Status: preliminary; not compared with conceptual translation
A:Accession: A49772
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|TyrAspGlnAlaGlyCysArgSerAspGluGlyGlyArgGlnValAlaGl
TIGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA 521
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    C:Species: Caenorhabditis elegans
    C;Date: 17-Apr-1993 #sequence_revision 17-Apr-199
    C;Accession: S27799
    R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P.
    submitted to the EMBL Data Library, July 1991
    A;Reference number: S27799
    A;Accession: S27799
    A;Accession: S27799
    A;Molecule type: DNA
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ibrary, July 1991
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A;Cross-references: EMBL:M55997; NID:g156271; PID:g156272 C:Genetics: A;Gene: CUT-1 A;Introns: 245/3
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Percent Similarity:
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alignment_block:
US-09-323-427-3 x S17855
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C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolog
C;Keywords: oxidoreductase
F;131-342/Domain: peptidylglycine monooxygenase I homology <PGM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptidylglycine monooxygenase (EC 1.14.17.3) - African clawed frog
N;Alternate names: peptidylhydroxyglycine N-C lyase
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: S17855
R;Iwasaki, Y; Kawahara, T.; Shimoi, H.; Suzuki, K.; Ghisalba, O.; Kangawa, K.; Matsuo,
Eur. J. Biochem. 201, 551-559, 1991
A;Title: Purification and cDNA cloning of Xenopus laevis skin peptidylhydroxyglycine N-C
A;Reference number: S17855; MUID:92037609
A;Accession: S17855
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Quality:
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A;Molecule type: mRNA
A;Residues: 1-935 <IWA>
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Percent Similarity:
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                                               563 nTrpGlyGluGluThrSerSerAsnValProArgProGlyGlnPheArgI 580
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1077 CTCAAT :: 823 lSerPh	1027 GTAAT 807 ValSe	977 TGCCAG 790 lyVals	936 TGATA : : 773 aGlyV	904 GCA 757 AlaG1	854 CAGCA :: 742 alGlu	804 ACAAT ::: 725 rGluI	766ATT 709 HisArg	725 ATGCGG 692 lyAspA	675 GGAATA :::: 675 eAspMe	631 AATGC	581 TCCAT ::: 652 alGln	531 TCATA 646 r	481 GGACC 635 Gly	431 AAACTC :::: 628 laValS	384 AACAGT : 612 nPheVa	334 AAAGT 597 Aspar	580 lePro
GTTTATGGGTT : ::: eValLeuIleI	ACTTGCTGCAGTACAAAAT ::: rThrGlnGluLysGlnSer	TTGATTTACGTCAC ::: erThrGlnGluLys	ATCAACACCCTTGAA ::: ValProThrGlnGluLys	GAACCG yValSerThrGlnGluLys	CAAAACCTGCTGCAGCTGCGCAAC ::: LuLysGlnThrGlnGluLysGlnG	GTTCAGAACCACAAGGA ::: lePheGluThrHisIle	TACCATTAAAGAACCAAA :::::: ::: :gSerValLysLysAlaGl	GATCGATCACAGCTTTTC :::::::: AlaHisAlaAsnAlaVal	ATCCAACAGATTTAATGG	AATGCTGATGGATGTGCTCTTG	TCCTGCTTTGTCGATGAT::::::::::::::::::::::	AAATGGACATGCGATTCTG	AACCGGTCAACCAGTTC	CAAATTGTCCCGATGCC::: : c::	TTAGTGCACAGATTGAG ::: ::: alLysGlnIleLys	TTGATCGTGCATATCGAC :::::::: rgGluAsnGlyArg:	::: ::: ProHisSerLeuThrMetVa
ATTGCATTGATT ::: :: LeuLeuIleIlePro	rGGAATCTGCATGT : :: :ValvalGlnGlus	CGTGCACTTCTGCAACATA ::::::::::: :::: GlnSerValValGlnGluS	ATTAGCGATG	GAGAATATCATT. ::: ::::: GlnAsnValValo	TTCGTTT ::: lnLys	GGATTCGGAGCTGTTAAAACAG ::: : IleArgSerArgProLysThr <i>A</i>	TAGCGA : ::: yIleGluValGluGl	TATCAATGCCAGAT :::::: TrpLysPheSerPr	GGCTGGCCAAGAAGCTC. :::::::::: aAlaAlaAspAspGlyT	GATAAATATTTG AspThrPheIleProAl	GGTAACGGTGAT ::: SerAsnGlyAsp	rgaaaccgttgatacttt :: glyty	AATTTGCTATCATTC ::: ::: euTyrAlaValAsnc	CAGTATGCCGTTATGAA	GTATCTGAAATCA ::: ::: HisGlnGluPheGlyA	TATCGAGTACAATGCTTTTACATGGAAGC	::: lProAspGlnG
GCTGCCGTCATTA ::: IleAlaValLeuI	CACCATTTGGCTT 	PAATGGACAACCT SerSerAlaGly	BATAATCAAGCTT :::::::: SluSerSerAlaG	::::::::::::::::::::::::::::::::::::::	ACTCAAGAAAAGATCT ::: ::: GlnLysAsnSer	\CAGGTGGTGCCG ::: :::: hrAsnGluSerV	AATGTGTTCGACC :::::: LulleThrGluTh	CAGT coSerLysAlaGlu	CACGTATACAAAT hrValTyrValG	CTAAATAATTT ::: :: laArgLysAsnPh	ACTGTGGAAATTCTA	PTCTGCGCGGTTG ::: 	GTCAGCCAGTTTA ::: LyLysProTyrTy	AATTTTGGATGGT	ACAACTGCTTTTC ::: ArgGluValPheA	rGGAAGCTGATAA ::: aGluThrGlyAs	::: lyGlnLeuCysValAla
1123 840	1076 823	1026 806	976 790	935 773	903 756	853 742	803 725	765 708	724 692	674 675	630 663	580 652	530 646	480 634	430 628	383 612	596

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C:Accession: A40970
R:Just, M.; Herbst, H.; Hunmel, M.; Duerkop, H.; Tripler, D.; Stein, H.; Schuppan, D.
J. Biol. Chem. 266, 17326-17332, 1991
A:Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular management of the fibronectin type III repeat homology (Finascin family of extracellular management of the fibronectin type III repeat homology (Finascin fibronectin fibronectin type III repeat homology (Finascin fibronectin fibronectin type III repeat homology (Finascin fibronectin fibrone
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366
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                                                                                    440 TTGTCCCGATG......CCAGTATGCCGTTATGAAATTTTGGATGGT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 CATTCGAAGGACATGTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           840 leAlaIleAlaIlePheIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 ProLeuThrGluGlyLeuAlaGlyAspGluLysGluMetLysIleGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uThrHisThrAspIleGluLeuSerGlyLeuLeuProAsnThr.....
euThrProLeuThrGluTyrThrIleAlaIlePheSerIleTyrAspGlu
                                                                                                                                                                                 uIleAsnGluValGluValAspProIleThrThrPheProLeuLysGlyL 406
                                                                                                                                                                                                                                                                      TAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAA 439
                                                                                                                                                                                                                                                                                                                                                               IleAsnGlyTyrArgIle.....ValTyrAsnAsnAlaAspGlyThrGl 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGTTGACAATGGTGTCGAAGGT...GAGCCAGAAATTGAATGTGGACC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspProValThrGlyGlnGluThrThrLeuAlaLeuSerProPro...Ar 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTAATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....GluTyrThrValThrValTyrAlaMetPheGlyGluGluAlaSer 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
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6
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0.578
53.086
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Percent Identity:
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19
22.222
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A; Molecule type: mRNA
A; Residues: 12139-121167, 'T', 12169-13288 <EC3>
A; Cross-references: GB: M61883; NID: 9454837; PID: 9
R; Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.;
J. Biol. Chem. 263, 1081-1088, 1988
                                                                                                                                                                                            R;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L. J. Biol. Chem. 266, 9678-9686, 1991
A;Title: Porcine submaxillary mucin contains a cystine-rich, carboxyl-terminal domain A;Reference number: A40009; MUID:91236743
A;Accession: A40009
                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-13288 <ECK>
A;Cross-references: EMBL:AF005273; NID:g2581863; PID:g2581864
A;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 272, 33204-33210, 1997
A;Title: The complete cDNA sequence and structural polymorphism A;Reference number: Z14839; MUID:98070526
A;Accession: T03099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Sep-1999
C;Accession: T03099; A40009; A268528; B29789
R;Eckhardt, A.E.; Timpte, C.S.; DeLuca, A.W.; Hill, R.L.
J. Biol. Chem. 272, 33204-33210, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
mucin, submaxillary - pig
   A; Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N; Alternate names: apomucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:T03099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  909 ACCGGAGAATATCATTGATG 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 hrIleValPro...ThrThrSerValThrSerValPheGlnThrGlyIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552 ArgAsn.............LeuValValGlyAspGluTh
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Porcine submaxillary gland apomucin contains tandemly repeated, identical se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt rThrSerSerLeuArgValLysTrpAspIleSerAspSerAspValGlnG}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAA 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGTATTACCATTAAAGAACCAAATAGCGAATGTTCGACCACAATGTT
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                                                                                            PID:g164374
                                                                    Hill, R.L.
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A;Cross-references: GB:J03512
A;Experimental source: submaxillary gland
A;Experimental source: submaxillary gland
R;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson Jr.,
J. Biol. Chem. 262, 11339-11344, 1987
A;Tittle: Structural properties of porcine submaxillary gland apomucin.
A;Reference number: A92606; MUID:87280230
A;Accession: B29789
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C;Keywords: tandem repeat
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A; Residues: 12139-12167, T, 12169-12641 <TIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13124 AspThrCysCysGluIle......GlyHisCysGluLysArgThrCy 13137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 AAAACAGTTAGTGCACAGATTGAGGTATCTGAA...ATCACAACTGCTTT 428
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| sThrCysThrGluAlaLysThrValAspCysLysProLysGluCysProS 13107
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                                                                             s...GlnAsnThrGlyPheThrAlaValValGlnAsnCysProLysGlnT 13178
                                                                                                                                   TTCAGAACCACAAGGATTCGGAGCTGTTAA.....
                                                                                                                                                                                   ValGlySerSerPheAspAspProAsnAsnProCysValThrTyrSerCy 13162
                                                                                                                                                                                                                                      ATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATG 809
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40.724
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Gaps: 12
Percent Identity: 23.982
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                             ....AGCAAAACCTGCTGC...
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        =
                                                                                                                                                                                                                                                                                    ....AACA 843
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A; Residues: 1-875 <OHS>
A; Cross-references: GB:M20191
A; Experimental source: skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: URXLA2 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
584 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
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                                                  ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
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0.945
43.103
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6
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C;Accession: A27715
R;Ohsuye, K.; Kitano, K.; Wada, Y.; Fuchimura, K.; Tanaka, S.; Mizuno, K.; Matsuo, Biochem. Biophys. Res. Commun. 150, 1275-1281, 1988
A;Title: Cloning of cDNA encoding a new peptide C-terminal alpha-amidating enzyme h A;Reference number: A27715; MUID:88134244
A;Accession: A27715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:40-385/Product: peptidylglycine monooxygenase II *status predicted <MAT> F:133-344/Domain: peptidylglycine monooxygenase I homology <PGM> F:133-944/Domain: transmembrane *status predicted <TMN> F:764-787/Domain: transmembrane *status predicted <TMN> *status predicted <PMN> *status predicted <PMN> *status predicted <PMN> *status predicted <PMN *status predicted <P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of p le and dismutates to 91yoxyLate and the corresponding desglycine peptide alpha-amide. hormones. The other enzyme is peptidyl alpha-amidating enzyme I.
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homo C;Keywords: copper; 91ycoprotein; monooxygenase; oxidoreductase; transmembrane protein; 1-24/Domain: signal sequence #status predicted <SIG>
F;24-39/Domain: propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptidylglycine monooxygenase (EC 1.14.17.3) II precursor - African clawed frog N;Alternate names: C-terminal alpha-amidating enzyme II (AE-II); peptidyl alpha-amida C;Species: Xenopus laevis (African clawed frog) C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Jun-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             530 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 246
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hav

600

GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC

377

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Experimental source: SMBL:U00065; NID:g495681; PID:g495684; PIDN:AAA50735.1; CESP:D1044.
A;Experimental source: Strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Pauley, A.
submitted to the EMBL Data Library, June 1994
submitted to the sequence of C. elegans cosmid D1044
A;Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein D1044.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15881
                                                                                                                                                                                                                                                               alignment_block:
US-09-323-427-3 x T15881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:D1044.3
A:Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2;
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A; Accession: T15881
                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                        Align seg 1/1
1165 nAsnTyrArgLeuValTyrGlyTyrCysValProIleThrSerSerIleC
                                                                                                 1149 GlnCysIleAspAsnSerValCysMetAsnGlnMetCysThrCysAsnAs
                                              296 CAAC......TGTTGTCATTTCGTTTCATCCATTATTT
                                                                                                                                                     246 CAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632 laValSerTyrAlaPro.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG 580
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Identity:
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DNA mismatch repair protein (mutL) homolog - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Date: 13.-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Jun-1998 C; Accession: C70126 C; Accession: C70126 C; Catheren C. M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997 A; Authors: Smith, H.O.; Venter, J.C. A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A; Reference number: A70100; MUID:98065943 A; Accession: C70126
                                                                                                                                                                                                                                                   A; Status, Francis DNA
A; Molecule type: DNA
A; Residues: 1-610 <KLE>
A; Cross-references: GB: AE001131; (
A; Cross-references: GB: AE001131; (
alignment_block:
US-09-323-427-3 x C70126
                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: pir2:C70126
                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1307
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                                                                                                                                          Quality:
                                                                                                                Ratio:
                                                                                   93.50
0.519
46.272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 AGCCAGAAATTGAA.....TGTGGACCAACTTCAATAACAATCAAT 123
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                                                                                               ATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCA......
                                                                                                                                                                              ACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCG
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                                                                                                                                                                                                                                                                                                                                          TTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProIleAspGlnLysAspLeuLeu........GluAlaIleThrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              etCysLeuLys.....ValLeuGluGluLysIleIleThrHisProGlu
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                                                                                                                                       sPro......GlnLysLysGluValArgPheTyrAsn......
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R;Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V. submitted to the EMBL Data Library, October 1995
A;Reference number: 217300
A;Accession: T11616
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2244 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-323-427-3 x Tl1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: SPAC22G7.06c
C; Keywords: ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z54328; NID:g1009451; PID:g1009456 A;Experimental source: strain 972h(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T11616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) - fission yeast
C;Species: Schlzosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: T11616 from: 1
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Percent Similarity:
                                                                                                                                                                                           1012
405
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                                                                                                                                                                                                                                124 TTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         958 AGCGATGATAATCAA......989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 luMetThrAsn.....Gln..ProGluAsnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316
                                            256 CGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGT 305
                                                                                        lyValTyrArgIleGlySerSerValGluPheAspTrpCysAlaValArg 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A...CGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTG 1036
                                                                                                                                                                                    .....AsnAspLysGlyValMetValLeuGlySerG
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Gaps: 17
Percent Identity: 20.274
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1048 AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGT 1092
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                                                                                                                                                                                                                                                                                                      1282 eGlnPheIleAlaLysAspAsnGluIleLysValIleGluCysAsnValA 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151 rPheAspGlu...AlaAspLysPheCys............................ 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1216 IleGluLeuAspAlaValAlaArgGluGlyLysMetValMetHisValIl 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1171 SerTyrValLeuSerGlyAlaAlaMetAsnThrValTyrSerGlnSerAs 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1085 GluGlnGluSerSerGlyIleIleIleAlaMetGlyGlyGlnThrAl 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1266 AlaAlaAlaLysIleGlyGluAlaLeuAsnIleThrGlyProTyrAsnIl 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1249 alLeuProProGlnAspLeuAlaProThrThrIleGluArgIleValAsp 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1204 alValIleSerLysTyrIleGluAsnAlaLys...............Glu 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1118 hrSerProGluMetIleAspGlyAlaGluAsnArgPheLysPheSerArg 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1101 aAsnAsnTleAlaLeuProLeuHisArgGluAsnValLysIleLeuGlyT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         715 ....GTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                640 GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 CGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 CCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATG 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCA.... 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pLeuHisSerTyrLeuGlnGlnAlaValAlaIleAsnLysAspHisProV 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGATGATGGTAACGGTGATACTGTG.....GAAATTCTAAATGCTGAT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetLeuAspAspIleGlyValAspGlnProLysTrpLysGluLeuThrSe 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATT.. 441
...GlyValAspMetIleSerMetAlaThrAspValIleMetGly 1325
                                                                                                                                                                                                                            GTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAA 1047
                                                                                                                                                                                                                                                                                                                                                                                 CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACAC 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eSerGluHisValGluAsnAlaGlyValHisSerGlyAspAlaThrLeuV 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTA.............ATGGCTGGCCAAGAAGCTCAC.... 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rgLeuTyr...PheGluAsnIleGlyLeuGluThrValLeuAspIleTyr 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTTCGTTTCATCCATTATTTGTTACC.....AAAGTTGATC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....GCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAA 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .SerArgSerPheProPheValSerLysValIle...
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C;Accession: A36054
R;Bhargava, A.K.; Woitach, J.T.; Davidson, E.A.; Bhavanandan, V.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 6798-6802, 1990
A;Title: Cloning and cDNA sequence of a bovine submaxillary gland mucin-like protein A;Reference number: A36054; MUID:90370871
A;Accession: A36054
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-563 <BHA>
A;Cross-references: GB:M36192; NID:g163400; PID:g163401
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US-09-323-427-3 x A36054
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C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 IleGlnThrGlyIleThrGlyThrGlySer.......GlyThrThrSe
518 GTCAGCCAGTTTATCATAAATGGACATGC...GATTCTGAAACCGTTGAT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 LysGluAlaSerGluThrThrThrGlyProGlyIleSerThrThrGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 alSerGlyArgValThrGlyValSerGluSerSerSerProGlyThrSer 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 rSerThrGlyValGlyArgGln.....ThrSerThrAlaValV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 ThrThrVal......IlePro...GluSerSerAsnThrGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homolog -
                                                  ......GlyProLeuGlyGluLysLysSerProGlyAspIleT
                                                                                                             AATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTG
                                                                                                                                                               LysThrGlyCysThrThrSerLeuProProProProAlaCysTyr....
                                                                                                                                                                                                                       ACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGA
                                                                                                                                                                                                                                                                               yrProGluThrThrValValAlaThrGlyGluGlnGlu...ThrGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AAAGTTGATCGTGCATATCGAGTACAATGCTTTT 367
                                                                                                                                                                                                                                                                                                                                       ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATC
                                                                                                                                                                                                                                                                                                                                                                                                  rThrSerLysSerAsnArgIleThrThrSerSerArgIlePro....T
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0.612
42.609
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Gaps: 18
Percent Identity: 20.290
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A;Genome: plastid
A;Note: this apparently degenerate plastid is referred to as the apicoplast
C;Keywords: hydrolase; plastid; serine proteinase
                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-95,'N',96-765 <WIW>
A;Cross-references: EMBL:X95276; NID:g1171591; PID:e220210; PID:g1171612
                                                                                                                                                                                                                                                                                                                        R;Wilson, R.J.M. submitted to the EMBL Data Library, January 1996 A:Reference number: S78483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Wilson, Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium A;Reference number: S72277; MUID:96346169
A;Accession: S72278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
seq_documentation_block:
ATP-dependent Clp proteinase (EC 3.4.21.-) homolog - Plasmodium falciparum plastid C:Species: plastid Plasmodium falciparum
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
C:Accession: S72278; S78483
                                                  alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: S78483
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-765 <WIL>
                                                                                                                                                                                                         A;Gene: clpC
                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: X95276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: pir2:S72278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown
           Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 CysLysLeuLysGluCysProSerProProThrCysLysProGluGlu.. 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    snProCysIleSerTyrSerCysHisAsn...ThrGlyPheValAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpThrAlaAsnCysHisLysCysThrCysThrAspAlaGluThrValAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValGlnAspCysProLysGlnThrTrpCysAlaGluGluAspArgValTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....GluValGlyAlaSerPheAlaAspProLysA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....ACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGG
      90.00
0.720
55.556
Length: 225
Gaps: 20
Percent Identity: 27.111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.; Why
                                                                                                                hypothetical protein YHR102w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change
         A; Description: The sequence A; Reference number: S46691
                           submitted to the EMBL Data Library, May 1994 A;Description: The sequence of S. cerevisiae
                                                                       R; Latreille,
                                                                                              C; Accession:
                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                            seq_name: pir2:S48944
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A;Gene: SGD:NRK1
A;Cross-references: SGD:S0001144; MIPS:YHR102w
A;Map position: 8R
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein
C;Keywords: ATP; serine/threonine-specific protein
F;21-276/Domain: protein kinase homology <KIN>
F;29-37/Region: protein kinase ATP-binding motif
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A;Molecule type: DNA
A;Residues: 1-1080 <LAT>
A;Cross-references: EMBL:U00059; NID:g529116; PIDN:AAB68860.1; PID:g529127; MIPS:YHR102xC;Genetics:
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US-09-323-427-3 x C71618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-1712 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:C71618
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Ratio:
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seq_name: pir2:C71618

seq_documentation_block:
hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13 -Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C;Accession: C71618
R;Gardner, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: C71618
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-1712 <GAR>
A;Residues: 1-1712 <GAR>
A;Residues: 1-1712 <GAR>
A;Cross references: GB.AE001386; GB:AE001362; NID:g3845148; PID:g3845151; TIGR:PFB031
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0315w

alignment_scores:
Cuality: 90.00
Caps: 12
Percent Similarity: 45.161 Percent Identity: 19.941
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1116 rValTyrGluTyrValIleGluLysTyrLysArgValHisValLeuTyrL 1102 MetLysLysLysLysThrGlnGluTyrValAspIleGlu.....Th 1116 173 ATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGA 222 223 ATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAA 272 LysTyrSerPheHisLysLeuArgIlePheTyrGluTyrLysIleGluMe 1166 ACGGTGATACTGTGGAAATTCTAAATGCTGATG.....GATGTGCTCTT 651 euLeuLeuLysGluLysSerAlaTyrGlnAsnHisLeuGlyLysAsnTyr 1238 TGATACTTTCTGCGCGCTTGTCCATTCCT...GCTTTGTCGATGATGGTA uSerSerPheIleAsnTyrGlnIleLysThrAsnAspMetLeuTyrAsnL CAGCCAGTTTATC.....ATAAATGGACATGCGATTCTGAAACCGT 560PheAsnHisIleIleAsnSerTyrGl 1205 TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT ysLeuGluPheLeuIleLysLysLysMetGlnHisTyr..... AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 469 tGluLysLeuLysLysAsnTyrIleHisCysIleTyrAspIleSerAspL 1183 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC CATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTAC euGlyArgLeuLeuGlnIleValGluLysLeuPheLysLysTyrIleLeu TC...CACGTGGTATTTTTGTAACAACAGTGTTGTCATTTCGTTTCATC from: Percent Identity: Ċ: Ξ 1712 519 419 1149 1133 607 1222 1195 369 319

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posterior-group protein tudor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999
C;Accession: A41519; S19019
R;Golumbeski, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E.
Genes Dev. 5, 2060-2070, 1991
A;Title: tudor, a posterior-group gene of Drosophila melanogaster, encodes a novel prote A;Reference number: A41519; MUID:92038995
A;Accession: A41519
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-2515 <GOL>
  alignment_block:
                                                                                                                                     alignment_scores
                                                                                                                                                                                                                     C; Superfamily: posterior-group protein tudor
                                                                                                                                                                                                                                               A; Cross-references: FlyBase: FBgn0003891
                                                                                                                                                                                                                                                                                                          C;Genetics
                                                                                                                                                                                                                                                                                                                              A;Cross·references: GB:X62420; NID:g8753; PIDN:CAA44286.1; PID:g8754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:A41519
                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1005 TCTGCAACATAATGGACAACCTG 1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1255 aIleTyrPheArgSerPheValTyrAsnAsnIleLysValŞerLysLysL 1272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1289 TyrGluArgArgIleLysSerPheIlePheSerLysLeuLysPheAsnTy 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATT 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....CAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGC 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnVallleGluLysAsnValTyrArgLeuValLysLeuIleSerLysIl 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euCysAsnAsnLeuAspLysIle 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ......CysAspAsnLeuIleTyrAlaAsnAsnGluL 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCGATGATAATCAAGCTTTGC...CAGTTGATTTACGTCACCGTGCACT 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnLysMetIle.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....AGCTTTTCTATCAATGCCAGAT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....LeuGlnLysTyrValTyrGluGlnAsnGluLysLys 1378
                                                                               Quality:
Ratio:
                                                   90.00
0.552
44.414
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                                                      Percent Identity:
                                                      19.074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1936 lnLeuLeuLysProGlyGlnAspHisValThrIleAspLeuLeuLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1919 uAlaLysPheAlaGluLeuThrGlyGluGlyGluLeuValPheThrThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1904 SerLeuGlnLeuPro...AspAlaTyrIleSerTrpSerProGluAlaGl
                                                2125 rAlaSerProProValValArgLeuThrThrLysAspLysArgSerLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2035 AlaAspAspLeuGluPheTyrArgSerArgIleLeuGluValLeuGluAs 2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2018 lnProLysThrGluLysAlaAlaValAspAspMetCysValValGlnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001 sAspSerLeuMetAspIleIleCysGluLysLeuAsnGlySerLysLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 GTAATGCATTCGAAGGA.....CATGTTTATGTGAAAGGTCTTTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 TGAT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC 377
722 AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...ThrHisValGluAsnThrSerArgIleTyrLeuGlnPheSerGluLy 2001
                                                                                                                                                                                                                                                                                                                            GCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTG 621
                                                                                                                                                                                                                                                                                                                                                                                  uProSerAlaIlePheGluLysAsnLysAlaLeuThrLeuThrThrPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spTyrGlyAsnThrThrValValAspLysLeuTyrGluLeuProGlnGlu
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                                                                                                         TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA 721
                                                                                                                                                            .....LysGlyValValAlaValGluPheValAsnLysSe
                                                                                                                                                                                                                     GAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAA 671
                                                                                                                                                                                                                                                                        spAlaLeuLeuAspSerCys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                  A.....ACCGTTGATACTTTCT 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PheThrLeuIle...LysProValAlaGlu.....IleCysSerMetGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....GTATCTGAAATCACAACTGC
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hypothetical protein yob1 - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 24-Sep-1998
C:Accession: H6998
C:Accession: H6998
C:Accession: H6998
C:Accession: H6998
C:Accession: H69998
C:A
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Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-323-427-3 x H69898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:299114; GB:AL009126; NID:g2634230; PID:e1185369; PID:g2634290 A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-1201 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                           552 LeuLeuGluLeuGluArgGluLysGlnGluIleArgAlaGlnSerLeuGl
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                                                                                                                                                                                                                                                                62 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yobI
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Gaps: 17
Percent Identity: 18.367
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4	G nG nA aVa T cAsnTvrVa AsnA	w
803	CCAAATAGCGAATGTGTTCGACC	754
ω c	roAsnIleThrTyrAlaAlaValLysAsnSerAsp	827
752	A A OTTATTOTA DA COTATOTA COTATOTA TOTATOTA A	704
703 826	"TTAATGGCTGGCC	660 816
Ė	ThrileTyrAspPheValValGlnArgAsnLeuTyrGluIleAsnI	799
ÚT.	TGATACTGTGGAAATTCTAAATGCTGATGGATGTGTCTTTGATAAATA	610
609 799	ATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAAC .::: ::: ::::::::::::::::::::::::::::	563 783
562 782	ACATGCGATTCTGAAACCGTTG ::: GluGluLysIleLysGluLeu	513 771
771	tSerPheThrLeuSerLysTyrLeuAsnLeuLeuS	758
512	ATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTAT	463
758	yrAlaAspIleAlaAspIleIleArgMetAsnLysGluSerVa	744
462	CAAACTCAAATTGTCCCGATGCCAGTATGCCGT	428
743	AsnTyrThrGlnGlnLysLysGluGluTyrLeuSerAspIleLeuThr	727
427	AGATTGAGGTATCTGAAATCACAACTGCTT	398
727	erSerLysTrpAspAspPheTrpSerPheIleGluLeuArgS	710
397		397
710	uArgAlaIleAsnLysAlaAlaPheIleGl	694
397		397
693	lySerLysGluSerValThr	677
397	CTGATAAAACAGTTAGTO	369
677	: :	664
368	ATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG0	319
318 664	TGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCAT :::::: ::: :::: :::	269 648
647	TyrSerPheGluLeuAspAsnIl	631
268	TGTTG	249
631	 LeuSerLeuSerAspIleLysPheValPheSerIleLysAsn	614
248		242
614	 HisTyrIleThrTyrPheTyrProG	598
241	GGAATTTCACTTCCATTTG	212
597	:::::: :::: ::: spLysLeuTyrGluLysLysLeuLeuValTyrLeuLeuArgHisGly	582
211	GAAAGGTCTTTATGATCAAGAAGGT	162

	ValLysHisAlaMetIleMetLys 890	883
	948 CCTTGAAATTAGCGATGATAATCAAG 973	948
882		877
947	898 AGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACAC 947	898
877	865 GluProGluSerPheLeuGluLeuLeuAsnArgGl 877	865
897	TTCGTTTACTC!	851
864	848 spAsnIleAspIlePheValGluLysValLeuThrGluGluIleGlu 864	848
850	804 ACAATGITCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTG 850	804

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P12435 bluetongue virus

saccharomyces

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SWISSPTOT_38:NRK1_YEAST +
SWISSPTOT_38:NRK1_YEAST +
SWISSPTOT_38:SRS_RAP +
SWISSPTOT_38:AMD_HUMAN +
SWISSPTOT_38:CGE1_CHICK +
SWISSPTOT_38:YAGE_SCHPO
SWISSPTOT_38:YAGE_SCHPO
SWISSPTOT_38:SRBM_YEAST +
SWISSPTOT_38:SRBM_YEAST +
SWISSPTOT_38:PITA_FUGRU +
SWISSPTOT_38:PITA_FUGRU +
SWISSPTOT_38:PITA_FUGRU +
SWISSPTOT_38:RPOD_SPIOL +
SWISSPTOT_38:RPOD_SPIOL +
SWISSPTOT_38:RWS_CLODI +
SWISSPTOT_38:RWS_CLODI +
SWISSPTOT_38:RWS_DYHG_CHIRE +
SWISSPTOT_38:RWS_EMENI +
SWISSPTOT_38:RWS_EMENI +
SWISSPTOT_38:RMS_EMENI +
SWISSPTOT_
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SwissProt_38:YQH3_CAEEL +
SwissProt_38:YAY3_SCHPO +
SwissProt_38:APMU_PIG +
SwissProt_38:GALU_PSEAE +
SwissProt_38:AMD2_XENLA +
SwissProt_38:YR1_SCHPO +
SwissProt_38:PYR1_SCHPO +
SwissProt_38:MUCS_BOVIN +
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Query: US-09-323-427-3
Query length: 1161
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Database sequences: 82229
Database length: 29864866
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Copyright (c)
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1.08 11.88
1.96 9.44
1.6 10.88
1.49 11.33
1.20 11.69
1.33 12.21
1.29 12.25
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SEQ_documentation_block:
ID CUTI_CABEL
AC Q03755, Q18693;
DT 01-FEB-1994 (Rel. 28,
DT 15-JUL-1998 (Rel. 37,
DE CUTICLIN 1 PRECURSOR.
GN C4762.1.
OS Caenorhabditis elegar
OC ENKARYOCA; Metazoa; N
CUT-1 OR C4762.1.
OS CAENORHABGITIOL N2;
RX SEBASTIANO M. A. SEQUENCE FROM N.A.
SERAIN-BRISTOL N2;
RX MEDLINE; 91323673.
RA SEBASTIANO M. LASSAN
TCUT-1 a CAENORHABDITOL
RY CUT-1 a CAENORHABDITOL
RY STRAIN-BRISTOL N2;
RA SEBASTIANO M. LASSAN
TCUT-1 a CAENORHABDITOL
RY CUT-1 a CAENORHABDITOL
RY STRAIN-BRISTOL N2;
RA SEBASTIANO M. A.
RC STRAIN-BRISTOL N2;
PALMER S.;
PALM
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SwissProt_38:PHY4_AVESA +
SwissProt_38:YEW2_YEAST +
SwissProt_38:P11A_HUMAN +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (APR-1995) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: COMPONENT OF THE CUTICLES, IT FORMS A RIBBON
-- APPROXIMATELY 2 MICRONS WIDE RUNNING ALONG THE LATERAL LINES
UNDERNEATH THE ALAE. CONTRIBUTES TO THE FORMATION OF EXTRACELLULAR
ENVELOPES PROTECTING THE ORGANISM FROM THE ENVIRONMENT.
-- SUBCELLULAR LOCATION: SECRETED.
-- TISSUE SPECIFICITY: LOCALIZED IN A NARROW BAND NOT EXPOSED
TO THE EXTERIOR, RUNNING UNDERNEATH THE ALAE.
-- DEVELOPMENTAL STAGE: EXPRESSED DURING DAUER LARVA FORMATION.
-- DOWAIN: THE SMALL REPEATS A-A-P-[AVI] ARE ALSO PRESENT IN MANY
PROTEINS CONSTITUTING THE PROTECTIVE ENVELOPE OF OTHER SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUT1_CAEEL STANDARD: PRT; 424 AA. Q03755; Q18693; 01-FEB-1994 (Rel. 28, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) CUTICLIN 1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cut-1 a Caenorhabditis elegans gene coding for a dauer-specific noncollagenous component of the cuticle.";
Dev. Biol. 146:519-530(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M55997; AAA27995.1;
EMBL; Z49125; CAA88934.1;
PIR; A49772; A49772.
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                                                        Nematoda; Secernentea; Rhabditia; Rhabditida;
oidea; Rhabditidae; Peloderinae; Caenorhabditis.
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P -> G (I

A -> G (I

A -> S

SS

FA -> LP

IG -> MR
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105.70
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CUTICLIN 1.
4 X 4 AA REPEAT OF A-A-P-[AVI].
          08E05529
                             P (IN REF. 1).
G (IN REF. 1).
G (IN REF. 1).
NG (IN REF. 1).
SS (IN REF. 1).
LP (IN REF. 1).
MR (IN REF. 1).
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P32634 saccharomyces
P42336 homo sapiens
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alignment_block:
US-09-323-427-3 x CUT1_CAEEL
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   258
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24 nValGluGlyGluProGluValGluCysGlyProAsnSerIleThrValA 41
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            ATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACA 821
                                                                                          AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC
                                                                                                                                        GlnIleLeuAsnGluGluGlyCysAlaLeuAspLysPheLeuLeuAsnAs
                                                                                                                                                              GAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAA 671
                                                                                                                                                                                                 GCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTG
                                                                                                                                                                                                                                                                               TTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA
                                                                                                                                                                                                                                                                                                                           CTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATT 471
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ysTyrAlaAspArgSerGlnLeuPheTyrGlnCysGlnIleSerIleThr
                                                                                                                                                                                    ysAlaValValHisSerCysThrValAspAspGlyAsnGlyAspThrVal
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Seq_documentation_block:
ID YQH3_CAEEL STANDARD;
AC Q09276;
AC Q00276;
AS QUANTION (Rel. 35, Last DT Q1.NOV-1997 (Rel. 35, Last DT Q1.)
ARP SEQUENCE FROM N.A.
ARC STRAIN-BRISTOL N2;
ARA SULSTON J.;
ARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1102 GCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCA 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 55.1 KD PROTEIN C43C3.3 IN CHROMOSOME
                                                 WORMPEP; C43C3.3; CE01525.

Hypothetical protein; Transmembrane; ATP-binding TRANSMEM 11 31 POTENTIAL.

TRANSMEM 426 446 POTENTIAL.

NP_BIND 171 178 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. That is are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              EMBL; 247067; CAA87330.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aLeuValSerGlu.....GluSerValArgArgArgAlaThrSerThrG
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| AlaAlaProValAlaAlaProValAlaAlaAlaAlaAlaAlaProAlaVa
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MW; ATP

TP (POTENTIAL).
09C77468 CRC32;

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alignment_block:
US-09-323-427-3 x YQH3_CAEEL
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                       258
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                                                                                                                                                                                                                                                              LysIleThrPhe.....ValGlnGlyGlyCysProValAsnGlyMetAs
                                         GCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTG.....
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                                                                                ..IleIleAspProLeuAlaAsnValAsnAspGlnIleTyrPheSerLys 306
                                                                                                                             CGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAAT 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAA 298
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PheArgThrPheArgPheGlyAsnGlnSerThrValPheValHisCysGl
                                                                                                                                                                                                                                                                                                         ....ACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAA 608
                                                                                                                                                                                                                                                                                                                                                                                            ......TGCGATTCTGAAACCGTTGAT.........
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Gaps:
Percent Identity:
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alignment_block:
US-09-323-427-3 x YAY3_SCHPO
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                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                        Align seg 1/1 to: YAY3_SCHPO
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHRO
                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMILTED (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 hrAspAspAsnGlySerLeu 378
                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Transmembrane.
TRANSMEM 265 285 POTENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z69380; CAA93342.1; -.
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36 LeuAspGlySerValGluMetMetCysTrpPro.....As
                                                                     73 GTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATCAA 122
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                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                               97.50
0.554
43.672
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584
646
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                                                                                                        from: 1
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POTENTIAL.
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22.333
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J. Biol One-
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01-OCT-1989 (Rel. 12, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat APOMUCIN (MUCIN CORE PROTEIN) (FRAGMENT).
            porcine submaxillary mucin tandem repeat glycopeptide. Model proposed for the polypeptide:qainac transferase peptide binding site.";
J. Biol. Chem. 272:9709-9719(1997).
-i- FUNCTION: APOMUCIN IS PART OF MUCIN, THE MAJOR GLYCOPROTEIN SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE THE ORAL CAVITY AND TO PROTECT IT FROM THE EXTERNAL
                                                                                                                                                                 CARBOHYDRATE-BINDING SITES, TISSUE=SUBMAXILLARY GLAND;
                                                                                                                                                                                                                                                                                                                                   TIMPTE C.S., ECKHARDT A.E., ABERNETHY J.L., HI "Porcine submaxillary gland apomucin contains identical sequences of 81 residues.";
J. Biol. Chem. 263:1081-1088(1988).
                                                                                                                                                                                                             JOHNSON W.C. JR., HILL R.L.; "Structural properties of porcine submaxillary gland J. Biol. Chem. 262:11339-11344(1987).
                                                                                                                                                                                                                                                         MEDLINE; 87280230.
ECKHARDT A.E., TIM
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                                                                                                                                                     MEDLINE;
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CHANG H., LEE C., PENG H.;

Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases

Submitted (DEC-1993) to The EMBL/GenBank/DDBJ databases

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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE
PYROPHOSPHORYLASE) (UDDGP) (ALPHA-D-GLUCOSYL-1-PHOSPHATE
URIDYLYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria;
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-i- CATALYTIC ACTIVITY: UTP + ALPHA-D-GLUCOSE 1-PHOSPHATE
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                                                             AsnGlnIleLysGlyThrAspLysGluLysTyrLeuValGlyIleArgLy
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Seq_documentation_block:
ID AND2_XENLA STANDA
AC P12890;
DT 01-OCT-1989 (Rel. 12,
DT 01-DCT-1989 (Rel. 37,
DT 15-DEC-1998 (Rel. 37,
DE PDTIDYL-GLYCINE ALPH
DE (EC 1.14.17.3) (PEPTI
OS Xenopus laevis (Afric
CC Eukaryota; Metazoa; C
C Batrachia; Anura; Mes
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKIN;
RX MEDLINE; 88134244.
RA OHSUYE K., KITANO K.,
RA MATSUO H.;
RT "Cloning of cDNA encc
enzyme having a putat
skin.";
RL Biochem. Biophys. Reg
CC -!- FUNCTION: C-TERM:
CC -!- CATALYTIC ACTIVI)
CC (THE PRODUCT IS (
CC CORRESPONDING DE;
CC -!- COFACTOR: COPPER
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01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE II PRECURSOR (BC 1.14.17.3) (PEPTIDE C-TERMINAL ALPHA-AMIDATING ENZYME II Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodi
                                                                                   -!- FUNCTION: C-TERMINAL ALPHA AMIDATION OF BIOLOGICAL PEPTIDES
-!- CATALYTIC ACTIVITY: PEPTIDYLGLYCINE + ASCORBATE + O(2) =
PEPTIDYL(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)0.
                                                                                                                                                               Biochem. Biophys. Res.
                                                                                                                                                                                                           "Cloning of cDNA encoding a new peptide C-terminal alpha-amidating enzyme having a putative membrane-spanning domain from Xenopus laevis
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             COPPER,
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             ASCORBATE
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Xenopodinae;
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                                                                    AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
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DE PUTATIVE SERINE/THREC
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GN 01044.3
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Submitted (JUN-1994) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: STRONG, TO ZC84.1.
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PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3
(EC 2.7.1.-)
                                                                                                                                                                                                                                        WORMPEP; D1044.3; CE01206.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
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HSSP; Q63450; 1A06.
WORMPEP; D1044.3; CE01206
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Eukaryota; Metazoa; Nematoda;
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      (Rel. 32.)

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                                                                                                                                                         SerGlnCysValGlySerGlnGlnCysLeuSerAsnSerGlnCysIleSe 1323
                                                                                                                                                                               GAA.....
                                                                                                                                                                                                        hrAsnGlnValCysIleSerAsnGlnCysTyrAsnTyrValSerIleGly
                                                                                                                                                                                                                                CGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAA
                                                                                                                                                                                                                                                       lCysThrAsnAsnIleCysValSerThrPheCysSerValSerCysSerT
                                                                                                                                                                                                                                                                                                                              CTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                  SerSer.SerSerCysAsnSerAsnGlnVal.....SerI 1248
                                                                                                                                                                                                                                                                                                                                                                                                                         TTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                               hrCysGlnCysThrAsnGlyAlaThrAlaMetTyrGlyTyrCysIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTT
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 (Rel. 32, Created)
(Rel. 32, Last sequence (Rel. 39, Last annotation)
                                                 STANDARD;
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0.940
47.847
32, Last sequence update)
39, Last annotation update)
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 DOMAIN
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                                                                                                                                                    PF00117; GATase; 1.
PF00185; OTCase; 1.
PF00289; CPSase_L_chain; 2.
PF00744; Dihydrooratase; 1.
PF00988; CPSase_sm_chain; 1.
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1525

1515

(BY SIMILARITY).
BOUNDARY BETWEEN |
(BY SIMILARITY).
DEFECTIVE DHOASE |

DOMAINS

SYNTHASE)

CPSASE (CARBAMOYL-PHOSPHATE (BY SIMILARITY).
BOUNDARY BETWEEN ENZYMATIC

(BY SIMILARITY)

DOMAINS

478 438 biosynthesis;

Ligase; Transferase; Multifunctional enzyme GATASE (GLUTAMINE AMIDOTRANSFERASE)

1854

1935 1853 1524 1514 477

(BY SIMILARITY).
BOUNDARY BETWEEN ENZYMATIC DOMAINS (BY SIMILARITY).

DOMAIN ENZYMATIC

```
AND ATCASE) (BY SINILARITY).

C -!- CATALYTIC ACCTIVITY: 2 ATP + GLUTAMINE + CO(2) + H(2)O = 2 ADP + CATALYTIC ACCTIVITY: 2 ATP + GLUTAMINE + CO(2) + H(2)O = 2 ADP + CORTHOPHOSPHATE + GLUTAMINE + CARBAMOYL PHOSPHATE.

C -!- CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE = COTHOPHOSPHATE + N-CARBAMOYL-PHOSPHATE + ASPARTATE = COTHOPHOSPHATE + N-CARBAMOYL-PHOSPHATE BIOSYNTHESIS.

C -!- MISCELLANEOUS: GATASE (GLUTAMINE AMIDOTRÂNSFERASE) AND CPSASE (CARBAMOYL PHOSPHATE SYNTHASE) FORM TOGETHER THE (CARBAMOYL PHOSPHATE SYNTHASE) FORM TOGETHER THE (GATASE (GD-CPSASE) (EG 6.3.5.5).

C -!- SIMILARITY: THE GATASE DOMAIN BELONGS TO OTHER CPASES.

C -!- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-1 GLUTAMINE DOMAIN.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; PROSITE; PS00442; GATASE_TYPE_I; 1. PROSITE; PS00866; CPSASE_1; 2. PROSITE; PS00867; CPSASE_2; 2. PFAM; PF00117; GATASE; 1.
                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                           EMBL; X81841; CAA57433.1; -. EMBL; Z54328; CAA91130.1; -. HSSP; P00968; JJDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "As in Saccharomyces cerevisiae, aspartate transcarbamoylase is assembled on a multifunctional protein including a dihydroorotase-like cryptic domain in Schizosaccharomyces pombe."; Curr. Genet. 28:138-149(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BADCOCK K., CHURCHER C.M., E Submitted (OCT-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URA1 PROTEIN [INCLUDES: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5); ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3 URA1 OR SPAC22G7.06C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOLLIER M., JA
SOUCIET J.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCK K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., milted (OCT-1995) to the EMBL/GenBank/DDBJ databases. FUNCTION: THIS PROTEIN IS A "FUSION" PROTEIN ENCODING ENZYMATIC ACTIVITIES OF THE PYRIMIDINE PATHWAY (GATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDOTRANSFERASES.
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                     640 GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA 689
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                                                                                                                                                                                                                                                                                                                                                                                            aAsnAsnIleAlaLeuProLeuHisArgGluAsnValLysIleLeuGlyT 1118
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                                                                                                  TCGATGATGGTAACGGTGATACTGTG.....GAAATTCTAAATGCTGAT
                                                                                                                                                                                  CGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTG
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GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GIC -> RYF (IN REF. 1).
CAVRA -> LQFAQ (IN REF. 1).
ELL -> DV (IN REF. 1).
G -> E (IN REF. 1).
G -> E (IN REF. 1).
OG MW; 582E9CD7 CRC32;
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Gaps: 17
Percent Identity: 20.274
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ATCASE (ASPARTATE TRANSCARBAMYLASE) (BY SIMILARITY).
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  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: SwissProt_38:MUCS_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          810
                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                             MEDLINE: 90370871.
BHARGAVA A.K., WOITACH J.T., DAVIDSON E.A., BHAVANAN "Cloning and cDNA sequence of a bovine submaxillary protein containing two distinct domains.";
Proc. Natl. Acad. Sci. U.S.A. 87:6798-6802(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SUBMAXILLARY MUCIN-LIKE PROTEIN.
                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=SUBMAXILLARY GLAND;
                                                                                                                                                                           -i- TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.
-i- SIMILARITY: TO PORCINE APOMUCIN.
-i- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
-i- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P98091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUCS_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...GlyValAspMetIleSerMetAlaThrAspValIleMetGly 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgAla.....SerArgSerPheProPheValSerLysValIle...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eGlnPheIleAlaLysAspAsnGluIleLysValIleGluCysAsnValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaAlaAlaLysIleGlyGluAlaLeuAsnIleThrGlyProTyrAsnIl 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alLeuProProGlnAspLeuAlaProThrThrIleGluArgIleValAsp 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....GCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eSerGluHisValGluAsnAlaGlyValHisSerGlyAspAlaThrLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAGAACCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCGCA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IleGluLeuAspAlaValAlaArgGluGlyLysMetValMetHisValIl 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTA.....ATGGCTGGCCAAGAAGCTCAC....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos.
                                                                                                                                                                                                                                                                                                                                               WOITACH J.T., DAVIDSON E.A., BHAVANANDAN V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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US-09-323-427-3 x MUCS_BOVIN
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HSSP; P00214; 1FTC.
PROSITE; PS01208; VMFC; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PFAM; PF00007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00007; Cys_knot; 1
Repeat; Glycoprotein.
DOMAIN 61 158
REPEAT 61 71
REPEAT 148 158
DOMAIN 338 404
DOMAIN 338 404
DOMAIN 471 555
SIMILAR 1 282
DISULFID 471 518
DISULFID 498 532
DISULFID 498 548
DISULFID 498 550
DISULFID 394 394
CARBOHYD 394 394
CARBOHYD 394 394
CARBOHYD 394 394
CARBOHYD 394 394
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SIMILAR
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CARBOHYD
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CARBOHYD
418 ACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGA 467
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                                                                                                                                                                                                                                                                                                                       258 TACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCA 307
                                                                                                                                                                                                                                                                                                                                                                                                               222 rgThrThrGluThrArgIleLeuSerGlyThrThrArgGlyArgSerGly 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTC 110
                                                                                                                                                                                                                                                      TTTCGTTTCATCCATTATTTGTTACC.....
                                                                                                                                                                                                                                                                                    rSerThrGlyValGlyArgGln.....ThrSerThrAlaValV 263
                                            yrProGluThrThrValValAlaThrGlyGluGlnGlu...ThrGluThr 326
                                                                                                      rThrSerLysSerAsnArgIleThrThrSerSerArgIlePro.....T
                                                                                                                                                                                                                              alSerGlyArgValThrGlyValSerGluSerSerSerProGlyThrSer 279
                                                                                                                                                                                                                                                                                                                                                                                   CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGA 207
                                                                          ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATC
                                                                                                                                    .....AAAGTTGATCGTGCATATCGAGTACAATGCTTTT
                                                                                                                                                                                                                                                                                                                                                     ThrThrVal.....IlePro...GluSerSerAsnThrGlyTh
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0.612
42.609
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Gaps: 18
Percent Identity: 20.290
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CTCK.

TO PORCINE APOMUCIN.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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RSTEN J., S., MOUSER L., VAUGHAN K.,	DU Z., FAVELL KUCABA T., HI LATREILLE P., NHAN M., RIFK	
	SEQUENCE FROM N.A. STRAIN-S288C / AB972; STRAIN-S288C / AB972; MEDLINE; 94378003.	
·		
	SEQUENCE FROM N.A.	
comycetales;	visiae (Baker's yeast). Ascomycota; Hemiascomycetes; Sacchar ; Saccharomyces.	
CH KINASE 1).	OFFERFIXED (NET. 33, Last annotation update) SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1) (N-RI NRK1 OR YHR102W.	
	01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update)	
	seq_documentation_block: ID NRK1_YEAST STANDARD; PRT; 1080 AA.	
	<pre>seq_name: SwissProt_38:NRK1_YEAST</pre>	
	901 TCTGCAGAACCGGAGAATATCATTGATGTACGAAC 935 :::::::::::::::::::::::::::::::	
900 470	855AGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA !	
854 458	838 AAAACAGGTGGTGCCGC	
837 441	788 GCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTT	
787 426	738 ACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATA ::::::::::::::::::::::::::::::	
415	415	
737	688 GATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGATC	
687 415	656 AATATTTGCTAAATAATTTGGAATATCCAACA	
401	:::::::::::::::::::::::::::::::::::	
605 386	CTGCTTTGTCGATGATGG : : rCysLysProGluGlu	
564 370	GTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGAT	
51 <i>7</i> 354	468 AATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTG	
341	7 LysThrGlyCysThrThrSerLeuProProProProAlaCysTyr	

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alignment_block:
US-09-323-427-3 x NRK1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                                          612
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Science 265:2077-2082(1994).
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
                               293 ArgTyrLeuLeuPheArgAspLysAsnLysAsnLysTyrLysIleGluGl
                                                                      712
                                                                                                              276
                                                                                                                                                                                       263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 LysValAspIleTrpSerLeuGlyIleThrThrTyrGluIleAlaThrGl
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P24941; 1AQ1.
SGD; L0001276; NRK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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762 CAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAUDIN M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIGNATI D.,
                                                                    CACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGAT
                                                                                                                                               GATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGG
                                                                                                                                                                                                                          TGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATT
                                                                                                                                                                                                                                                          LysGluPheIleAlaLeu.....CysLeuAspGluAspProLys..
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                                                                                                                                                                                                                                                                                                                                                                          TCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTT
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                                                                                                          leArgAlaHisLysAlaThrProThrSerIleLeuLysGluLeuIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine/threonine-protein kinase; ATP-binding
23 276 PROTEIN KINASE.
29 37 ATP (BY SIMILARITY).
52 52 ATP (BY SIMILARITY).
                                                                                                                                                                                   .GluArgLeuSerAlaAspAspLeuLeuLysSerLysPheI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pkinase;
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0.833
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ID TUD_DROME STANDARD;
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US-09-323-427-3 x TUD_DROME
                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOLUMBESKI G.S., BARDSLEY A., TAX F., BOSWELL R.E.;
"Tudor, a posterior-group gene of Drosophila melanogaster, en
novel protein and an mRNA localized during mid-oogenesis.";
Genes Dev. 5:2060-2070(1991).

Genes Dev. S:2060-2070(1991).
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01-MAY-1992 (Rel. 22, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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                                                                                                                                                                                      FLYBASE; FBgn0003891; PFAM; PF00567; TUDOR;
                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
-I- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
-I- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR
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MIZNIK H.B., SRIKANT C.B., PAYEL Y.C.;
"MOLecular cloning, functional characterization, and chromosomal
localization of a human somatostatin receptor (somatostatin receptor
type 5) with preferential affinity for somatostatin-28.";
MOL Pharmacol. 45:417-427(1994).
-i- FUNCTION: RECEPTOR FOR SOMATOSTATIN-28. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: PROMINENT IN THE PITUITARY AND SMALL
INTESTINE. LOW LEVELS IN ISLETS AND SPLEEN. NOT DETECTED IN
                                   EMBL;
                                                                                       modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'CARROLL A.-M., LOLAIT S.J., KONIG M., MAHAN L.C.; "MOLECULAR CLONLING and expression of a pituitary somatostatin receptor with preferential affinity for somatostatin-28."; Mol. Pharmacol. 42:939-946(1992).
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
SOMATOSTATIN RECEPTOR TYPE 5 (SS5R).
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                                                                                                                                                                                                                                         KIDNEY, PANCREAS, CEREBELLUM, OR CORTEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 93125499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=PITUITARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94195267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PITUITARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS TO C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnLysArgAsnGluAsnSerGluCysIleIleSerTyrGlyAsnSerPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuIleAspProThrThrAsnSerAsnGlyValCysTyrSerGlnGluAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCTGCGCAACTTCGTTTACTCAAGAAAGATCTGCAGAACCGGAGAAT
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                 L04535; AAA17029.1;
U01152; AAC09011.1;
X74828; CAA52825.1;
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                                                                                                       (See http://www.isb-sib.ch/announce/
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Rattus.
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                                                                                                                                commercia
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GCR_0514;

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alignment_scores:
    Quality:
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US-09-323-427-3
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1
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DOMAIN
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                           672 TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA 721
                                                                                                                                                                                                                                                                                106 GlySerPheLeuCysArgLeuValMetThrLeuAspGlyIleAsnGlnPh
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                                                                                                                                                                                                                                                                                                                                        89
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                                                                                                             LysMetAlaSerAlaAlaValTrpValPheSerLeuLeuMetSerLeuPr
                                                                                                                                       GTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCA 437
erTrpProGluProValGlyLeuTrpGlyAlaAlaPheIleThrTyrThr
                                                       oLeuLeuValPheAlaAspValGlnGluGlyTrpGlyThrCysAsnLeuS
                                                                                  CTTGATA.....
                                                                                                                                                                   alValHisProLeu...ArgSerAlaArgTrpArgArgProArgValAla
                                                                                                                                                                                              TTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCG
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                                                                                                                                                                                                                                                                                                                                      lyLeuProPheLeuAlaThrGlnAsnAlaValValSerTyrTrpProPhe
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E; PS00237; G_PROTEIN_RECEPTOR;
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Gaps: 6
Percent Identity: 24.342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
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5 (POTENTIAL)
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2 (POTENTIA)
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6 (POTENTIA
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3 (POTENTIAL).
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human peptidylglycine alpha-amidating monoxygenase: cDNA, cl and functional expression of a truncated form in COS cells.";

L Biochem. Biophys. Res. Commun. 169:551-558(1990).

-!- FUNCTION: C-TERMINAL ALPHA-AMIDATION OF PEPTIDES.

C -!- FUNCTION: C-TERMINAL ALPHA-AMIDATION OF PEPTIDES.

C -!- CATALYTIC ACTIVITY: PEPTIDYLGLYCINE + ASCORBATE + H(2) - PEPTIDYL(2-HYDROXYGLYCINE) + DEMYDROASCONBATE + H(2) O.

(THE PRODUCT IS UNSTABLE AND DISMITATES TO GLYOXYLATE AND CORRESPONDING DESGLYCINE PEPTIDE AMIDE).

-!- COFACTOR: COPPER, AND ASCORBATE.

-!- SUBCELLULAR LOCATION: SECRETORY GRANULES.

C -!- SUBCELLULAR LOCATION: TO THE COPPER TYPE II, ASCORBATE-DEPEN MONOOXYGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   documentation_block:
                                       CARBOHYD
SEQUENCE
                                                               DOMAIN
TRANSMEM
DOMAIN
METAL
METAL
METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P19021;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE
(EC 1.14.17.3) (PAM).
                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205
                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                    use
                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                             Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                       Oxidoreductase; Monooxygenase;
                                                                                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                                                                             PROSITE; PS00084; CU2_MONOOXYGENASE_1; PROSITE; PS00085; CU2_MONOOXYGENASE_2;
                                                                                                                                                                                                                                                                                                                        MIM; 170270;
                                                                                                                                                                                                                                                                                                                                    EMBL; M37721;
PIR; A35477; I
                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLAUDER J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=THYROID CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                722 AATATG
                                                                                                                                                                                                                                                                                   PFAM;
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                                                                                                                                                                                                                                                                    PF01082; Cu2_monooxygen; PF01436; NHL; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                       URHUAP
                                                                                                                                                                                                                                         Phosphorylation;
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                                                                                                                                                                                                    30
974
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                                       108475
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                                        W.
                                                                                                                                                                                                                                                                                                                                                                                          agreement
                                                                                                                                                                                                                                                                                                                                                                                                     is not removed.
                                                                COPPER
COPPER
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COPPER
                                                                                                                                  CYTOPLASMIC (POTENTIAL).
COPPER (POTENTIAL).
                                                     POTENTIAL
                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                        MONOOXYGENASE
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                                                                                                                                                                                                                   PROBABLE
                                                                                                                                                                                                                              PROBABLE.
                                                                                                                                                                        INTRAGRANULAR (POTENTIAL).
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                                                                                                                                                                                                                                                      Copper; Vitamin
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                                       05A75C07 CRC32;
                                                                                         (POTENTIAL).
(POTENTIAL).
                                                                (POTENTIAL)
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                                                                              POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                    its content
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                                                                                                                                                                                                                                                         Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                      commercial
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Quality:

87.00

Length:

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alignment_block:
US-09-323-427-3 x AMD_HUMAN
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TAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
                                                                                                                                                                                                         {\tt saspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT}
                                                                                  AGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT
                                                                                                                         hr {\tt AsnThrValTrpLysPheThrLeuThrGluLysLeuGluHisArgSer}
                                                                                                                                                                      CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT
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alignment_block:
US-09-323-427-3 x CGE1_CHICK
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     Align seg 1/1 to: CGE1_CHICK
                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U28981; AAA74981.1; -... EMBL; U28990; AAA81647.1; JOIN EMBL; U28982; AAA81647.1; JOIN EMBL; U28983; AAA81647.1; JOIN EMBL; U28985; AAA81647.1; JOIN EMBL; U28986; AAA81647.1; JOIN EMBL; U28986; AAA81647.1; JOIN EMBL; U28987; AAA81647.1; JOIN EMBL; U28988; AAA881647.1; JOIN EMBL; U28988; AAA881647, U2898; AAA888; AAA888; AAA8888; AAA8
                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p49707; Q91032;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
61/S-SPECIFIC CYCLIN E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LI H., LAHTI J.M., VALENTINE M., HOUSTON J., KIDD V.J.; SUBMILTED (JUN-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE (START) TRANSITION. INTERACTS WITH A MEMBER OF THE CDC2/CDK PROTEIN KINASES FAMILY TO FORM MPF (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN E SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               833
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Cyclin; Cell cycle; Cell division.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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AC P06503;
DT 01-JAN-1988 (Rel. 06, Creator P07 01-JAN-1992 (Rel. 21, Last D7 01-JAN-1992 (Rel. 21, Last D7 01-JAN-1992 (Rel. 38, Last D7
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PFAM; PF00360; phytochrome; PFAM; PF00512; signal; 1. PFAM; PF00989; PAS; 2. PFAM; PF01590; GAF; 1.
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HERSHEY H.P., BARKER R.F., IDLER K.B., LISSEWORE J.L., QUAIL P. "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic sequences for phytochrome: "Analysis of cloned cDNA and genomic seque
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Avena sativa (Oat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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PROSITE; PS00245; PHYTOCHROME_1;
PROSITE; PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X03242; CAA26999.1; -. EMBL; M18822; AAA76820.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS FR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBBNIT OF RIBULOSE-BISSHOSPHATE CARBOXYLLAS, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
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alignment Percent	ent_scores: Quality: 86.50 Ratio: 0.618 nt Similarity: 48.951 Percent Identity: 23.776	
us-09-	ent_block: -323-427-3 x PHY3_AVESA	
Align	seg 1/1 to: PHY3_AVESA from: 1 to: 1128	
7	71 TTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTC 520	
7:	21 AGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTT 561	
5(7)	62 GATACTITCTGCGGGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGG 611	
8 6	112 TGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATT 661 ; ;; ;; ;; ;; 106 nAlaSerCysProLeuLysAsnArgAspAlaPheValSerLeuCysValL 823	
66 82	62 TGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC	
71 83	12 CACGTATACAAATATGCGGATCGATCACGCTTTTCTATCAATG 755 ::: ::: !!!!!!!! 34 GluLysalaproPheGlyPhePheAspArgSerGlyLysTyrIleGluCy 850	
75 85	56 CCAGATCAGTATTACCATTAAAGAACCAAATAGCGAA	
79 86	93TGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTT 837 ::: ::: 67 alpheCys.pheIleHisValalaSerHisGluLeuGlnHisAlaLe 882	
88	38 AAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACT 881	
88	B2 TCGTTTACTCAAGAAAAGATCTGCAGAAACCGGAGAATATCATTGATGTAC 931 ·	
93 91	32 GAACTGATATCAACAC 947 ::: 16 SerArgLysAlaLeuLysAsnThrAspLeuAsnGluGluGlnMetLysGl 932	
94 93	48 CCTTGAAATTAGCGATGATATCAAGCTTTGCCAG 982 	
983 948	TTGATTTACGTCACCGTGCACCTTCTGCAACAT::: ::: ::::: ::: ::: ::: ::: :::	
102 96	21CAACCTGTAATACTTGCTGCAGTACAA 1047 ::::: ::: 55 GluMetalaGluPheLeuLeuGlnAspValValValAlaAlaValSerGl 981	

1048		1066 .	
981	981 nValLeuIleThrCysGlnGlyLysGlyIleArgIleSerCysAsnLeuP 998	866	
1067		1095	
998	998 roGluArgPheMetLysGlnSerValTyrGlyAspGlyVal 1011	1011	
1096		1145	
1012	1012 ArgLeuGlnGlnIleLeuSerAspPheLeuPheIleSerValLysPheSe 1028	1028	
1146	1146 TCCA 1149		
1028	1028 rPro 1029		

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sp_invertebrate:Q3YVV7
sp_invertebrate:Q3YVV7
sp_invertebrate:Q3997
sp_invertebrate:Q2680
sp_invertebrate:Q19586
sp_invertebrate:Q21573
sp_invertebrate:Q21576
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sp_invertebrate:Q2627
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sp_invertebrate:Q21587
sp_invertebrate:Q216274
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sp_invertebrate:093115 + 1653
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sp_invertebra+~ ~~~
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Query length: 1161
Database: SPTREMBL_12:*
Database sequences: 228878
Database length: 69334122
                                                  sp_bacteria:09ZEG6
sp_bacteria:051229
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sp_invertebrate:Q22164
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sp_invertebrate:Q21540
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            sp_invertebrate:097239
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-Q=/cgn2_1/USPTO_spool/US09333427/runat_14042000_170514_19920/app_guery.fasta.
-Q=/cgn2_1/USPTO_spool/US09333427/runat_14042000_170514_19920/app_guery.fasta.
-DB=SPTREMBL_12 -QEMT=fastan -SUFFIX=backtrans.rspt
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=4.000 -MINMATCH=0.100 -XGAPOP=10.000
-XGAPEXT=0.000 -GAPOP=4.500 -GAPEXT=7.000 -XGAPOP=10.000
-XGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.400 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
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312 | Q18213 caenorhabditis elegans 
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315 | Q23587 caenorhabditis elegans 
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                                          ! 077509 bos taurus (bovine).
! Q9zeg6 carnobacterium divergo
! 051229 borrelia burgdorferi
                                                                                                                                                                                                           1 020550 caenorhabditis elegans
1 062672 bos taurus (bovine). bo
1 091697 xenopus laevis (african
1 005707 homo sapiens (human). un
                                                                                                                                                                         018758 sus scrofa
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odium falciparum
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sp_virus:Q66951 +
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sp_human:O94829 +
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seq_name: sp_invertebrate:Q93115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ascaris lumbricoides (common roundworm).
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Ascaridida;
Ascaridoidea; Ascarididae; Ascaris.
                                                                                                                                                            "cut-1-like genes of Ascaris
Gene 193:81-87(1997).
                                                                                                                                                                                                                               154 GTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGG
                                                                                                                                                                                                                                                                                               104 CAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACAT
                                                                                                                                                                                                                                                                      33 roThrSerIleThrValAsnPheAsnThrArgAsnProPheGluGlyHis
                                                                                                       CGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTT
                                                                                                                                                                                                                                                                                                                          aIleProValAspAsnGlyValGluGlyGluProGluIleGluCysGlyP
                                                                                                                                                                                                                                                                                                                                                    GATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGAC
AlaTyrValLysGlyLeuTyrAspGlnGluGlyCysArgSerAspGluGl
                                                                                                                                                                                                                                                                                                                                                                                                         ATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTC
                                                                                                                                                                                                                                                                                   U73005; AAB66646.1;
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Ratio: 4.593
milarity: 92.784
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1 094829 homo sapiens (human).
44 1 096440 leishmania chagasi.
1 1 066951 feline infectious pe
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Q1-NOV-1996 (TremBLrel. 0:
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01-JAN-1999 (TremBLrel. 0:
F22B5.3 PROTEIN.
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BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
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SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
234
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EMBL; Z50044; CAA90355.1;
SEQUENCE 389 AA; 42983
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   Eukaryota;
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|AlaIlePheIleThrTyrMetIleValSerArgMetMetValProSerA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE GIORGI C., DE LUCA F., DI VITO M., LAMBERTI F.;
"Modulation of expression at the level of splicing of cut-1 RNA in infective second-stage juvenile of the plant parasitic nematode meloidogyne artiellia.";
                                                                                                                       150
                                                                                                                                                                       133
                                                                                                                                                                                               389
                                                                                                                                                                                                                                               339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                     AAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ePheThrValArgAlaIleProValAspAsnGlyValGluGlyGluProG
                                                                                                                                                                                                                                  TGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAG
                                                                                                                                                                                                                                                                                                                      spSerCysAsnValAlaArgThr...AspAlaGluProLysGlyValPhe
                                                                                                                                                                                                                                                                                                                                                                                               CCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                GCATTCGAAGGACATGTTATGTGAAAGGTCTTTATGATCAAGAAGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetArgLysLeuLeuPheAlaIleGlyValPheValAlaLeuAsnAlaIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCT.....
TGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGA
                                              GGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCC
                                                                                                                      ValValProMetProValCysLysTyrGluIleLeuGluGlyAlaAlaLe
                                                                                                                                                                                                                     lAspArgAlaTyrArgValGlnCysPheTyrMetGluAlaAspLysThrV
                                                                                                                                                                                                                                                                                                                                               ATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        luIleGluCysGlyProThrSerIleThrValAsnPheAsnThrArgAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 AA;
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Percent Identity: 63
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                                                                                      Q9XVM7 PRELIMINARY;
Q9XVM7 PRELIMINARY;
Q9XVM7;
Q1-NOV-1999 (TrEMBLrel. 12, Li
Q1-NOV-1999 (TrEMBLrel. 12, Li
Q1-NOV-1999 (TrEMBLrel. 12, Li
E53F1.1 PROTEIN.
F53F1.1 PROTEIN.
F53F1.1 Echenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
SEQUENCE FROM N.A. MEDLINE; 94150718.
BURTON J.;
"2.2 Mb of contiguo
                                                                                                                                                                                                               _documentation_block:
Q9XVM7 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 1078 TCAATGTTTATGGG.TTTAAGCATTGCATTGATTGCTGCCGTCATTATTA 1126
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                                                                           Rhabditina; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spLeuThrAlaGlyGlnGluAlaHisValTyrLysTyrAlaAspArgSer
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                                                                                                                                                                                                                                                                                                                                                                                                            {\tt rgPheIleTyrGlnGlyGlnGlnValCysMetSerSerPheArgAla}
                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGCTGCAGTACAAATGGA.....ATCTGCATGTCACCATTTGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eArgHisHisHisLeuMetGluAsnLeuSerAlaGluProGlnArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGTCACCGTGCACTTCTGCAACATAAT.....GGACAACCTGTAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTT
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                                                                         Nematoda; Secernentea;
pidea; Rhabditidae; Pelc
 nucleotide
                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                 PRT;
 sequence
                                                                                                                                                                                                                 364
                                                                           Peloderinae;
                                                                                                                                                                                                                 AΑ
from
                                                                                           Rhabditia; Rhabditida;
 chromosome
                                                                           Caenorhabditis
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alignment_scores:
Quality:
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US-09-323-427-3 x Q9XVM7
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AN MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

A BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

A CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

A GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

A LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

AR PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

THIERRY-MIEG J., THOMAS K., VAUDIN N., VAUGHAN K., WATERSTON R.,

AN WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RELEGATS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 uArgGlnArgValLeuAsnProLysGlyLeuAlaValArgThrThrIleT
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EMBL; Z81088; CABO3124.1;
SEQUENCE 364 AA; 40843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 GCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 TTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 rArgThrIleSerValGlnIleLySThrGluLysProPheValGlyValI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 ValProIleGlnAsnSerLeuTyrGlyAspValGlnValGluCysAspSe
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                                            hrCysThrTyrGlnIleLeuSerGlyGlyProPheGlyGluProValGlu
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                                                                                              TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA
                                                                                                                                                                                        TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA
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ACCGTTGATACTTTCTGCGCGGTTGTCC
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alignment_block:
US-09-323-427-3 x Q9XYU9
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                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q9XYU9 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

RAMZY R., HELMY H., ADELY M., CURTIS K., WEIL G.;

"Wuchereria bancrofti L3 cuticulin-1 cDNA partial sequence.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF125580; AAD28743.1; -.

NON_TER

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SEQUENCE 206 AA; 22602 MW; 4DEE20D0 CRC32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9XYU9;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
CUTICULIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9XYU9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wuchereria bancrofti.
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Wuchereria.
                                                                                                                                                       606 TAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATA 655
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ValIleSerPheHisProLeuSerValThrLysValAspArgAlaTyrAr 17

403

US-09-323-427-3 x Q21808

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Seq_documentation_block:
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DT 01-NOV-1996 (TrEMBLTel. 02
DE 01-JAN-1999 (TrEMBLTel. 02
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DE 01-JAN-1999 (TREMBLTEL)
CEUKATYOTA; Metazoa; Nemato
OC EukaTyOta; Nemato
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alignment_block:
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DUBEN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTLMORE B., O'CALLACHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SUUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
EMBL; Z49207; CAAB9068.1;
SEQUENCE 290 AA; 33215
                                                                                                                                                                                                                                                                                                                                            WATSON A., WEINSTOCK L., WILKINSO "2.2 Mb of contiguous nucleotide elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Ratio:
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                                                                                                                                AsnPhe.....AspMetArgIleSer....
                                                                                                                                                                  AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT 927
                                                                                                                                                                                               spTyrIleIleProAsnAspAspIleIleSerLeuAsnTrpLeuGlnArg
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sp_invertebrate:Q21540

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alignment_scores:
Quality:
Ratio:
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Q21540 PRELIMIN
Q21540;
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BONFIELD J., BURTON J., CONNELL M., COOPSEY J., COUDSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
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JONES M., KERSHAW J., KIRSTEN J., LAISTER N., COALLAGHAN M.,
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THIERRY-MIEG J., THOMAS K., VADUIN M., VAUGHAN K., WATERSTON R.,
WATENSTON A., WEINSTOK L., WILKINSON-SPROAT J., WOLLDMAN P.,
"3.2 M. Def contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Phabditina: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
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                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGCGTACACGATC
                                                                                                                                                                                                                                                                                                                                          TACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATC
                                                                                                                                                                                                                                                                                 AAGAAGGTTGCCGT.....AATGATGAAGGTGGACGTCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                        GlyThrProGluIleIleCysGlyProAspArgIleGlyValLysAlaSe
                                                                                                                                                                                                                                                spGluGluCysArgAlaGlyProGluLysPheProAspSerArgSerIle
TACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAAT
                                                                  ATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTT
                                                                                                       rLeuAsnProLysGlyIlePheValGluValSerIleValPheMetPheH
                                                                                                                                          TCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTC
                                                                                                                                                                         \dots \texttt{GlyLeuThrValProPheSerAlaCysAsnValHisArgTyrArgSe}
                                   isSerLeuPheMetThrLysThrAspGlnThrValLysValGlnCysPhe
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seq_documentation_block:
ID 019053
AC 019053;
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AC 019053;
AC 01908 (TYEMBLrel. 01
DT 01-JAN-1998 (TYEMBLrel. 05
DT 01-JAN-1999 (TYEMBLrel. 09
DE 204D5.3 PROTEIN.
GN E04D5.3 PROTEIN.
OC Eukaryota; Metazoa; Nematoo
OC Enhabditina; Rhabditoidea; RN [1]
RP SEQUENCE FROM N.A.
RA MCMURRAY A.;
RB SEQUENCE FROM N.A.
RA SUBMILTED J., BURTON J., CO
                                                                                                                                                                                                                                                                                                                                                                  seq_name: sp_invertebrate:Q19053
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                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
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   ANDERSON K
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Rhabditidae; Pelc
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 K., BAYNES C., BERKS M., COULSON A.,
                                                                                                                                                                                                                                                                                                                     484
                                                                                                                                                         Peloderinae;
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                   BERKS M.,
                                                                                                                                                           Caenorhabditis
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alignment_block:
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  194
                                      626 TTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG
                                                                                                                                                                                                                                              145 luAla...GlyGlySerProIleLysTyrAlaArgIleGlyAspGlnVal
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EMBL; Z66496; CAA91280.1; -.
SEQUENCE 484 AA; 53325 MW;
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alIleAspAlaAsnGlyCysSerValAspGlyValIleLeuGlnAsnLeu
                                                                                                                                                               TyrHisLysTrpThrCysValAlaGluLeuGluAsnValTyrCysMetLy
                                                                            sValHisSerCysThrValTyrAspGlyGlnGlyGlyProProValThrV
                                                                                                                     TGTCCATTCCTGCTTTGTCGATGATGGT...AACGGTGATACTGTGGAAA
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                                                                                                                                                                                                                                                 US-09-323-427-3 x Q93532
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROPPRA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
Belegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
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                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 278542; CAB01742.1; SEQUENCE 315 AA; 35785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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                 110 CAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTAT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
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                                                       41 nIleAspAsnGlyLeuGlnGlyGluProLeuIleArgCysGlySerGluS
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                                                                                                                                                                        10 CGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCC
                                                                         TGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTA 775
                                                                                                                                ArgIleProLeuPheCysLys.....TyrHisAlaGluGl
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                          Length:
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erLeuSerIleAsnPheLysThrGlnGlyAlaPheGluGlyHisValTyr

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Sequence of the sequence of th
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                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
01-JAN-1999
                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                               T04F8.4 PROTEIN.
SEQUENCE FROM N.A
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191 sLeuAsnAspProSerThrGluGluArgIleSerTyrAsnValProLeuP
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aProGlyGlnAsnGlnThrSerProPheCysValThrValHisSerCysA 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uThrGlyGlnLeuSerGlnValCysSerTrpThrValArg 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTT 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spIleAlaLysGluGlnGluLysLysIlePheValMetValGlyAspGlu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nCysPheTyrAlaGluAlaGlnLysThrValThrGlnGlnLeuAsnValA 158
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                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 01; Created)
(TrEMBLrel. 01; Last sequence update)
(TrEMBLrel. 09, Last annotation update)
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alignment_block:
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VADRIAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994),
EMBL; Z66565; CAA91480.1;
SEQUENCE 384 AA; 43964
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAA 112
AGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG
                                                                                                                                                                        ATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACC
                                                                                                                                                                                                                                                               laIleAspValSerAsnLeuProThrGluSerValGlnSerAspLeuPro
                                                                                                                                                                                                                                                                                                                                                     AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGC
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                                                                                  MetProThrCysSerTyrThrIleArgArgAspGlnLeuAspGlyProIl
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seq_name: sp_invertebrate:Q9XVN2
SEQUENCE FROM N.A. MEDLINE; 94150718. WHITE S.; "2.2 Mb of contiguo
                                                                                                                                                                                                                           _documentation_block:
Q9XVN2 PRELIMINARY;
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O9XVN2;

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 12,
                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                               F53B6.6 PROTEIN. F53B6.6.
                                                                                Rhabditina; Rhabditoidea;
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of contiguous
 nucleotide
                                                                                Rhabditidae;
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Last annotation update)
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                                                                                               Secernentea; Rhabditia; Rhabditida;
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sequence
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                                                                                Peloderinae;
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   chromosome
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.
GARATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                          161
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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EMBL; Z81086; CABO3116.1;
SEQUENCE 610 AA; 68585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTEN J., COLALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONHAMMER E., STANDEN R., SULSTON R.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VANGHAN K., WATERSTON R.,
WALTSON A., WELNSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                          Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. EMBL; Z81143; CAB03520.1; -. EMBL; Z75713; CAB03520.1; JOINED. EMBL; Z75713; CAB00057.1; -. EMBL; Z81143; CAB00057.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q93967; Q94405;
Q13967; Q94405;
Q1-FEB-1997 (TIEMBLIEL 02,
Q1-NOV-1998 (TIEMBLIEL 08,
Q1-JAN-1999 (TIEMBLIEL 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 94150718.
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                                                                                                                                                                                                                                                                                                                                  LENNARD N.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
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MW: 3F2BBBA2 CRC32;
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Last sequence update)
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Length:
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US-09-323-427-3 x Q93967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q93967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ATTCGTCTTATTGCTTCTGTACTACACTTATTGCATTGTCTTATTCGAT
CATTAAAGAACCAAATAGCGAATGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgValLeuHisGlnTrpHisCysAsnAspGln......MetTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yAsnGlnLysThrArgLysProHisPheAspLeuGlnPheGlyAlaCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spGluIleArgIleTrpValLysThrArgLysIlePheAlaGlyArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAA
                                                                                                                                                                                  {\tt leArgTyrSerSerAspLeuGlnArgAlaTyrAlaGluSerSerValPhe}
                                                                                                                                                                                                                                                   TGGAATATCCAACAGATTTAATG...GCTGGCCAAGAAGCTCACGTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTGGA...CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleProGlyCysThrTyrSerIleHisArgSerThrIleAspGluLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG::::: |||||| ||| |||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::::
||||||||::::::|||||||||:::::::|
lyMetLysSerLeuArgSerValAspProArgGlyMetTyrTyrGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrAlaLysGlyArgAlaGluLeuGluAspCysTyrLysAspAspPheGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eSerTleAspAsnGluTleTleGlyGluProAspIleGluCysLeuGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuLysIleLeuIleIleAlaTrpThrGlyTrpArgValAlaAsnAlaIl
                                                          LysPheAlaAspLysProGlyValTrpPhePheCysGlnValGlnMetCy
                                                                                                                           AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC
                                                                                                                                                                                                                                                                                                                        pValIleAspAspLysGlyCysProIleAspProIleLeuIleThrGlyI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValLeuIleAsnAsnCysTyrValThrAspGlyPheGlyLysLysAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGCCAGTATGCCGTTATGAAATT.....TTGGA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luLeuGlyValSerMetIleProThrThrGluLeuGluAlaArgHisGly 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aTyrHisValLysCysPhePheGluGluAlaAsnLysGlyLeuThrAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrValValValSerPheHisProLeuPheIleThrLysValAspGlnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGTCAAGTTGCC......GGAATTTCACTTCCATTTGATTCATGCA
                                                                                                                                                                                                                                                                                                                                                                                         AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pAlaGlyArgProAlaGlyAsnValIleGlnPheAlaArgValGlyGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.296
65.000
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Percent Identity: 33.438
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.GTTCGACCACAATGT.
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103

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53

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347

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137 397

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217

swetLysLys...HisGlyMetCysAspGlyIleThrProProSerCysG

283

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alignment_block:
US-09-323-427-3 x Q23097
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                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q23097 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER M., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VANDIN M., WAPERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W01A8.3 PROTEIN.
W01A8.3.
Caenorhabditis elegans.
Cuenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q23097;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
EMBL; Z71267; CAA95850.1; -.
SEQUENCE 387 AA; 43212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   903
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                                                                                                                                                                                                                                                             85 CCAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACG
                                                      GTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCA 234
                                                                                                      rLysProPheArgGlyAsnIlePheValLysGlyArgAlaLysAspLysS
                                                                                                                                                       TAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAG
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erCysArgGlnSerTyrAlaAsnAsnGlyThrAsnSerTyrSerLeuPro
                                                                                                                                                                                                          ProLysValIleCysAlaGluAsnAspLeuAlaLeuAspIleValThrSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lySerMetSerArgValIleSerValGlyGlyGluAspAsnGlyGlyPhe
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  476.00
2.235
59.167
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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6
                                                                                                                                                                                                                                                                                                                   387
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SOR FRIDA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 lAsnPheMetValThrValIleValSerPheHisProAlaGlyPheIleT
                                                                                                                                                                                                                                                                ysArgGluAlaAspArgSerAspTyrGluIleAspValAlaThrSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluIleValThrGlnAsnIleAspValSerMetIleProThrThrGluLe
                                         TCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATTGCA 1104
                                                                                                                                  TCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACCAAAT....AGCGAATGTGTTCGACCACAATGT.......
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                                                                                                                                                                                                                                                                                                            CAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAA
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Quality:
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Percent Similarity:
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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

ABONFIELD J., BURTON J., CONNELL M., CORRESY T., COOPER J., COULSON A.,

ABONFIELD J., BURTON J., CONNELL M., CORRESY T., COOPER J., COULSON A.,

ABONFIELD J., BURTON J., CONNELL M., COPER M., FULTON L.,

ABONFIELD J., BURTON J., LAISTEN J., FULTON L.,

ABONFIELD J., LAISTEN J., LAISTER N., LATREILLE P.,

ALLIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

ALLIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

ABONFIELD J., SONNHAMMER E., STADEN R., SUNDERS D., SHOWNKEEN R.,

ABONFIELD J., THOMAS K., VAUGHAN K., WATERSTON R.,

ABATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

THIERRY-MIEG J., THOMAS K., VAUGHAN K., WATERSTON R.,

ABATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

THE CONTROL OF THE CONT
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\text{\cappa2680} \text{\text{PRELIMINARY;}
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
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EMBL; 249071; CAA88879.1; -.
HSSP; P03000; LTIF.
SEQUENCE 609 AA; 68882 MW;
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                                                                                                                                  nValMetValHisPheSerCysGlnIleThrThrCysGlnLysGlnGluA
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Total number of hits satisfying chosen parameters:
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     GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                821193 seqs, -1518192014 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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1161
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-728.156 Million cell updates/sec
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9b_om:*
9b_om:*
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9b_pl2:*
9b_pr2:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
em_hum1: *
em_in : *
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45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_p13:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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45	44	43	42	41	40	39	ა 8	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	1 -	כי	οœ	7	σ	տ	4	ω	N		Result No.
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11163	1310	190000	2296	35955		124181	91894	6100	5214	110000	12976	9901	95713	82652	110000	102195	37872	165302	164399	27770	t n	_	23953	164548	\sim	34368	$\overline{}$	m	25284	~	~	~ '	0.6	. 1 -	3 10		637	2584	5792	724		34831	N	Length
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AE001500	EGU21005	AC004479	AF044022	CEF53B7	SGU40026	AF207067	AC005739	AB017910	F090	CEY53H1_2	CEY53H1B	\sim	AF085279	ATAC007020	G	CEY71H9	CET04F8	AC009451	PFMAL3P6	CET22C8	CELB0511	CELK03H9	CELK06A1	CEY70D2	EF20D1	CEW06D12	CEM28	CELF10E7	EW01A	CEZK265	EM142	CEY39A1 3	CERO7E3	つがけんない しゅうしゅうしゅう	CERULE:	BPA012618	BMA012617	MAMTCUT1	ALU73005	AF125580	CELCUT1	EC47G	CEF22B5	ID
Helico	glena ge	Homo sap	4022 Eurytide	0	reptococo	Homo sap	Homo sap	AB017910 Dictyoste	Dictyost		51	0 ме	AF085279 Arabidops	20 A		575	Caenorhab	C00945	98551	71 Caenorhabd	08 Caenorha	8 Caenorhabd	Ö	AL008880 Caenorhab	a	82073	_	U41264 Caenorhabdi	67 Caenorhabd	w	Caenorhabd	nuation (4 o	Caenorhahd	781086 Caenorhabdi	8 Caenornabd	-	617	M.artiel	Ascaris lu	80	55997 C.elegans	49125 Cae	044 Ca	Description

ALIGNMENTS

KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	CEF22B5/c	RESULT 1
HTG; Cuticulin; Elongation factor; GTP-binding ADP-ribosylation	Z50044.1 GI:899234	250044	Caenorhabditis elegans cosmid F22B5, complete sequence.	"CEF22B5 25823 bp DNA INV 02-SEP-1999		

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SOURCE
ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bin/display7db=wormace&class=Sequence &object=F22B5
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F22B5. It may be shorter because we only sequence overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
The true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-JUL-1995) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor; Phenylalanyl-tri
Caenorhabditis elegans
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence z66523.

The true left end of clone M05D6 is at 25723 in this sequence. The true right end of clone F14E5 is at 4610 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neighbouring submissions.
The true left end of clone F22B5 is at 24607 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 Mb of contiguous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 25823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end of this sequence (25723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phenylalanyl-tRNA synthetase; RNA binding
                                                                                                                                               gene"
                                                                                                                                                                                                                                              /gene="F22B5.2"
join(411. .462,584. .663,745. .1127,1216. .1471)
/gene="F22B5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z66523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              right end of clone F22B5 is at 16002 in
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/db_xref="GI:3876226"
/db_xref="SWISS-PROT:Q19706"
                                                                                                                                                                                    comes from this
                                                                                                                                                                            /note="similar to RNA binding protein; cDNA EST yk390d8.5 comes from this gene; cDNA EST yk499d6.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:6239"
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                                                                                                          /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              /clone="F22B5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence from chromosome III of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .25823) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elegans"
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complement(join(10849. .10984,11033. .11343,11397.
11578. .11832,11917. .12154))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="sptrembl:q19707"
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dkellnuleveydllkagagvegalpvkadasolfvqcqtvgtuppkecarprocsepog
Egaykganqtagefrylkkrsapvmenildvraelttlevlegnlpssltqagalvas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="Mofikilirkqraberematiligidnakitytikkefideetdti
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hsikshhwkifsccalsgdrivqamtwlcddvgsrlfild"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILDVQEDKQTAKTTSREHCRHCKGNDHWSTHCPYKVMYQLDEEADADKDTEKDRMAMG
MRPDGRQIDRNRSDENTCRVTNLPQEMNEDELRDLFGKIGRVIRIFIARDKVTGLPKG
FAFVTFESRDDAARAIAELNDIRMYHMVLKVEWTRPSN*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(10849. .12154)
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/gene="F22B5.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAEIWLDRSNSKAPWDWERLRDTYWKMPTVAFDLDGRTRKRCELMEQLQDEMLEAAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA90356.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /hote="cDNA EST yk304c8.3 comes from this gene; cDNA EST /k304c8.5 comes from this gene; cDNA EST yk594h3.3 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F22B5
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/db_xref="GI:3876227"
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                                                                                                                         CAACTGTCGTCGTCTTTCCATCCCCAATTTGTCACCAAGGTTGATCGGTAAGACTATG 3812
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/translation="MSWMPLDEVDILPKLPPNFDELRESKKWQERKEALEALLKVLT/
/translation="MSWMPLDEVDILPKLPPNFDELRESKKWQERKEALEALLKVLT
DNERRISTKASY AELIGHLQMVLAKDANINCQALAAKCIGKFATGLRAKFSSFAGPLLP
VIFEKMKEKKPMLREPLYDCSNEVGRTWOSLETGQEDILAALAKPNPQIKQQTALFVA
RQLDLVVPAKQPKGFIKAVVPVFGKLTGDADQDVREASLQGLGAVQRIIGDKWKNKLL
GDASSDEGKMKKIGEYAEKSTASFACHTSPIESASAASGDPSGTATA
VVSSGAEVAEADPWDFLDAFDVLSKMEDGFDTNIESKKWQERKEALEGLLDLITANPK
LDPKANYGALVERLOKVLEKDANINVAALAANCITGIANGLRYKFOFFAVSVYFPIIFE
LDPKANYGALVERLOKVLEKDANINVAALAANCITGIANGLRYKFOFFAVSVYFPIIFE
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LAQYHIIHESSNIISKIMKNASSRGKIVNENATNTHFGLTCVTTAFLCIITSLIIVDIL
FKTHETTFRYVVFMNIAVVAGGLFVTGYLLGHIVEIWFAKMSTIYSCROLGIQTYLITS
NSTGEEVRKLESAGCETAISSEFKNVFFDLLIQAVFIPLHILLTAFSWTFSGLIRPRW
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18794. .18946,18996. .19449,19497. .19843,20042. .20554,
20672. .21600,21677. .21812)
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/gene="F22B5:6"
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/db_xref="GI:3876232"
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/db_xref="GI:3876230"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgttaaaacaggtggtgccgcagcaaaacctgctgcagctgcgcaacttcgtttactcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAGGAACCAAATGAGGAGTGTGCTCGCCCAACGTGCTCTGAGCCACAAGGATTTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgtatacaaatatgcggatcgatcacagcttttctatcaatgccagatcagtattaccat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAGTTCTTGCTCAACAATTTGGAATATCCAACTGATTTGATGGCTGGACAAGAGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTGATGATGGAAATGGTGATACCGTGCAAATTTTTGGATGAGAACGGTTGTGCTCTTGA
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        Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Yaughan,K., Waterston,R., Watson,A., Weinstock,L.,
                                                                                                                                                                                                                                                                                                                                               HTG; Cuticulin; Fork head.
Caenorhabditis elegans
Caenorhabditis elegans
Cuticulario elegans
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z49125
Z49125.1 GI:790365
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Caenorhabditis
                                                                                                                                                                                                                                                                                         Rhabditina; Rhabditoidea; Rhabditidae; l (bases 1 to 34831)
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and Wohldman, P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                  Secernentea; Rhabditia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C47G2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete sequence.
                                                                                                                                                                                                                                                                                                                              Peloderinae;
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                                                                                                                                                                                                                                                                                                                              Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                     Rhabditida;
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FEATURES
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TITLE
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                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IT may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2 Mb c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neighbouring submissions.
The true left end of clone C47G2 is at 1 in this sequence. The true right end of clone C47G2 is at 6388 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence Z49912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-APR-1995) Louis, MO 63110,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palmer, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 34831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end of this sequence (34731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="cut-1"
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yk262c12.3 comes from this gene; cDNA EST
yk262c12.5 comes from this gene; cDNA EST yk665h3.5 comes
from this gene; cDNA EST yk278g8.3 comes from this gene;
cDNA EST yk78g8.5 comes from this gene; cDNA EST
yk439e8.3 comes from this gene; cDNA EST
yk439e8.3 comes from this gene; cDNA EST
yk439e8.3 comes from this gene; cDNA EST
yk380a11.3 comes from this gene; cDNA EST
yk380a11.5 comes from this gene; cDNA EST
yk380a11.5 comes from this gene; cDNA EST
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15433. .17108
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join(15433. .157
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                                                                                                     LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGICLTP
IGFASFLGIGTIVATALSATIFYVARPTSHKH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="C47G2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .34831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4878
   .15770,16205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .34831) overlaps with the start of
   .16531,16772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             computer analysis,
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CDS

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/note="similarity to Trichostrongylus colubriformis 11 kd /note="similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); CDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D36149 comes from this gene; cDNA EST EMBL:D36149 comes from this gene; cDNA EST EMBL:C13631 comes from this gene; cDNA EST yk358b10.3 comes from this gene; cDNA EST yk358b10.5 comes from this gene; cDNA EST yk358b10.5 comes from this gene; cDNA EST yk301f4.3 comes from this gene; cDNA EST yk301f4.3 comes from this gene; cDNA EST yk295f2.3 comes from this gene; cDNA EST yk295f2.5 comes from this gene; cDNA EST yk295f2.5 comes from this gene; cDNA EST yk295f2.5 comes
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL:C13621 comes from this gene; cDNA EST yk227d8.5 comulting this gene; cDNA EST yk257e7.5 comes from this gene; cDNA EST yk357e7.5 comes from this gene; cDNA EST yk3104.5 comes from this gene; cDNA EST yk335b12.5 comes from this gene; cDNA EST yk335b12.5 comes from this gene; cDNA EST yk35b12.5 comes from this gene; cDNA EST yk35b12.5 comes from this gene; cDNA EST yk366d7.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /di_xref="Stftembi:Q18695"
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TLSPAAFVTEYASTRPHYKYTQFVAFGIIVLITSAYFTIFRLQIYKYYHLDRGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(24417. . .24975,2504:
25668. .25907,25967. .26054,26106.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(30076. .30134,30184. .30492,31050. .31274,31321. .31480,
31534. .31653,31701. .31835,31889. .32104,32160. .32570,
32639. .32935,32998. .33215,33263. .33651,33802. .34049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENSILFSAILLCRLTPPICLNFLGMIHMDSHISMAKSFGIETQFTKLMGHLDVIPILA
KGINIYLPICIILLCAIHYYRVGAYVLHNIGFDQFVEADEMTNDMINSGRSLVQIERN
SIKRSNDRSQRTQNWTNSFGSSNAGNGSTTSKFKRSNKNDEERPMLEDDDEEVEESST
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/translation="MLFSMESILSSTKPKLEPPPKLEPEVTINEQVVDLPRSNTRLSE
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FEYYKEKFPAWONSIRHNLSLNDCFVKYAGNEGENFGKCGYWALDPNCEDMFDNGSFLN
RRKRYKKKNSDTYHEMMSHHYMPFPFPIPOGMPFPRMMHANIPMAVIMNURPAVPN
MPAFFIPONIDSOKILSMMASRIMPMDAPVSSGOKRTSSSSSPNENGSSAVSDKLSA"
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EMBL:Cl3621 comes from this gene; cDNA EST yk227d8.5 co
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/gene="C47G2.5"
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/db_xref="GI:3875033"
/db_xref="SPTREMBL:Q18696"
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.6054,26106. .26227,26277. .26608,
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                                 cuticle protein; cuticlin 1.
C.elegans DNA.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 2310)
Sebastano, M., Lassan
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C.elegans cuticlin
M55997
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MDETLIAKIADNLIVEEGCPAEELVKKSALISASAKILEAFIKIMFVSNAPAQQLEEI
ERNLIEERHYSYGLMREQMDNDPYEHSYQPDERIVEGILANELPNILQPULRDIEAN
GSVWQPLLRLIIELCNTNCMSTHEKIAVAFRSLPFINLKAAKMLPRASVLHCLLVKV
VILLHBSSFPCDELSPAAEYLLTEGGLLONIVDTATSENPGSSVACSGLRSFNONLGD
AINRAKKAGIPNQKLLAILSADNTWTELEDIIHLYNLKHRPQMQHDFNDSSVVSSIRN
DSHGFNDSEWTDASTKRAEMDATSSAKQAFSGFSSPFENMQRESDFEGGFDDTPDE
DEFRKLCSERANSSSCAGISFETSPIKWPGEAEKTSEKASEPSVVASTYPQQTNGNQ
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WADFSSFPTISPTAAANSASSSSSDAWPGSDIHLQGEASDWPLNNSHESKASDPVMVG
LAASISHPGDSSEA"
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                                   Caenorhabditis
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                                                                                                                                                                                                                                                                            CCATGCTTCTACATGGAGTCCGACAAGACTGTGTCCACACAGATCGAAGTCTCGGATCTC
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gaaccaaatagcgaatgtgttcgaccacaatgttcagaaccacaaggattcggagctgtt
                                TACAAATATGCCGATCGCTCCCAACTCTTCTATCAATGCCAAATCTCCATCACCATCAAG
                                                | tacaaatatgcggatcgatcacagcttttctatcaatgccagatcagtattaccattaaa
                                                                                            TGGACTTGCGATTCTGAGACCACTGACACCTTCTGCGCCGTCGTTCACTCTTGCACTGTC
                                                                                                                                                                                                                                     tggacatgcgattctgaaaccgttgatactttctgcgcggttgtccattcctgctttgtc
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91323673
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/product="outiclin 1"
/protein_ld="AAA27995.1"
/protein_ld="AAA27995.1"
/protein_ld="AAA27995.1"
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DKFLINNLESTPTDLMAGCAHIYKADHSQLFYQCQISITIKDPGSECAFPTCSEPQE
EGAVKQAGAGGAHAAAAPQAGVEEVQAAPVGAAPVAAAAAAPAVPRATLAQLRL
LRKKRSFGENEGILDVRYEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGISSTP
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567 c 433 g
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join(1186. .1920,1971.
/gene="cut-1"
join(1186. .1920,1971.
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/product="cuticlin
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/db_xref="taxon:6239"
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75.1%;
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Pred. No. 2e-64;
0; Mismatches 130;
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                               GTCAACGACCACAATGCACTGAACCGCAAGGTTTTTGGCGCAATTAAAACGCGCAATGGTG
                                               TAGAATATCCAACAGATTTAATGGCTGGACAAGAAGCACACGTATACAAATACGCTGATC 180
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Wuchereria
AF125580
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Ramzy,R., Helmy,H., Adely,M., Curtis,K. and Weil,G
Direct Submission
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Filarioidea; Onchocercidae; Wuchereria.
1 (bases 1 to 724)
Ramzy,R., Helmy,H., Adely,M., Curtis,K.
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VIVARMTQGICMSITGEFTLAGMLIFVIVSVATIVAITLLRSHSTKV"
112 c 128 g 236 t
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/db_xref="taxon:6293"
/dev_stage="L3 larvae"
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/db_xref="GI:4741875"
/translation="TVDTFCAVVHSCEVDDGNGDKVELLNADGCALDKELLNNLEYPT
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U73005
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Submitted (01-OCT-1996) GA3,
NA 80125, Italy
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Gene 193 (1), 81-87 (1997)
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Timinouni, M. and Bazzicalupo, P.
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             /translation="MCRAVSFLALFGLAAAIPVDNGVEGEPEIECGPTSITVNENTRN
PFEGHAYVKGLYDQEGCRSDEGGRQVAGISLPFDSCNVARTRSLUPRGIFVTTTVVIS
FHPLFITKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFQTQIVPMPVCKYEILDGGF
TGQPTQFATIGQQVYHKWTCDSETVDFFCAVVHSCFVDDGSGDTIQILMEEGCALDKY
LLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQITITIKEPNSECPRPTCSEPQGFGA
                                                                                              /product="CUT-1-like cuticlin protein precursor"
/protein_id="AAB66646.1"
/db_xref="GI:1657625"
                                                                                                                                                                /note="cuticlin gene; proteins of other nema
VRPGGSIAPKKQRRCQLRLIKKSGGDYDNTLDVRTDFSALDISDRDEALPMDLRHRAF
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/gene="ascut-1"
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Direct Submission
Submitted (15-MAR-1996) C. De Giorgi, Dipartimento di Biochimica
Biologia Molecolare, Via Orabona 4, 70126, Bari, ITALY
2 (bases 1 to 2584)
De Giorgi,C., De Luca,F., Di Vito,M. and Lamberti,F.
Modulation of expression at the level of splicing of cut-1 RNA in
                                                                                                               Meloidogyne artiellia
Eukaryota; Metazoa; Nematoda; Secernentea; Diplogasteria;
Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae;
Meloidogyninae; Meloidogyne.
1 (bases 1 to 2584)
                                                                                                                                                                                                                                     M.artiellia Mtcut-1
X96677
                                                                                                                                                                                                      X96677.1 GI:2648040 cuticle protein; cut
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                                                                                                   De Giorgi,C
                                                                                                                                                                                         Meloidogyne artiellia.
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5064. .5070
/gene="ascut-1"
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join(930. .954,2851. .3239,3583. .4083,4499. .4690)
/gene="ascut-1"
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Pred. No. 7.7e-49;
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Best Local Similarity
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                 aacaacaactgttgtcatttcgtttcattcattatttgttaccaaagttgatcgtgcata
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                                                                                                                                               CTTTGACCAGGCCGGATGCCGTTCGGATGAGCACGGCCGACAAGTGGCCGGAATTGAGCT
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2518. .252
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/translation="MERLLFAIGUFVALNAIFTVRAIPVDNGVEGEPEIECGPTSITV/translation="MERLLFAIGUFVALNAIFTVRAIPVDNGVEGEPEIECGPTSITVNETRUFEGEHYYKGLEDOAGCRSDEHGRQVAGIELPEDSCHVARTDAEPKGVFVSTTVVISFHEQEFYYKUDRAYRVQCFYMEADKTVSAQLEVSEITTQFGTQVVPMPVCKYEITDEGAALGQPTQFATAQQVYTSGTCDSETIDTFCAVVHSCVVDDGNGDTVQILMEGSCLEGAALGQPTQFATAQQVYTSGTCDSETIDTFCAVVHSCVVDDGNGDTVQILMEGSCALDKRELSHEELANLEQAFTQFTATAQQAYTSGTCDSETIDTFCAVVHSCVVDDGNGDTVQILMEGSCALDKRELLANLEGAALGQPTQGATAGQARAAAAATPPPAAAAPPAPIAPAIPARTQRLRTRQLRLLRK
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CMSSFRANHLLRYGHCNGCSHWWVHSTYCLFIVVFFSNEIK"
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join(<467. .943,1139.
/gene="Mtcut-1"
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/protein_id="CAA65452
/db_xref="GI:2648041"
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/db_xref="taxon:42426"
/clone_lib="lambda7-2(1)"
/clone="pUc(3000)"
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Mol. Bio
99339397
                    cut-1-like genes are present in the filarial nematodes, pahangi and Brugia malayi, and, as in other nematodes, components of the cuticle
                                                                  Filarioidea; Onchocercidae; Brugia.

1 (bases 1 to 637)
Lewis, E., Hunter, S.J., Tetley, L., Nunes, C.P.,
                                                                                               Brugia malayi
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
                                                                                                                                                      Brugia malayi cut-1 ge
AJ012617
AJ012617.1 GI:3858954
                                                          Devaney,E
                                                                                                                               Brugia malayi.
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            Biochem. Parasitol.
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          101 (1-2),
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                                                                    Bazzicalupo, P. and
                                                                                                                                                                                            29-JUN-1999
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              gaaattctaaatgctgatggatgtgctcttgataaatatttgctaaataatttggaatat
                                                                                                gatactttctgcgcggttgtccattcctgctttgtcgatgatggtaacggtgatactgtg
                                                                                                                                                                                                                                                                                                                 cttttacatggaagctgataaaacagttagtgcacagattgagggtatctgaaatcacaac
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GAAATTCTGAGTGCAGATGGTTGTGCTCTCGATAAATACTTGCTGAATAATTTGGAATAT
                                                CTTCTATATGGAAGCTGACAAAACGGTCAGCACCCAGATTGAGGTGTCTGAAATCACAAC
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Direct Submission
Submitted (06-NOV-1998) Devaney E., Veterinary Parasitology,
University of Glasgow, Bearsden Road, Glasgow, G61 1QH, UK
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/gene="cut-1"
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/translation="visfhplsvtkvdrayrvqcfymeadktvstqievseittafqt
Qivpmpvcryeildgcptgqpiqfatigqpvyhkwtcdsetvdffcavvhscfyddgn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="cuticlin"
/protein_id="CAA10074.1"
/db_xref="GI:3858955"
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join(<2...164,266.
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/db_xref="taxon:6279"
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                                                                                                                                                                                                                                                                                                                                                                                                               16.4%;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 190.6; DB 34; Pred. No. 4.4e-35; 0; Mismatches 54;
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Best Local Similarity
                                                                                                                                                                      Matches 171;
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                                                               accgttgatactttctgcgcggttgtccattcctgctttgtcgatgatggtaacggtgat 615
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                                               ACCGTTGATACCTTTTGCGCAGTTGTCCACTCCTGCTTTGTGGATGATGGCAACGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (06-NOV-1998) Devaney E., Ve
University of Glasgow, Bearsden Road,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cut-1-like genes are present in the filarial nematodes,
pahangi and Brugia malayi, and, as in other nematodes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brugia pahangi cut-1 gene, AJ012618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     components of the cuticle Mol. Biochem. Parasitol. 101 (1-2), 173-183 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 358)
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                                                                                                                                                                                                                                                                                                           /number=1350..356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brugia pahangi"
/db_xref="taxon:6280"
join(<1. .191,350. .>356)
/gene="cut-1"
                                                                                                                                                                                                                                                                                           /gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                      INADGCALDKYLLNNLEYPTDL"
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:096776"
/translation="PIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEI
                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA10075.1"
/db_xref="GI:3970656"
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                                                                                                                                                                    Score 156.6; DB 34;
Pred. No. 4.6e-27;
0; Mismatches 24;
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d, Glasgow, G61 1QH, UK
                                                                                                                                                                 24; Indels
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                                                                                                                                                                                                    358;
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTION THIS sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small contents of the specified clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, usir predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Latreille, P., Lightning, J., Lloyd, C., McMurray, A., McTtimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                             overlap between neighbouring submissions.
This sequence is the entire insert of clone F53F1. The true right end of clone M04G12 is at 21759 in this sequence. The start of this sequence (1...101) overlaps with the end of sequence z81103. The end of this sequence (39379. .39478) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans
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Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bin/display?db=wormace&class=Sequence &object=F53F1
Current sequence finishing criteria for the C. eleg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z81088.1 GI:1627965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nttp://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                           AL021448
                                                                                                                  complement(14923.
/gene="F53F1.1"
                              16033. .16271,1
/gene="F53F1.1"
                                                            complement(join(14923. .15347,15663. .15774,15835. .15984, 16033. .16271,16318. .16486))
                                                                                                                                                                               /clone="F53F1"
                                                                                                                                                                                                          /chromosome="V"
                                                                                                                                                                                                                                        /db_xref="taxon:6239"
/note="predicted using Genefinder; similar to cuticlin"
                                                                                                                                                                                                                                                                   ∕organism="Caenorhabditis elegans'
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                 .39478
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                                                                                                                                                .16486)
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for a small
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/Note="predicted using Genefinder; similar to cuticlin; cDNA EST EMBL:D72018 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C12451 comes from this gene; cDNA EST EMBL:C10189 comes from this gene; cDNA EST EMBL:C106b3.3 comes from this gene; cDNA EST yk37e9.5 comes from this gene; cDNA EST yk31h10.3 comes from this gene; cDNA EST yk31h10.3 comes from this gene; cDNA EST yk31h10.5 comes from this gene; cDNA EST yk31h3.5 comes from this gene; cDNA EST yk31h3.5 comes from this gene; cDNA EST yk191d9.3 comes from this gene; cDNA EST yk191d9.5 comes from this gene; cDNA EST 
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join(25572...25660,25850...26408)
/gene="F53F1.5"
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19919. .20008,20072. .20251)
/gene="r53f1.3"
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18714. . 20251
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NYEIVHLEELKTYAKVPPCANQLEYHPHFARIPLQKYCKEKNIFFQAFSSLARHEPKL
IEDPVVVELAKKHNTSVPLVLLAWALRQNVGIVPKSVTPSRIVENFKVIDIALTPEDI
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/LPPLQLPRFELPRLSLPSFGGGGGGBAPCGGAAPAYVAPPPAAGYAAPPPAGGYATA
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join(21582. .21670,21781. .22009)
/gene="F53F1.4"
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/gene="F53F1.2"
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18339. .185
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gene

/note="predicted using Genefinder; similar to cuticilin; cDNA EST predicted using Genefinder; similar to cuticilin; cDNA EST predicted using gene; cDNA EST EMBL:D7036 comes from this gene; cDNA EST EMBL:D7036 comes from this gene; cDNA EST EMBL:D7358 comes from this gene; cDNA EST EMBL:D7407 comes from this gene; cDNA EST

Query Match 9.3%; Score 107.4; DB 34; Length 39478; Best Local Similarity 61.7%; Pred. No. 2.1e-15; Matches 171; Conservative 0; Mismatches 106; Indels 0; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                               bin/display?db-wormace&class*Sequence &object=E04D5
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a smale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, F., Hawkins, T., Hiller, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Liatreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Waterston, J., and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
sequence Z48585.
The true left end of clone ZK673 true right end of clone T09F3 is
                                                                                neighbouring submissions.

The true left end of clone E04D5 is at 1 in this sequence. The true right end of clone E04D5 is at 2110 in
                                                                                                                                                                      overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone E04D5.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-OCT-1995) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McMurray,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 31536)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z66496
Z66496.1 GI:1041307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 31536)
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FEATURES
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The end of this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from this gene; cDNA EST yk45409.3 comes from this gene; cDNA EST yk45409.5 comes from this gene; cDNA EST yk450b11.3 comes from this gene; cDNA EST yk40b11.3 comes from this gene; cDNA EST yk40b12.3 comes from this gene; cDNA EST yk375c1.3 comes from this gene; cDNA EST yk375c1.3 comes from this gene; cDNA EST yk37468.3 comes from this gene; cDNA EST yk37468.3 comes from this gene; cDNA EST yk37468.3 comes from this gene; cDNA EST yk365e8.3 comes from this gene; cDNA EST yk256f12.3 comes from this gene; cDNA EST yk256f12.5 comes from this gene; cDNA EST yk256f12.3 comes from this gene; cDNA EST yk256f12.3 comes from this gene; cDNA EST yk360e3.5 comes from this gene; cDNA EST yk360e3.5 comes from this gene; cDNA EST yk59a6.3 comes from this gene; cDNA EST yk69a6.3 comes from this gene; cD
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/gene="E04D5.1"
join(6082. 6250,6307. 6379,6432. 6509,6564. .
5750. 6930,7003. .7283,7337. .8179,8228. .8326)
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CDNQVTRVFELATNKELILCVELKRTRKLIFSPKDNFLLTFEPMAVYGPRTAENOKPED
UNRVYSLADGKHVSTFSAPKEASMEPQFSDDESLAARMYGSEVFFYTNMSFDRYDKL
VEKGATNFALLSGPAPHHVAVYVPAVGSTPARVRVHRVSESFPVVGNRTFFKSDKAVM
TWNQRGQSLLILASVEVDKTNQSYYGEQSLYLINIQSGESVVVPLEKKGPIYAAKWNP
                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(8619. .8761,8813. .8988,9895. .10028, 10089. .10283,10330. .10614,10730. .10935,11582. .11629,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(8619. .11718)
/gene="E04D5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGREFAVCYGYMPAKVTFYNPRGVPIFDTIEGPRNDVFYNAFGNIVLICGFGNIAKGK
MEFWDVETKKEIISIEVPNTTLFDWAPDGQHFVTCTTAPRLRIDNSYRFWHYTGRMLA
ETHFESPKELWEVRWRPMTGYNKFAIKELTKTDKMAAGLPIRKKDASHPLNNVPAGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RQAGAYIPPHLRKPLGGGGSAGPPSAAAPTPGNQNQRPAQPRANGNGNAPOPFRPQQS
EQERKAFQLKKKYEEIKVLKQRVANGDQLQPNQMEKIQRENEYLSELSKLTI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA91279.1".
/db_xref="GI:3875451"
/db_xref="GI:3875451"
/translation="MPAPNTTPSRDSNFFVISSSFSNFLLLPEKFKTFSFFRLSQTLI
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/translation="MFGENLFYADIHSTIPFKCEKLKIRVFLSENAQKHLFGFFLKYP
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                                                                                                                                                      /protein_id="CAA91282.1"
/db_xref="GI:3875454"
                                                                                                                                                                                                                                                                                                                                                                                11691. .11718))
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YIVPVFFIAKVVQFAIPFILILITFERYLWTCTERKRFGITFQVLTLSLSFRKAFSAI

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DEFINITION ACCESSION
                                                                                   RESULT 11
CEF53B6/c
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Best Local Similarity 56.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 tggaccaaccggtcaaccagttcaatttgctatcattggtcagccagtttatcataaatg 539
                                                                                                                                                                                                                                                         agaaccaaatagcgaatgt 795
                                                                                                                                                                                                                                                                                                                     CTTCAAATTTGCTGACAAAGCTGGGCTTTATTTCAATTGTCAAATTCAATTAACAATCAA 28082
                                                                                                                                                                                                                                                                                                                                                                    atacaaatatgcggatcgatcacagcttttctatcaatgccagatcagtattaccattaa 776
                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGATCCTTCAGAATCTTGAGTACACCTCTGACTTGACAGCTGGAAAACTCGCACCAGT 28022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATGGACAAGGTGGACCACCAGTAACTGTCATTGATGCCAATGGATGTTCTGTAGATGG 27962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgatggtaacggtgatactgtggaaattctaa---atgctgatggatgtgctcttgatáa 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACTTGCGTTGCTGAACTTGAGAATGTGTACTGTATGAAAGTTCACTCATGTACGGTTTA 27902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAGCCGGTGGATCACCTATTAAGTACGCTCGAATCGGAGATCAAGTCTATCACAAATG 27842
                                                                                                                                                                                                       AGACGTAAATTATGGATGT 28101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179;
Caenorhabditis elegans cosmid F53B6, complete sequence 281086
                                                           CEF53B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10458 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA91281.1"
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/db_xref="SUTREMBL:Q19054"
/db_xref="SUTREMBL:Q19054"
/translation="MWSINLTVHIILLVTFSVSHVVTTAVTKATGETTVRGAGQDLGD
VSSSFFYETTTASTCADDPNTDCTQYTFLCSNAKYTPLLQQFCAKTCGFCGSGSTAAP
VACVDTSTQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPYDSHESGYPTRPANYPVASSRYPIPTTQAPASYPSSPAPPPPGADIDNGYPEPQPI
YIAETPENAYDGIVGFNDTEQPFTTSAAYTEDGVYSRLIKRNVVESTEQINASNKKRP
VTVGDIDLPERGILVEGLEEMEDGETTNAGDHGATRALREARNSQEKTCFSTSRMYFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSEPSCHTVGDGKTGHRFEVRHDSCGVRRQREINGVVISATVIISFHSIFITKIDRAY
RVSCFVVEGTKKVHNHVDISALTTQLLESETQLFVGKT8ILNEAGGSPIKYARIGDQV
YHKWTCVAELENYYCHKVHSCTVYDGOGGFPTVVIDANGCSVDGVILQNLEYTSDTA
GKLAPVFKFADKAGLYFNCQIQLTIKDVNYGCSNTQPQCPTSQYVVEPAQKTTETAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDFHVITAIQMMFPFVVLLLLNLTIIKRLVAEKRENMYPILRGAGTTTEVKKASFVQG
NLPENYVLLQVAADVIKESLIHRSSRSKRSQLRNAIYTMLAIVTSYLVCNGVHLFLTI
LERFDPSYLVESTDRMQSSTFYIVLSDTVSICYMASSAIRIFIYAKCNPKLRQEITDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA91280.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="E04D5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28158.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(25834. .25873,27277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="E04D5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKREKSIETNSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="E04D5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(29675. .29840,31127. .31214,31267. .31348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="E04D5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to cuticlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MPSRLAMKELKGGGEPEVVCETASISLLFKTRNSFNGKVFVKGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5592 c
                                                           32412 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .28410,28491. .28811,29092. .29213)
"E04D5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5636 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 83.8; DB 34; Pred. No. 7.8e-10;
                                                              DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137;
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AUTHORS
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ORGANISM
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Sandders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IT may be shorter because we only sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F53B6. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; Cuticulin; Human platelet tetraspan antigen like; Initiation factor associated protein; Thrombospondin like.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence Z81523.

The true left end of clone F32H2 is at 32306 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neighbouring submissions.
The true left end of clone F53B6 is at 1 in right end of clone F53B6 is at 5116 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                start of this sequence (1. .105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94150718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z81086.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bin/display?db=wormace&class=Sequence &object=F53B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 32412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end of this sequence (32306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z81523
                                                                                   platelet-endothelial tetraspan
/protein_id="CAB03120.1"
/db_xref="GI:3877452"
                                                                                                                                                                                                                              1480. .3649
/gene="F53B6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                        codon_start=
                                                                                                                                           /gene="F53B6.
                                                                                                                                                                      join(1480. .1638,1707.
3205. .3308,3430. .364
                                                                                                                                                                                                                                                                                                               'chromosome="I"
                                                                                                                                                                                                                                                                                    'clone="F53B6"
                                                                                                                                                                                                                                                                                                                                                  'db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                             organism="Caenorhabditis elegans"
                                                                                                                note="predicted using Genefinder; Similarity to Human
                                                                                                                                                                            .3649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secernentea; Rhabditia; Rhabditida;
                                                                                                                                                                                                    .1946,2437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .32412) overlaps with
                                                                                      antigen (SWLPET3_HUMAN)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this sequence. The true
                                                                                                                                                                                                    .2628,2969.
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В Š В δõ 밁 δõ В Š Ъ δÃ В Š

gene

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/note="predicted using Genefinder; similar to thrombospondin like; cDNA EST EMBL.214404 comes from this gene; cDNA EST BBL:C12571 comes from this gene; cDNA EST yk195c9.3 comes from this gene; cDNA EST yk195c9.5 comes from this gene; cDNA EST yk28697.3 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk333e3.5 comes from this gene; cDNA EST yk353h1.3 comes from this gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4270. .15311)
/gene="F53B6.2"
complement(join(4270. .4339,4493. .4547,5071. .5295, complement(join(4270. .4339,4493. .4547,5071. .5295, complement(join(4270. .4339,4493. .4547,5071. .5295, complement(join(4270. .4339,4493. .7287,7546. .7877,7546. .7877,7546. .7877,7546. .7877,7546. .7877,7546. .7877,7546. .13784,13931. .14132, 14183. .14294,14341. .14457,14994. .15155,15198. .15311))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKCSYTVVFLLFYLLIASFHVDALSWAAWSPWSSCTKTCGGGVS
RQLrRCLTSKCSGESVRRKVCAQKTCESKSRLARDTICGGEEIVSRGQCEVCBSRLT
GANELMRVDDGTPCQAATSRAVCSKGSCOIVGCDGLISSSFRFDACGVCGGRGDTOD
GKFIWKYSEEYTACASNCDDIVDWSGAGRSIASTSQPIVVCVNAITGRVVPEKLCADK
LRPKVEARPCPMLICPSRWMAADWTECVPHCGEGTRKREVYCYQTAHNVTVHVPDTFC
                                                                                                                                                                                                                                                                                             comes from this gene; cDNA EST yk193h3.5 gene; cDNA EST yk411f5.3 comes from this yk411f5.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OWRYGOMTOCSASCLGGKOKAALKCIQVSTĞKSVQMSQCDARRRPPEKSRPČNQHPCP
PFWLTSKYSDCSMSCGGGTARRSVKCAQTVSKTDGADAHIVLKDDRCHFKKPQETETC
NVVACPATWYSSLINKBHKIKIKLKKLYAQWTESCSRSCDSGERRRQVMCEIRDSRKKTD
RRPDVECDANTKPQTVEVCSFGSCSRPELLSNRVFEQNAEQKKLTLGIGGVATLYQGT
SIKIKCPAKKFDKKIXKKNCKKIKNDAHIKVSANGMLRVFHARMEDAGVYECCTDR
LOGNVTLNFKYRDFPARSTVDLAPKDQIPSTKNAQRVUVSKEDVLREQASVLHKNNYSL
LEALLTAPNDEKAREQLRKYGNELVARWDIGHWSECROKTCHVAGYQARGISCKVTFH
                                      SSKAKHSKRSSKSSKKGTSGKSGKGSSKRGGKSSKSKSKKVKTATTSGSQVSTVSAA
TGVSDKQSNSSKSSRKSSKSSKSRKNRRLDSDAQKKMEKSGKSGKVALIPKTQQTTGS
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VPLTAIVTTSLPMVAAIAFCAKNRKTVHAKNKNKNKNKSSKSAKSSKSTRGASKSGKSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(20516. .20602,20648. .20953,20999. .21424. 21609. .21818))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(20516. .21818)
/gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(19892. .20022,20241. .20283))
/gene="F53B6.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEIRNVDNSICESLASVRPPETRPCHREDCPRWEASQWSECSSQRCVSSMLAQKRRNV
TCRFTNGTSVDIQHCDITNRPATTMDCPNQNCKAEWRTSDWGSCSSECGTGGVQLRLL
SCVWISSGRPAGRNCEQMRRPHSARACVADEPLPPCMPTASALYQRDASCQDQSRFCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTRPAAEENCVSTSCGRWEAGKWSKCTASCGQGVRRRHVACVGGSDCDEGGRPRQE
TTCYAGIPCSIATNSLDWNDRAYLDGNTFGSWDNHNDWQAPRLVAGEWSTCSSTCGTG
VMSRTYECVAVNPISSAPIKLPMSECQDQEQPKLFESCEVRSCPLQEDSKLSEDEAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKWYMHQRAPKLLIPESCCIPSEIERCRSNPFDQDAPPPYYTSTCYEPLQNDLLHVMN
VASWLCITNAIVQVIFVSLKTIKLLNFILLKT"
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LYVDVGRILVIISILSILNYLICFYAIFKEMRCFVTSCAVASIVIAVMLIIGGCIGLN
FRDQLTHYTPLNLKMLTSLRELYGTHDMKGITESWDALQSNFKCCGVNGTDNAQIWKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGYYQSNYWGKRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB54255.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(19892. .20283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIKLFHSCDSLEVROKCCSTCTFVERKKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB03121.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F53B6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F53B6.8"
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YRVNPVYGFAEPRSSVKIDVLRLNGEQKTDKLVLLTANANGSTNPHEAFANQAEHREM
                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted using Genefinder; cDNA EST yk193h3.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F53B6.4"
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                                                                                                     407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cacttccatttgattcatgcaatgttgcgcgtacacgatctctgaatccacgtggtattt 286
                                  TTGGGTATGTTAACTCTGAAGTATTAAATCAATT 29618
                                                                                                                                                                                                                                                                                                    CATTTTCCTTCACAATGATCACCTCGTTTCATCCATTCTTTGTGACGGGAATGGATCGAG
                                                                                                                                                                                                                                                                                                                                                                   ttgtaacaactgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtg 346
                                                                                                                                                                                                                                                                                                                                                                                                                                     CAATTCCAATTGGAGCATGCAATATGCGGAGGCAACGAACACTGCATCCACGTGGAATAT 29772
                                                                                                 tatctgaaatcacaactgcttttcaaactcaaat 440
                                                                                                                                                                   CATTCAGTATTCGATGTTTCTTCCTCGAGTCAATTAAAGGATTGAACGCGGAAATTGATG
                                                                                                                                                                                                                              catatcgagtacaatgcttttacatggaagctgataaaacagttagtgcacagattgagg 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="Cab03116.1"
/db_xref="GI:3877448"
/db_xref="GI:3877448"
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hpfytgendrafsircfflesikglnaeidvgtlapohvdgeyslpvcayhlkdgieg
hVlrfaqvggkvyhvwrcdodashvygilihscyaddohgkrelvdraecstopfle
hVlrfaqvggkvyhvwrcdodashvygilihscyadoggesipvcayhlgegeshfgi
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EVFCSPDMKSVQTAAFLIKGLGLSYTTINIDPALLSYROMLPTNFQEMLLSPKAFFNM
GYPINIQYLPSQGFIRAENIEDYNLRIQAFFKKNIAKIEQKQVVVISDNVMVDLTRNE
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GQSIAQCRIHTEKTVPIVKGGEQARMEENEIYAIETFGSTGKGYFHDDMETSHYMKNF
ELADEKIPLRLQKSKGLLNLIDKNFATLAFCRCWIDRLGETKYLMALKGKCSYSTASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(27666. .27862,27919. .27959,28076. .2877
28905. .29001,29330. .29417,29467. .29606,29648. .29915,
30107. _30301,30478. .30589))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(27666. .30589)
/gene="F53B6.6"
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/db_xref="GI:3877450"
/translation="MSRESPVSLAQLVERETFNLKVRGSSPLVSHAESMGLIFPNWVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="TTT Lys K-tRNA; predicted preliminary prediction; similar (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F53B6.7"
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26258. .27459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB03119.1"
/db_xref="GI:3877451"
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/gene="F53B6.5"
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23555. .24160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(26258. .26342,26501. .2
27153. .27288,27334. .27459)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 74.8;
Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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le-07;
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to tRNA-Lys"
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28770,

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TITLE
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone R07E3. The true right end of clone F41E7 is at 36774 in this sequence. The start of this sequence (1..115) overlaps with the end of sequence Z68106.

The end of this sequence (39633..39736) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, M., Laister, M., Johnston, L., Johnning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson, Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jes@sanger.ac.uk or rwênematode.wustl.edu
On Nov 21, 1995 this sequence version replaced gi:798823.
Coding sequences below are predicted from computer analysis, usin
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-MAY-1995) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elegans
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Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cottage, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z49207.1 GI:1067021
HTG; ADP,ATP carrier protein; Cuticulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans cosmid R07E3, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CER07E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea;
Rhabditina; Rhabditoidea; Rhabditidae; Pelo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2 Mb of contiguous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 39736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 39736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL032624.
/note-"Serine and threonine rich protein, Carboxyl terminus is glycine rich; cDNA EST EMBL: COB296 comes from this gene; cDNA EST yk259b4.5 comes from this gene; cDNA EST yk559c11.3 comes from this gene; cDNA EST yk574h3.3 comes from this gene; cDNA EST yk597h8.3 comes from this
                                                                                                                                                                    5080. .8873

//gene="R07E3.6"

join(5080. .5246,5409. .5769,5826. .5942,6381. .6905,

6955. .7075,7125. .7448,7495. .7787,7831. .7980,8037. .8174,

8222. .8405,8470. .8873)
                                                                                                                                                        /gene="R07E3.6"
                                                                                                                                                                                                                                                                                                                                      /clone="R07E3"
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:6239"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               þ
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Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
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                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                   CDS
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complement(join(21213.
22011. .22170,22220. .;
23254. .23259))
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                                                                                                                                                                                                                                                                                                                                                     complement(21213. .23259)
/gene="R07E3.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(17917. .18025,18074. .18331
18604. .18751,18800. .18877,18947. .19072))
/gene="R07E3.4"
/note="similar to ADP,ATP carrier protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="cDNA EST yk278a10.3 comes from this gene; cDNA EST yk278a10.5 comes from this gene; cDNA EST yk486f8.5 comes from this gene; cDNA EST yk603d8.3 comes from this gene" /codon_start=1 /protein_id="CAA89072.1" /db_xref="GI:3878960"
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/translation="MASTSATLDVLETSKKCLAGSAAAAISKTTTAPFDRVKLVLQLQ
ROSEFAMAEY MGIRDCISKIBLEQGAMALWRCNGAGYVARCLPHHTLNPAFRDIYRNTL
LKNVDRNESFGKFLAGTFVSGGLGGATTLFMLYPFDFARTRLALDVKKDGSRKYKGMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(17917. .19072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEIGSTIYPIAVKYDTRLTDAFWNSSAQSYGRYLWSMMTSWAIICDVWYLPAMTRGEN
EDSISFAKRVKRAIAKKGGLIDLEWDGALKRERVSSKLVTLQOKLYFERLARTTTLNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(11510. .14654)
/gene="R07E3.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NSLRSTGGALIITFYYEFSKYM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQISITTSGMVCYPLDTVRRSMMMQSGKQIKQYTSTKDCWKTLYKKDGINGFYRGALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCLKKIKASEGVASWYKGLSSALQFVIASRAIFFGIFDSIRTSVEDPKSLNFAACWAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLEEKSSDILNIMQGISEEERDELLKQIDEQDDEEEMIRKISSLKPKFKIGDHDADEH
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EGYEQGRDGVKTTFHGDSGVMTGGGHSAPTFDYLNMPSESFGLAPVAPPAPPPPPATQ
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QQLAGRLYQPDMDSGEPESAEDGIDKKKTAEKVDFTDDNNYSOSDADAKDSTHENGG
EHVSTTPEESITENTTAEVPASTASTKOTKLSVKIRSEDEKREEDKLSDDDEKPNYKKK
EHVSTTPEESITENTTAEVPASTASTKOTKLSVKIRSEDEKREEDKLSDDDEKPNYKKK
LEEIYKKEEELVERELAEMSVAAEIFEKEVVIKTTKVTPTSTTTEIPTTTTEEATTTT
                                                                                                                                               codon_start=1
                                                                                                                                                                                'note="similar to cuticulin"
                                                                                                                                                                                                                     /gene="R07E3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="R07E3.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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                                                                                                                                                                                                                                                                                          3. .21359,21654. .21739,21787. .21886, .22335,22428. .22542,22637. .22779,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .18331,18378. .18555,
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KVIQISMPPPTMHSKQLNMPVCKYEVLDGSPTGPPVYFATVGQMVYHKWTCDTEHENT FCMLVHSCFVDDGNGQRVQLLNDKGCALDKYLLTNLEYPTDLMAGREAHVYKYADRDN

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Sin
                                                                                                                                                                                                                                                                                    GATGCGCTCTCGACAAATACCTCCTCACAAATCTTGAGTATCCCCACAGACCTGATGGCGG
                                                                                                                                                                                                                                                                                                                                  gatgtgctcttgataaatatttgctaaataatttggaatatccaacagatttaatggctg 700
                                                                                                                                                                          gccaagaagctcacgtatacaaatatgcggatcgatcacagcttttctatcaatgccaga 760
TTTCGATCACAGTCAAAGAGCCTGGTCTTGACTAT 22017
                                                                                                                                        GAAGGGAAGCCCACGTATACAAATATGCCGATAGAGATAACATGTATTTTGATTGTCAAA
                                                            tcagtattaccattaaagaaccaaatagcgaatgt 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to cysteine proteinase; cDNA EST EMBL:M89104 comes from this gene; cDNA EST EMBL:D69358 comes from this gene; cDNA EST EMBL:D69368 comes from this gene; cDNA EST EMBL:D6368 comes from this gene; cDNA EST EMBL:D69680 comes from this gene; cDNA EST EMBL:D69680 comes from this gene; cDNA EST EMBL:D73027 comes from this gene; cDNA EST EMBL:D6900 comes from this gene; cDNA EST EMBL:D73027 comes from
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LHKEAEFIEPIPESLTAKKGESSSPFPDFFDWRDKNVITPVKAQGQCGSCWAFASTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(26570. .26749,26841. 27330. .27815,27863. .27958,28006. .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:Q21814"
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/translation="MLINTSFSQCVVLFSFSQLALSLLSVKTGEEVVDTEAAVTWEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(29470. .29618,30123.
30963. .31067,31117. .31252))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEAAWA IAHGEKRNLSEQTLLDCDLVDNACDGGDEDKAFRY IHRNGLANAVDLPYVAH
RQNGCAVNDHWNTTR IKAAY FLHHDEDS IINWLVNFGPVNIGMAV IQPWRAY KGGVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL:C09692 comes from this gene; cDNA EST comes from this gene; cDNA EST EMBL:C12356 gene; cDNA EST EMBL:C12305 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(26570. .28295)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEVADKEDGHQCQTKQCRLLDDLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVEDTVEVVIMEEDMVAEVTMEEAAMEVAETWEVDTDTEVVTADMVATEVADTEEVVIM EAATEWEEDTEEVVTADMVANTEVADTEEVVIM EAATEEETWEVVVDTDTOTTEDHUNQWEDSKEVMVDNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(29470. .31252)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSEYACKNEVIGLHALLITGYGTSKTGEKYWIVKNSWGNTWGVEHGYIYFARGINACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA89070.1"
/db_xref="GI:3878958"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yk587h4.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="R07E3.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA89074.1"
/db_xref="GI:3878962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(23363.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTSPKLEKTKSTML"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="R07E3.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MLAVIAGILAVLLILILFFCIRSKDKKQPPSPAEPNRRLPTRAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="R07E3.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 34;
Pred. No. 7.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene;
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.28071,28119. .2
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RESULT
CEY39A1_
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VERSION
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CEM142
                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence split into 5
Fragment Name
CEY39A1_0
CEY39A1_1
CEY39A1_2
CEY39A1_3
CEY39A1_4
CEY39A1_4
                                                                                                                                                                                                                                                                                                                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agtattaccattaaaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGATGGGAATGCATTGAAGTGGAGGGTGCTGATAAGGACACTTTCGGAATGTTAGTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaatggacatgcgattctgaaaccgttgat-----actttctgcgcggttgtccat 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gatggtggaccaaccggtcaaccagttcaatttgctatcattggtcagccagtttatcat 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCTAGACGCGGTGCTTCTCTCAACTCCGGACTACGATACTTCTCTGCGTCTCGCCACG 82172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gctcttgataaatatttgctaaataatttggaatatccaacagattt---aatggctggc 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTGCTATGTGGATAACGGCTACGGTGATAGAGTGGATATTCTTGATTCGAATGGTTGT
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197; Conserv
                                                   Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                              Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; 1 (bases 1 to 36306)
                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEM142
    Nature
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                               HTG; Cuticulin; Homeobox protein EVX1 like
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    368
                                                                                                                                                                                                                                                                                                                                                                                                        GI:1657678
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                                       contiguous nucleotide
  (6466),
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200001
300001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                36306 bp
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52.3%;
32-38 (1994)
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210000
310000
410000
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Pred. No. 3.4e-05
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                                                                                                                                                                                                                                                                                                                         Secernentea; Rhabditia; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300001 (299293 Caenorhabditis elegans
                                     sequence from chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANI
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                                                                                                                                                                                                                                                                                                  Caenorhabditis.
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.17468,18628. .18766,20758. .20915,22487. .22677

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MEDLINE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone M12. The true right end of clone C44B9 is at 5059 in this sequence. The start of this sequence (1..104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-MAY-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on Nov 4, 1996 this sequence version replaced gi:1370039. Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bin/display?db=wormace&class=Sequence &object=M142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McMurray,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 36306)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end of this sequence (36203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submission
GVGTIDVFTDSVTVLEQEPACQQVTTYSFRFSISTNQKIENS"
                                                                                                 SMCKTEFRPGTPEIICGPDRIGVKASTKQPFEGNVFVMDHYHDEECRAGPEKFPDSRS
IGLTVPFSACNVHRYRSLNPKGIFVEVSIVFMFHSLFMTKTDQTVKVQCFYMEADKHV
TVPLSVSMITTVFREQIYQMPQCAYTLRKGAPDGPIVRFATLGESVYHRWECIEVEGA
                                                                                                                                                                                                                                           /db_xref="Sptrembl:Q21540"
/translation="MRPIPYDISLSITSFLSLILICSANPIDNGLVDSELTHECVTHK/translation="MRPIPYDISLSITSFLSLILICSANPIDNGLVDSELTHECVTHKAVETLLLESSLGSHMALIQYAETPKLEFSLGOFNHFTQLEMAIQRIEYQSGATNTGQALRLTLEKGLQGARPGIPKVAIVITDGQSQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SWISS-PROT:010658"

/translation="MKAEQQQOSIAFESQMPRPPPVTEQAITTEAELLAKNQI
TPNDVLALPGITQGFLCSPSANVYNEFTKFQIRDLDTEHVLFEIAKPENETEENLQA
QAESARYVRYRFAPNFLKLKTVGATVEFKVGDVPITHFRMIERHFFKDRLLKCFDFEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z99276.
                                                             DKDTFGMLVHSCYVDNGYGDRVDILDSNGCGLDAVLLSTPDYDTSLRLATKPYHVFKY
                                                                                                                                                                                                       VSEPSQLLRDADVMVYAIGVTNLVNVHQLHQMTGNPVRVFTVESFEQLDRALADSLTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(8540. .8572,9335. .9416,9468. .9679,10373. .10721,
10772. .10974,11033. .11175,11871. .12501)
/gene="M142.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFCMPNSRNNCEHIYEFPQLSQQLMDDMINNPNETRSDSFYFVENKLVMHNKADYSYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="cDNA EST yk258al.3 comes from this gene; cDNA EST yk258al.5 comes from this gene; cDNA EST yk532all.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(3511. .3570,4639. .4750,4821. .5201,5689. .5795)
/gene="unc-119"
                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA97806.1"
/db_xref="GI:3878735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA97807.1"
/db_xref="GI:3878736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted using Genefinder; similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3540. .12501
/gene="M142.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="unc-119"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="M142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5795
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MIEITISIOSNTHVSSQLWSAVRARGCOFLGPAMQDDVLRLILMTLETGECIARKILV
MYVVQTLASDYPQVSKTCVGHVQLLVRARGCOFLGPAMQDDVLRLILMTLETGECIARKILV
MYVVQTLASDYPQVSKTCVGHVQLLVRASCFNVLKROESSCLMQLKEEFRTYESLRR
EHDSQIVQIAFESGLRIGPDWSALLYADGSHRSHMOSIIDKLOSKNSYQOGVEELRA
LAGSQTSMLVPAYRYFLTQVIFCLEFFAGIEHDDTSMRNIGDALHQIRILLKLHCSQD
DLRKMPKEERRGVILQAEVPGGMGGGPGSGGAEAGRIGCHPLYSQLDETGRSISRT
NFKDNSHNSPOTPPKOPROKRYQMGIPPNRMGYSSDAPPFIPSHQQPPPQFFNSOHL
PQRFRGGRQRGAPPPPPPQPMMLIGYDMFGAFMMQATEVLTADGQMVNGTPQRFVIM
QSETHLPGGPVMLPQQOMVPPPQSMTPVGGEPMGPMGPMTPSIPVQVPPNTMMTATSP
TGSVIYPAASPPGQPPHTIHIQSIGVFKRKSNFLKIVRKISFLUFYDFFLILRKLKK
EKKGADIEFFEKIKSTDFKKYPSSFSRTDGNSFPMEDRGSGGMWGGFGTMLRESGADA
EQULAKRYELIKRLOPSEDDDDPEDGGIGHVSYTVASSVLDDRMDHHPLTMIPVFID
LPAIPISFANMPTEETMTMIGEMVQNRPRAPSLTAPSSNQPMNVNASASATVQAECEN
RKILDFPLKYRKMTLMFEKVSTCFHVTLLKDYMVFYULNTLKFAKSMFPRRRRAATIPQ
PVIPMVQVPVQVPIYPAENKNPNVPPPPPPQGQPMLVDSAIGLLTPRRPILVAHPQN
PVIPMVQVPVQVPIYPAENKNPNNPPPPPPPQGQPMLVDSAIGLLTPLRPILVAHPQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            jóin(34039. .34101,34448. .34750,35530. .3
299276.1:405. .698.299276.1:3164. .1566.29
299276.1:4495. .2795,299276.1:3714. .3982,
299276.1:4056. .4104,299276.1:5846. .5958,
299276.1:6478. .6729,299276.1:7169. .7338)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(34039. .34101.34448. .34750,35530. .36306,

299276.1:105. .698,299276.1:1364. .1566,299276.1:1666.

299276.1:2495. .2795.299276.1:3714. .3928,

299276.1:4056. 4104,299276.1:5846. .5958,

299276.1:6478. .6729,299276.1:7169. .7338)

79ene**M142.6**
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mAPTGQGGQWQEVLCCSICNRHFNETFLFVSLICGHVICRKCAE
KPENQTKPCPHDDWKTTHSPSEYPNNVALLSVIFPRKQCMTLSGAVSEAEKRVDQLSI
QIAKFFREADSERGGTVSSREISRTLQRKVLALLCYQWREVDGRLKTLKMCRGISERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D67323 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVAAALEGSEARPARIGCVSSPTLVKFFHETEEYKTGQIQLTLFEFDDRFGLKFPTEF
VHYDYKHPTDLPAELLAKFDVIIADPPFLAAECLIKTAHSIRLLGKSDVKVLLCTGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKEMAINKPMIRIFNSEHLKNIKVLSEALEESEKFARAKTEQFAQNNPVNGTRTTERL
DKTIGELTPNLMKSPAISIRGQQAYLOLKRTILDTCWGGEDIRVIGLVLVHKRYEVSD
VTKDAKATGFDESRRESSAVLQVYKLISKPMTEYTARAPLDFTIGAIVANYSSSEMSDT
DDIPOLSADTLAALSMFQAEQQEKIEQLOSGIIEKIDEDWQLSQFWYDDETSRKLVAE
VVSNSLDKIVDVKERISEAQGNASEAENAHLRMELRMAESQMAHLDPYTKNNCLLRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDYASRLMAMHRTSFEPRHANNLANDFSCFANYQTLTFC"
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31500. .31763,32933. .33043)
/gene="M142.5"
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AELNLPEGTIKVWFQNRMKDKRQRVGGLAWPFPPQMAAYMLNPFAYEMWMKTAAASQ
FGATGPGNGAYGNNGSSTSPSAAGSLPFLPPLGFPSFLSQNSTKSPSSPHSDDSSKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA97810.1"
/db_xref="GI:3878739"
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/db_xref="GI:3878737"
/db_xref="SPTREMBL:Q21541"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted using Genefinder; cDNA EST EMBL:T01774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTSSDDDESKPVNFSNSPSSSSPSPYSTD"
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/db_xref="GI:3878738"
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22840. .230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="M142.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MQSFDIESLIGVNKVPSLVEMVAASRASSFSPPFEQQHHDPMGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 28499, 28558.
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.1566,299276.1:1666. .1772,
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ORGANISM
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                                                                                                     COMMENT
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11935 AAAGGCGCCCCTGATGGCCCAATAGTCCGTTTTGCCAACTCTCGGTGAAAGTGTATATCAT 11994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCTAGACGCGGTGCTTCTCTCAACTCCGGACTACGATACTTCTCTGCGTCTCGCCACG 12174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gctcttgataaatatttgctaaataatttggaatatccaacagattt---aatggctggc 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gatggtggaccaaccggtcaaccagttcaatttgctatcattggtcagccagtttatcat 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTGCTATGTGGATAACGGCTACGGTGATAGAGTGGATATTCTTGATTCGAATGGTTGT 12114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | tectgetttgtegatgatggtaaeggtgatactgtgggaaattetaaatgetgatggatgt 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaatggacatgcgattctgaaaccgttgat-----actttctgcgcggttgtccat 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196;
                                                        Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using Codictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                  Bonfield, J., Burton J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Watson, A., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 36069) 1 (bases 1, Anderson, K., Baynes, C., Berks, M., Polifold, R., Anderson, K., Baynes, C., Berks, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; Collagen; Cuticulin; Homeobox protein; Human G9A protein like Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans cosmid ZK265, complete sequence 281143
      For a graphical representation
                                         available information.
                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                    Dobson, R.
                                                                                                                                                                                                                                                                                                            Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                               elegans
                                                                                                                                                                                                                                                                                                                                                                        2.2 Mb of contiguous
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Similarity 52.0%;
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                                                                                                                                                                                                                                                      (bases 1 to 36069)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 169;
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   of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                        sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                  chromosome III of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jier, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ņ
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                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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IMPORTANT: This sequence is not the entire insert of clone ZK265.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small convertapping sections once, or longer because we arrange for a small convertapping sections once, or longer because we arrange for a small convertapping sections once, or longer because we arrange for a small convertapping sections once, or longer because we arrange for a small convertapping sections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               start of this sequence (1. .110) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The true left end of clone T01G9 is at 35964 in this sequence. The true right end of clone T02E1 is at 4168 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bin/display?db=wormace&class=Sequence &object=2K265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neighbouring submissions
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                                                                                                                                                                       /protein_id="Cab03515.1"
/db_xref="G1:388J551"
/db_xref="G1:388J551"
/db_xref="G1:388J551"
/db_xref="G1:388J551"
/db_xref="G1:388J551"
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/translation="MPVAKEDSWAFQPIGSPFPEAPVRPNQNNGYWYEMLPLKQRHEN
/TANNNOGVVECSFPYNKAELKGKLDLGGQIOILOYXGDYNSLGYWYEMLPLKQRHEN
NEGIREIVRGGNSVPVLAKLKDGTDKLGFLDTNTEVALSVAGTTEKYEGGATANFMT
IFRNLRPPFFGLKVYDDLMYDLRYGDNEPSNAVPADGRALNTETGPHMQYVALMYKHG
DPVFGRSYPSSAGKTMAHFGKNNQENAGPEVGSMQLLTVPPEASCMGLEYKMMPLSEGK
complement(join(6676. .7754,7804. .7870))
/gene="ZK265.2"
                                                                  complement(6676. .7870)
/gene="ZK265.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLHDDLHQPSSSTKPPVGHVPGLSLVCVPVFNKESVBVANSRYENLQKMVNLCHNQPE
MFDIHTKNMILLLERWLIDSQTFDSYFLSHFYKKESSTTRIKTCVHNPAFIDLØEQCI
RHMSHSVTSNVSSASADLDBRVHVANIAKIAKLRYNKETISVINPAFNDHFASEDSSC
VYFYPGIKQCRAQRAASSTSQDMRSRLYPLHKAAEDGNAEEIRRELKIGMDSNLRDDD
SWFPLHSACFHGHLEVVHELLMSPQMTAINAQNKGGATALQYAVINGNBYLVBILITSH
ASIDVNIQNNEGSYRPIDYCGNHPAIOKILEKQIFKSKINVDTSIGSFSIKSRSPEEAT
VGEVLDRLAGETQLNREQMNCFALFVYSESMSLQLOPDSLIDGKLKVDKWNTTIRKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(492.
/gene="ZK265.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z7573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:Q94400"
/translation="MAEVSVAIVRLKISALSDKAIPSAQDFEICVKEEPSTAKNEGPV
KHDYNIKKRVTVGGHTIGADVEKLPNESFEPSKVSTLEDMIHDVEKRTGNIIRRSYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDIPFETPRLKLKRNAYATARMEIVTVSIEAVIFINIFDIKKRNQRSYYSDQHY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(492..736,782..932,983..1189,1629..1758, 1943..2076,2124..2289,2385..2762,3174..3313,3365..3440
                                                            /gene="ZK265.
                                                                                                                                                       SSGWTTVHIGNSAPCILKDDKGLEVLGNLDLTIEKASAGYGGKEKIMTGAAVAKLKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(5062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB03514.1"
/db_xref="GI:3881550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein (TR:G287865)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ZK265.3"
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CCPAGPPGPPGNAGTAGDDGPAGRANPGSDSTEGDBMAFUNGDVKCPAGPPGPPGPPR
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/GOMPLEMENT (8777. .13818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSLFCSAVIYALVEYFNOORLMTLERDHRTTNYTLSIRYQLKENLKTLKVMRRFFISI
ILIILAMGLGNSLPVILNLNEDLILTVEVMDYVFHSNEVFLYDTAIFTIENTKYTF
NKARTTFGMRIJOSRKDEMEEKLDELEDDSRPSJIMSTRRSSTRADSTTKRASPNSTV
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AVHQMDGDREEHDRLTRCIQYFFVAMLFLHAFWFKQIIISVLYYHIFIEEILGAVAAV
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complement(join(8777. .8956,9538. .9646,9702.
9879. .9976,12270. .12598,13623. .13818))
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                                                                                                                                                                                                                                                                                                 /gene="ZK265.6"
/note="---
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liseleitylligystammetqkeflkyckytkefhakonnelshkukwyevlttpy
Llwaekynlaieiresikcolochhegoksyakmyebsiejaammyytwytytyty
Gilterifatilykdyekksrhwifglifyaqnifsctmavytttsgltfqyllisgvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="cDNA EST yk481g5.5 comes yk508e4.3 comes from this gene"
                        NLWQYTPKQWAKKIRTHKESEMCKFLETA"
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join(18275. .18:
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/db_xref="GI:3881553"
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                                                                                                                                                                                                                                                                                           /note="predicted using Genefinder"
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                         tgccagtatgccgttatgaaatt 471
                                                                TGACTGCTGAGTTGGGTGTTAGTATGATTCCAACGACAGAATTAGAAGCGAGACATGGAA 35175
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join(33403. 33428, 34402,34791. 34918,34995. 35304,

35555. 35799,35846. 36069,Z75713.1:107. 118,

Z75713.1:188. .290,Z75713.1:343. .430,Z75713.1:495. .556)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(27566. .27635,27677. .27835,28839. .28913,29226. .29
29467. .29631,29755. .29902,29982. .30024,30072. .30293,
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TTTARVTPKKSTKRIGTGTTAHPPLFPKDASKARVINIVDIRNKHATSLLNYCQFFVF
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56.7%;
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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L.lactis DB1341 Ad
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irst entry) N-acetylglucosamine-6-phosphate aureus protein; ribozyme; antis gene; regulatory element; bacte lococcal infection; food poison drome; ss. aureus. Location/Qualifiers	tcaatgccaga ttcagaacca TCCAAATCTTA AGCGGCAATATA	Score 40; DB Pred. No. 0.5 0; Mismatches itttaatggctggcc	TOCUS LOCUS End 210000 210000 310000 410000 610000
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etylase. sequence; control; gene expression; scaled skin syndrome			s jannasci 209
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a Staphylococcus aureus protein, that, based on homology with an Escherichia coli protein, is believed to be a N-acetylglucosamine-6-phosphate deacetylase. The present sequence was obtained from a library of clones of S. aureus WCHH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxite shock syndrome.
                                                                                                                                                                       s. aureus infection; diagnosis; therapy; central nervous system disorder; upper respiratory tract infection; otilis media; bacterial tracheitis; acute epiglottitis; thyroiditis; empyema; lung abscess; splenic abscess; cardiac infection; infective endocarditis; secretory diarrhoea; ulcer; retroperitoneal abscess; cerebral abscess; blepharitis; conjunctivitis; keratitis; endophthalmitis; preseptal cellulitis; orbital cellulitis; darcryocystitis; epididymitis; intrarenal abscess; perinephric abscess; toxic shock syndrome; impetigo; folliculitis; cutaneous abscess; cellulitis; wound infection; bacterial myositis; septic arthritis;
14-SEP-1998; U18987.
12-SEP-1997; US-058710.
(SMIK ) SMITHKLINE BEECHAM CORP BURDHAM MKR, Lonetto MA, Warren WPI; 99-229138/19.
                                                                                                        Staphylococcus
WO9912557-A1.
                                                                                                                                                             osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                         X33788 standard; DNA; 348
X33788;
25-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Black MT, Burnham MK, Hodgson JE, Knowles Pratt JM, Reichard RW, Rosenberg M, Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Pages 719-720; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to isolate antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptide(s) from Staphylococcus aureus strain WCUH29
                                                                                         18-MAR-1999
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(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 CAAGCACGTCTTGCAAATGGT 229
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                                                                                                                                                                                                                                                                                                                        aureus coding sequence SEQ ID NO. 45. aureus infection; diagnosis; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aatgcattcgaaggacatgtt 156
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74; Conser
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                        aureus
                                                                                                                                                             Helicobacter
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/*tag= a
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                  Warren PV;
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                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                          pylori infection; stomach cancer; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.6; D
Pred. No. 0.83
0; Mismatches
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Best Local Similarity
Thehes 75; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The polypeptides can be used for the treatment or prevention of disease. CC The polypeptides can be used to diagnose diseases content of their expression. The polypeptides and vectors containing them can also be used in immunisation methods. The products can be used for treating infection, e.g. infections of the upper respiratory tract, containing them cc an also be used in immunisation methods. The products can be used for treating infection, e.g. infections of the upper respiratory tract, contributed in bacterial tracheltis, acute epiglottitis, rective endocarditis), gastrointestinal (e.g. secretory conjunctivitis), respiratory (e.g. entrainervous conjunctivitis, keratitis, endophthalmitis, preseptal and orbital conjunctivitis, keratitis, endophthalmitis, preseptal and cribital conjunctivitis, intrarenal and perinephric abscess, cardictic (e.g. epididymitis, intrarenal and perinephric abscess, toxic shock conjunctivitis, wound infection, bacterial myositis), bone and joint confections, (e.g. causing stomach cancer, ulcers and gastritis). The products can also be used for treating in-devices and wounds. Sequence 348 BP; 108 A; 55 C; 78 G; 107 T;
                                                                                                                                                                                                                                                                                                                             S. aureus coding sequence SEQ ID NO. 8.

S. aureus infection; diagnosis; therapy; central nervous system disorder; upper respiratory tract infection; otitis media; bacterial tracheitis; acute epiglottitis; thyroiditis; empyema; lung abscess; splenic abscess; cardiac infection; infective endocarditis; secretory diarrhoea; ulcer; retroperitoneal abscess; cerebral abscess; blepharitis; conjunctivitis; keratitis; endophthalmitis; preseptal cellulitis; orbital cellulitis;
              New isolated Staphylococcus aureus polynucleotides Claim 20; Page 65-67; 102pp; English.
                                                                                                                                                                                            Staphylococcus WO9912557-A1.
                                                                                                                                                                                                                                                                       darcryocystitis; epididymitis; intrarenal abscess; perinephric abscess; toxic shock syndrome; impetigo; folliculitis; cutaneous abscess; cellulitis; wound infection; bacterial myositis; septic arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Staphylococcus aureus polynucleotides Claim 21; Page 90-91; 102pp; English.
This sequence represents a S. aureus polynucleotide The invention also relates to the polypeptides encoder.
                                                        WPI; 99-229138/19.
P-PSDB; Y05308.
                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP
Burnham MKR, Lonetto MA, Warren
                                                                                                                                   14-SEP-1998;
12-SEP-1997;
                                                                                                                                                                                                                                                      osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X33781 standard; DNA;
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US-058710.
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                                                                                                                                                                                                                  aureus.
                                                                                                                                                                                                                                                    Helicobacter pylori infection; stomach
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53.2%;
102pp; !
•nts a S.
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polynucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>, .</u>
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                                                                                                                                                                                                                                                    cancer; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention. by the
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invention

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V74344
ID V74344
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ID V7 V764344
ID V76444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptides can be used for the treatment or prevention of disease. The polypeptide or polynucleotide can also be used to diagnose diseases related to their expression. The polypeptides and vectors containing the can also be used in immunisation methods. The products can be used for
                                                                          misc_feature
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.4140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7563 BP
                                                                   "these bases represent a line of missing texthe sequence listing in the specification, are included to maintain the nucleotide nungiven in the specification for this DNA sec. 5940
                                                                                                                                                                                                                                                                                                                                                                                      these bases represent a line of missing
"these
                                                                                                                                                                                                                                                                                                                                           are included to maintain
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Pred. No. 1
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Best Local
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В Q В Ş 밁 Ş

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30-JUL-1997.
07-JAN-1997;
05-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                            This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The
                                                                                                                                                                            be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim 1; Page 321-325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC
Barash SC, Choi GH, Dillon P.
for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.

Sequence 7563 BP; 2584 A; 1028 C; 1476 G; 2229 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide(s) and proteins derived stored on computer readable medium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PJ,
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ATTGCTTACCGTATGAAAGGTAATGAACGTTTTTATTTAATTACCGATGCAATGCGTGCA CAAGCACGTCTTGCAAATGGT aatgcattcgaaggacatgtt 156 AAAGGTATGCCTGAAGGAGAATATGATTTGGGTGGACAAAAAGTAACTGTTCAATCGCAA 5595 gaaggtgagccagaaattgaatgtggaccaacttcaataacaattcaattttaatacacgt 135 attgctttctgtactacacttattgcattgtcttattcgattccggttgacaatggtgtc 75 l Similarity 75; Conser Conservative 3.0%; 53.2%; 0; Score 35.4; D Pred. No. 3.2; Mismatches DB <u>+</u>; Length 7563; 0; Gaps 5535 0

W09814583-A2. 09-APR-1998. 02-OCT-1997; 02-OCT-1996; 23-SEP-1998 (first entry)
P. falciparum gp190 DNA.
gp190; malaria; MSP-1; merozoite
monoclonal antibody; passive immu (BUJA/) BUJARD H. Bujard H, Pan W, T WPI; 98-240088/21. Plasmodium falciparum V35363; V35363 standard; E05441. DE-040817. 10. .4929 /*tag= a Tolle /product= DNA; 4940 ocation/Qualifiers ВP immunisation; surface protein; stability;

vaccine;

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RESULT
N50530/c
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Claim 2; Fig 1; 51pp; English.

The sequence encoding the P195 protein of Plasmodium falciparum (N50530) and a peptide comprising at least one of its epitopes (see P50777) are claimed. Also claimed is a vaccine for inducing immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the nev DNA sequence, together with a carrier.

Sequence 5760 BP; 2565 A; 630 C; 725 G; 1840 T;
                                                                                                                                                                                  Holder A,
WPI; 85-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes the Plasmodium falciparum gp190/MSP-1 (merozoite surface protein). This gene is used in a method for stabilising the gene sequences by reducing the AT content. Such products are useful in vaccines against malaria or for producing monoclonal antibodies (for passive immunisation). The complete gp190 protein can now be produced outside the parasite and has, at least over extended regions, the native pattern of folding. Larger amounts of the protein can be produced recombinantly than would be possible using the parasites as source. Sequence 4940 BP; 2196 A; 597 C; 687 G; 1460 T;
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                                                                                                         malaria
Claim 2; Fig
                                                                                                                                                     Cloned DNA sequence encoding
                                                                                                                                                                                                                           22-FEB-1984; GB-004692.
26-SEP-1984; GB-024340.
21-FEB-1985; GB-004429.
                                                                                                                                                                                                                                                           21-FEB-1985;
22-FEB-1984;
                                                                                                                                                                                                                                                                                         EP-154454-A.
11-SEP-1985.
                                                                                                                                                                                                                                                                                                                                                                    Plasmodium
                                                                                                                                                                                                                                                                                                                                                                               Malaria vaccine; epitope; antigen;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                N50530
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                                                                                                                                       useful for expressing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTCTTAAATAGTATTCTAATTCAAGTGG
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                                                                                                                                                                                             ) WELLCOME FOUNDATION CA, Sandhu J, Odink K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgcgcgtacacgatctctgaatccacgtgg
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
oding the P195 protein
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                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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45.6%;
                                                                                                                                        the
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                                                                                                                                       protein
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Pred. No. 3
                                                                                                                                                     plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                immunogen; ss
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se in vaccines agai
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Query Match Best Local S Matches 72

l Similarity 72; Conser

Conservative

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Score 34.8; DI Pred. No. 4.9; O; Mismatches

4.9;

Length 8395;

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Best Local
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04-MAY-1998;
14-NOV-1997;
                        A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosting Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X13154 standard;
X13154;
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                                                                                                                                                                                                                                         Claim 1;

    used to develop products for the detection of Enterococcus
    use in vaccines for prevention or attenuation of Enterococcus

                                                                                                                                                                                                                                                                                                  WPI; 99-045171/04.
New isolated Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; attenuation; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis; contig; detection; Enterococcus infection;
 Sequence
                                                                                                                                                                                                                                                        infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTACTTGGTTCTTTTGTATAATCAAATGGATTAATTAAATCACCAAAAGAATTAAGTTC 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                      Page 1103-1107; 2084pp;
 8395
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US-046655.
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45.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8395
2616 A;
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Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 147;
                                                                                                                                                                                                                                        English.
 1692 C;
                                                                                                                                                                                                                                                                                      polynucleotides and polypeptides detection of Enterococcus and for
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RESULT
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Best Local Similarity
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12-NOV-1998.
04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis genome contig SEQ ID NO:405. Enterococcus faecalis; contig; detection; Enteroco vaccine; attenuation; computer readable medium; ds Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4127
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Barash SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.
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                            351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated Enterococcus faecalis polynucleotides and polypeptides sed to develop products for the detection of Enterococcus and for vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used
tcgagtacaatgcttttacatggaagctgataaaacagttagtgcacagattgaggtatc 410
                                                                                                                                                                                                                                                                                                  | tatgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcact
                                                                    ATCACGTGTTGAAAACAATTCAAAAGGCCCACAAGTTTTTGTAAGCCGTAGTCATCCAGA
                                                                                                                  aacaacaactgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtgcata
                                                                                                                                                                        AAAACAAGATCAAATGCCAAATGAATTTTACCAACCGCATGRTCGGRTTAAAGTTTACGT
                                                                                                                                                                                                                   tccatttgattcatgcaatgttgcgcgtacacgatctctgaatccacgtggtatttttgt
                                                                                                                                                                                                                                                                      TGAACGTCAAGATCGTCGTTATATTTATGTAAACTTAGGTAAAATCGAAGCAGTCTTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34.6;
Pred. No. 2.
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735

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1918 AATGTTTATTTTCCAAAAATGCATAATTATAATATTATTTTAAACACTATGTATCAA 1974

atcacagcttttctatcaatgccagatcagtattaccattaaagaaccaaatagcga 791 GTAGTTGTAAACATTATTAATAGCAGCCATCCAATTGTATGCAAACTAATTAAGGTATTG

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RESULT
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                                                                                                                                  Query Match
Best Local
                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                         used for therapeutic modulation of IL-1 activity

Claim 2; Fig 1; 95pp; English.

This cDNA clone codes for human interleukin-1 receptor accessory molecule (IL1-R AcM) (see W53897), a new member of the immunoglobulin superfamily that forms a complex with type 1 IL1-R and which has higher affinity for IL-1 than the receptor itself, suggesting that the known high and low affinity forms of IL1-R are in fact the receptor with or without IL1-R AcM, respectively. The 2155 bp sequence is present in clone HMEEJ52 (deposited as ATCC 97666) derived from microvascular epithelium (no details of isolation given). Recombinant expression in Escherichia coli, mammalian and insect cells is described. Recombinant bost cells
                                                                                                                                                                                                                                                                                                                                         and recombinant vectors are claimed. Also claimed are isolated nucleic acid molecules encoding epitope-bearing portions (see w53898-915) of ILI-R ACM. Recombinant ILI-R ACM can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interleukin-1 receptor accessor;
signal transduction; infection;
rheumatoid arthritis; therapy;
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                                                                                                                                                                                                     might be linked to disease. Sequence 2155 BP; 709
                                                                                                                                                                                                                                    Nucleic acid fragments are useful as diagnostic probes and primers, for isolation of IL1-R AcM-encoding genomic sequences, for in situ hybridisation to determine chromosomal localisation of the gene, for chromosome identification and for identifying mutations that
                                                                                                                                                                                                                                                                                                         W53898-915) of IL1-R ACM. Recombinant IL1-R ACM can be used to identify IL-1R agonists and antagonists useful for therapeutic modulation of IL-1 activity, and to raise specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC. Bednarik DP, Olsen HS, Rosen WPI; 98-230267/20.
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26-AUG-1996; U13954.
26-AUG-1996; WO-U13954.
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ggaatatccaacagatttaatggctggccaagaagctcacgtatacaaatatgcggatcg
                                               TCCTGAACAAATAACAGAAAGGGAATTATATATACCTTTTTAATATTATTAGAAGCATTATCT 1857
                                                                             tactgtggaaattctaaatgctgatggatgtgctcttgataaatatttgctaaataattt 674
                                                                                                                  ch 3.0%; l Similarity 49.7%; 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; cDNA; 2155 BP
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354..1370
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                                                                                                                Score 34.6; I
Pred. No. 3;
0; Mismatches
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            734
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RESULT 11
V74396/c
TD V74396 standard; DNA; 9062
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CS.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences
                                                                                                                                                                                                                                                                              anti-S.aureus
                                                                                                                                                                                                                                                                                           stored on computer readable
                                                                                                                                                                                                                                                                                                                                          Rosen
                                                                                                                                                                                                                                                                                                                                                                                  EP-786519-A2.
30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861
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Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyalid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                            Polynucleotide(s) and proteins
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                                                                                                                                                                                                                                                             laim 1; Page 544-549; 3271pp; English.
                 their
                                                                                                                                                                                                                                                                                                                           97-374922/35
                                                                                                                                                                                                                                                                                                                                                       SC, Choi
               fragments) are useful as primers or probes for
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Dillon PJ, Fannon MR,
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06-MAY-1997;
16-MAY-1997;
                                                                           Claim 1; Page 615-626; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fo use in vaccines for prevention or attenuation of Enterococcus
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04-MAY-1998;
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W09850555-A2.
12-NOV-1998.
04-MAY-1998; U08985.
04-MAY-1997; US-046609.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
            New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and foruse in vaccines for prevention or attenuation of Enterococcus
                                           (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.
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31-JAN-1996;
31-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2022-2024; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
          Disclosure; Page 46-49; 63pp; English.

A Streptococcus mutans gene (T36122) codes for I/II antigen
(W02098), a 185 kDa cell surface protein at least partly responsil
for S. mutans adhesion to teeth. The I/II antigen includes a
series of overlapping T-cell, B-cell and adhesion epitopes.
Fragments (see also T36111-21) of the gene can be used to produce
recombinant polypeptides (W02087-97) carrying such epitopes for
use in vaccines for immunisation against dental caries. The DNA
                                                                                                                                              P-PSDB; W02098.

Nucleic acid encoding polypeptide for prevention or treatment of dental caries - which stimulates T or B cell response, and/or dental caries - which in competition with Streptococcus mutans antige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-1996 (first entry)
S. mutans anticon T.T.
                                                                                                                                                                                                                     (UNME-) UNITED MEDICAL Kelly C, Lehner T; WPI; 96-371434/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caries; antigen I/II; genetic immunisation; Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T36122 standard;
T36122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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that differs from amino acids 618-650
given on page 46 of the specification*
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be used as naked
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                                                                       781 cca 783
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US-08-781-802-5
US-08-317-844B-1
US-08-359-303B-72
US-08-754-100-17
US-08-764-100-17
US-08-764-100-17
US-08-764-100-20
US-08-397-236-1
US-08-397-236-1
US-08-311-316-6
US-08-322-760A-1
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Patent No.
Sequence
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Sequence 72, Appli
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Sequence 119, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 19, Appl	Sequence 1, Appli	Sequence 9, Appli	Sequence 41, Appl	Sequence 13, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli				

ALIGNMENTS

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RESULT 1
US-07-772-087-1
                                                                                                                                                                                                   FILING DATE: 19911008

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1675
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)83-4300
TELEPAX: (703)83-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 base pairs
TYPE: NUCLEIC ACID
STEAMLPONES: 40410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/07772087 Patent No. 5275945
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                                                                                 MOLECULE TYPE: D
ORIGINAL SOURCE:
STRAIN: 164A-1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/772,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEPEN: PC-DOS/MS-DOS
COPTUBRE: Datonth DC-DOS #1 0
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APPLICANT: FODGE, Douglas W.
APPLICANT: LALONDE, James J.
TITLE OF INVENTION: ALKALINE PROTEASES STABLE IN HEAVY-DUTY
TITLE OF INVENTION: DETERGENT LIQUIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
NAME/KEY: CDS
LOCATION: 716..1849
OTHER INFORMATION: /product- "mature protein of
OTHER INFORMATION: 164A-1"
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CITY: Alexandria
STATE: Virginia
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TOPOLOGY: lir
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                                                                                                       164A-1
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RESULT 2
518210 9/c
; Patent No. 5182210
; Patent No. 5182210
; CAMPBELL, JOAN I.A.; TOWLEY, FIONA M.
; CAMPBELL, JOAN I.A.; TOWLEY, FIONA M.
; TITLE OF INVESTION: FOWLPOX VIRUS PROMOTERS
; NUMBER OF SEQUENCES: 22
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA;
; CURRENT APPLICATION DATA;
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; LOCATION:
US-07-772-087-1
                                                          5352450-1; Patent No. 5352450
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Best Local Similarity 52.5%;
Matches 96; Conservative
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LOCATION:
FEATURE:
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/529,602
FILING DATE: 29-MAY-1990
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Local Similarity 55.6%;
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716..1021
                                                                                                                             TOSHIHIKO; OKAHASHI, NOBUO; TAKAHASHI, ICHIRO,
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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PCT-US96-05320A-705/c
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Best Local S
Matches 89
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              APPLICATION NUMBER: 08/476,102
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/487,429
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Eric K. Steffe
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                    ZIP: 20003-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                             COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 2.8%;
Local Similarity 48.6%;
les 89; Conservative
   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5177
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Rockville, MD 20850
United States of America
Johns Hopkins University
720 Rutland Avenue
                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamilton O. Smith J. Craig Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Owen White
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United States of America
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   (202)
371-2600
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2, 1996
                                                                                                                                                                                                                                                                                                                                    3.50 inch, 1.4Mb storage
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                                       014PC01
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US-08-781-802-5/c

; Sequence 5, Application US/08781802

; Patent No. 5969121
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Best Local Similarity
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,802
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1038 tgcagtacaaaatggaatctgcatgtcaccatttggcttctcaatgtttatgggtttaag 1097
                                                                                                                                           REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION UDATA:
APPLICATION UNMEER: US 60/019,580
FILING DATE: 12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1098 cartgcartgattgctgccgtcattattaccatttcgtttaaattt 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,995
FILING DATE: 01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 TGCCGTATAAAATGCAAATTTCACCGCACTTTTTGGCTTTGACATAGACATTGGGATCAG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US on APPLICATION NUMBER: US on APPLICATION NUMBER: US on APPLICATION NUMBER: US of APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                NAME: Chao, Mark REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 10
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                            312-913-0002
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CASADABAN, Malcolm
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VONSTEIN, Veronika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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AIKENS, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                    312-913-0001
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application Patent No. 5728810
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Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-TOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/425,069
                   ATTORNEY/AGENT INFORMATION: NAME: Murphy Jr., Gerald
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDITIFIC OF INVENTION: PROTEIN, A REPLICABLE VECTOR TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2655 AGAAGGAAACCCGCGGCTGTTTCGCGCCACAAATATTCTTGTTAATCAGA 2606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2895 ACATGTTTTGAATAACGTCCATATGGTGAAGAAAATAGCAGCAGATTGATATCTCATTA 2836
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2775 ATATCCGATCGCCAAACCCCTTGTAAATAAAGGGGGTTTCGGCATTTTATCTTTATATAGT 2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 tcaagttgccggaatttcacttccatttgattcatgcaatgttgcgcgtacacgatctct 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330 taccaaagttgatcgtgcatatcgagtacaatgcttttacatggaagctgataaaacagt 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 gaatccacgtggtatttttgtaacaacaactgttgtcatttcgtttcatccattatttgt 329
                                                    FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5728810th Washington Street CITY: Falls Church
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LOCATION:
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                                                                                                                                                                                                                                          COUNTRY:
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NAME: Murphy Jr., G
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4090 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08425069
                                                                                                                                                                                                                                                                                                                                                                                                                            Xu, Ming
Hinman, Michael B.
                                                                                                                                                                                                                                            U.S.A.
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197..1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
197..1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis
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                                                                      19-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Randolph V.
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Gerald M
ER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                             ISOLATED DNA CODING FOR SPIDER SILK PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "E011 sequence of longest
open reading frame; other possible start codons ATG/met4;
TTG/leu7; GTG/val8; GTG/val15; GTG/val36; ATG/met62"
                                                                                        US/08/425,069
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Pred. No. 6.
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                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
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                                                                                                                                                                                                                                                                                                                                                                             AND PRODUCTS THEREOF
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INFORMATION FOR SEQ ID NO: 1:

TELEPHONE: (703) 205-8000

REFERENCE/DOCKET NUMBER:

1447-106P

TELEFAX: (703)

205-8050

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RESULT 7
US-08-317-844B-1
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1615
                                    CURRENT APPLICATION DATA:
                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                    APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1555 GGAGGACTTGGAAGCCAAGGTTCTGGTCGAGGAGGATTAGGTGGACAAGGTGCAGGTGCA 1614
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2338 base pair
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
AUTHORS: Xu, Ming
                                                                                                                                                                STREET: 301 No. 5989894th Washington CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            850 gccgcagcaaaacctgctgcagctgcgcaacttcgtttactcaagaaaagatctgcagaa 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          790 gaatgtgttcgaccacaatgttcagaaccacaaggattcggagctgttaaaaacaggtggt 849
                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1..2154
OTHER INFORMATION:
OTHER INFORMATION:
APPLICATION NUMBER: US/0 FILING DATE: 04-OCT-1994
                                                                                                    MEDIUM TYPE:
                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE: Structure of a protein superfiber: TITLE: drafline silk
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LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                            1, 05,
NO. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGCAGCAGCTGGAGGTGCTGGACAAGGAGGATTAGGTGGACAAGGTGCTGGACAA 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65; Conserv
                                                                                                                                      22046
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                                                                                                                                                    U.S.A.
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                                                                                                                                                                                                                                                                                                                                    Xu, Ming
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                                                                                                                                                                                                                                                                                                                                                       Lewis, Randolph V.
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                                                                                                  Floppy disk
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                                                                                                                                                                                                    Stewart, Kolasch & Birch
989894th Washington Street
                   US/08/317,844B
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                                                     Version
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5.4;
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                                                     #1.25
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US-08-559-303B-72
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                                                                                                                                                                                                                                                                    Sequence 72, Application US/08559303B
Patent No. 5824501
GENERAL INFORMATION:
APPLICANT: NATHAN A. ELLIS, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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OTHER INFORMATION: drag
PUBLICATION INFORMATION:
AUTHORS: Xu, Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                     ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: MC-DOS
                                                                                                                                                                                                                      APPLICANT: GRODEN
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                    1615 GCAGCAGCAGCAGCTGGAGGTGCTGGACAAGGAGGATTAGGTGGACAAGGTGCTGGACAA 1674
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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LENGTH: 2338 base pair
CURRENT APPLICATION DATA:
                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 790 gaatgtgttcggaccacaatgttcagaaccacaaggattcggagctgttaaaacaggtggt 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
              COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: ASCII
                                                                                              COUNTRY: U
ZIP: 10016
                                                                                                                           CITY: NEW YORK
STATE: NEW YOR
                                                                                                                                              ADDRESSEE: AMSILII, CHREET: 90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGES: 7120-7124
DATE: Sept.-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE: Structure of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703
TELEX: 248345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 241-13
TELEFAX: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Murphy Jr., Gerald REGISTRATION NUMBER: 28,9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGGACTTGGAAGCCAAGGTTCTGGTCGAGGAGGATTAGGTGGACAAGGTGCAGGTGCA 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                           NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lewis, Randolph V.
                                                                                                           U.S.A.
                                                                                                                                                                                                                                                                      NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                         OF BLOOM'S
                                                                                                                                                                                                            78
                                                                                                                                                                          ROTHSTEIN & EBENSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Nephila clavipes dragline silk protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
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                                                                                                                                                                                                                         FOR DIAGNOSIS AND TREATMENT
M'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 4
Pred. No. 6.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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US-07-781-034-4 
; Sequence 4, Application US/07781034 
; Patent No. 5442050
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                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                 STREET: 1 CONTY: Lexington CITY: Massachusetts
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       APPLICANT: Fishman, Jay A.
TITLE OF INVENTION: Molecular Cloning of Antigens Shared By
TITLE OF INVENTION: Rat- and Human-Derived Pneumocystis Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3727
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REFERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELECOMMUNICATION TO THE TELEPHONE: (212) 697-5995
                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3607 AAACTGTACTAAATGGCAATTTAAAGGTAGACTTTATGGAAACAGAAAATTCCAGCAGTG 3666
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NAME: ELIZABETH A. BOGOSIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
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nes 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                               AGGTTTTGCTTCAAATTGATGGTGTTACTGAAGACAAACTGGAAAA 3892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAATATTTTTAATACCGTCACTCTCAAGAAGCTTGCAGAATCTTTATCTTCTGATCCTG 3846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAAAAAACAAAAAGCGTTAGTAGCAAAAGTGTCTCAGAGGGAAGAAGATGGTTAAAAAAAT 3726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttaatacacgtaatgcattcgaaggacatgtttatgtgaaaggtctttatgatcaagaag 184
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                                                                                                                                                 Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINEAR
                                                                                                                                                                 Hamilton, Brook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER NUCLEIC
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                                                                                                                                                                 Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                         Pneumocystis Carinii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application PC/TUS9208328 GENERAL INFORMATION:
APPLICANT: Fishman, Jay A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 861-95
INFORMATION FOR SEQ ID NO:
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/781,034
FILING DATE: 18-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,166
FILING DATE: 30-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT. INFORMATION: NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
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LENGTH: 1189 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: MGH91-02A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     636 ACATGGACACGATCATGATCATGAA 660
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                                                                                                                                                 APPLICATION NUMBER: POFILING DATE: 19920930
                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                        STREET: Two Mil CITY: Lexington
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: U: FILING DATE: 19911018
                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGACGAATGTGATGAATGTGAGGAATGCGGTGAATGTGAGCCAGATGAAGGATGTGGCTG 575
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Granahan,
                                                                                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                                                                                                                                                                                                                                          Two Militia Drive
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular Cloning of Antigens Shared By
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Pred. No. 6.8;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
TELEFAX: 951794
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.7%;
Best Local Similarity 51.0%;
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: van Grinsven J., Martinus Q.
APPLICANT: De Haan, Petrus T.
APPLICANT: Gielen L., Johannes J.
APPLICANT: Peters, Dirk
APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 27
                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-WAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-WAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5773700ris, Allen E.
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                           FILING DATE:
                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 STREET: 975 Card
                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                Floppy disk
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Pred. No. 6.8;
0; Mismatches 71;
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RESULT 12
US-08-764-100-21/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
            APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY,AGENT INFORMATION:
NAME: NO. 5773700ris, Allen E.
REGISTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: van Grinsven J.,
APPLICANT: De Haan, Petrus
APPLICANT: Gielen L., Johan
APPLICANT: Gielen L., Johan
                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Improvementitle OF INVENTION: Compounds
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/764,100 FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                               CLASSIFICATION:
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nes 77; Conserv
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Pred. No. 12;
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Best Local Similarity
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                         APPLICATION NUMBER: US 08/U3/...
APPLICATION NUMBER: US 08/U3/...
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773700ris, Allen E.
REGISTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-1061
TELECOMMUNICATION INFORMATION:
"PRIEDPHONE: (415) 354-3592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08764100 Patent No. 5773700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5773700 GENERAL INFORMATION:
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TELEFAX: (415) 857-1125 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3414 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                              FILING DATE: 06-DEC-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                               94304
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Peters, Dirk
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Pred. No. 12;
0; Mismatches
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US-08-764-100-20
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Best Local S
                                                                                                                        FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773700ris, Allen E
REGISTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-
TELECOMMUNICATION INFORMATION:
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                                                                                TELEFAX: (415) 857-1125 INFORMATION FOR SEQ ID NO:
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LENGTH: 4970 base pair
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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COMPUTER: IBM PC c
OPERATING SYSTEM:
SOFTWARE: Patentin
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CITY: Palo Alto
                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US 0
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9
                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/764,100 FILING DATE: 06-DEC-1996
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STREET: 975 California Avenue
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STRANDEDNESS: single
                        STRANDEDNESS:
                                         TYPE:
                                                                                                            TELEPHONE:
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                   nucleic acid
DEDNESS: single
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De Haan, Petrus T
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                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible SYSTEM: PC-DOS/MS-DOS
            linear
                                                                                                               (415) 354-3592
                                                                                                                                                                                                UMBER: GB 9206016.9
19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                        Allen E.
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Pred. No. 14;
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US-08-989-478-1/c
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Best Local Similarity
Matches 77; Conserv
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INFORMATION FOR SEQ
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FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:
CLASSIFICATION: PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                     APPLICATION NUMBER: US 60/0:
AFILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
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                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/034,382 FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: No. 5986082artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082th Carolina
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Ryals, John
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Best Local Similarity
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1366 GATAAACTTTAGATAAACACCCAATTGCCAAAT 1334
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(c) 1993 - 2000
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69 pb set44: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	Result
2	No.
390.2	sult Query
372.2	No. Score Match Length DB ID
390.2 33.6	Query
372.2 32.1	Match
	Length
42 37	DB
665 42 AIII1196 628 37 AA701731	ID
AIIII196 SWOV3MCAI	esult Query
AA701731 SWOV3MCAI	No. Score Match Length DB ID Description

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Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                        Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                              mRNA sequence.
AI111196
AI1111196.1 GI:3510080
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                                                                                                    On Sep 12, 1996 this sequence Contact: Steven A. Williams
                                                                                                                                  Genes expressed in molting Unpublished (1997)
                                                                                                                                                      Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
                                                                                      Molecular Parasitology
                                                                                                                                                                                                                                                                Onchocerca
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AI665774
AA625005
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AI438781
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AA624955
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A1322108 SWOV3MCAM
A1317939 SWOV3MCAM
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A1352993 SWOV3MCAA
AA625073 SWOV3MCA6
A1665774 SWOV3MCA1
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                                   alcataaatggacatgcgattctgaaaccgttgatactttctgcgcggttgtccat
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                   -CCATAAATGGACATGTGATTCTGAAACAGTTGATACATTCTGGGCTGGTGGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome@smith.edu
Seq primer: pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The Library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The Library is available from Dr. Sara Lustigman (email: sissistigmapyc.org)."
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/db_xref="taxon:6282"
/clone="SWOv3MCA1232"
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(SL96MLW-OvmL3)"
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REFERENCE AUTHORS TITLE

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JOURNAL

KEYWORDS SOURCE ORGANISM

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ACCESSION VERSION

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ORIGIN
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AUTHORS
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Best Local
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ttatgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcac
                                                                                      caataacaatcaattttaatacacgtaatgcattcgaaggacatgtttatgtgaaaggtc 169
                                                                                                                                                   ATGCTATTCCGGTTGATAACGGTGTAGAAGGTGAACCAGAAATTGAATGTGGTCCAACAT 171
                                                                                                                                                                            attcgattccggttgacaatggtgtcgaaggtgagccagaaattgaatgtggaccaactt 109
                                                                                                                                                                                                                                            431;
                                                                 CAATTACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATGTATACGTGAAAGGCT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
On Sep 19, 1997 + 4.7 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA701731 628 bp mRNA EST 19-DEC SWOV3MCA1144SK Onchocerca volvulus molting L3 larva cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Sep 19, 1997 this sequence version Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AA701731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onchocerca
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                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: pBluescript
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                              ۵
                                                                                                                                                                                                                                                                                                                                                                                           slustigm@nybc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _/clone="SWOv3MCA1144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Onchocerca volvulus molting L3
(SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Onchocerca volvulus"
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).3e-90;
les 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405188.
Contact: Steven A. Williams
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SWOV3WCA1879SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO1879 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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primer: pBluescript
                      /dev_stage="molting L3"
/lab_host="XLI-Blue MRF'"
/lab_host="XLI-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Eco 
                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="SWmL3CO1879"
/clone_lib="Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:6282"
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/strain="Kumba, Cameroons"
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and converted to double-stranded cDNA using
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Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 639)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1 Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                             Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
                                                                                                                                                                                                                                                                                          AI322117 639 bp mRNA EST 22-E SWOv3MCAM12G08SK Onchocerca volvulus molting L3 larva
                                                                                                                                                                                   Onchocerca volvulus.
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                                                                                                          CCGAAATGACAACTGCATTTGCAACACAAATTGTACCGATGCCTGTATGCCGATATGAGA
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//dev_stage="molting 
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/db_xref="taxon:6282"
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Pred. No. 4.2e-86;
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TITLE
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Best Local Similarity
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                                                                                                                                                                         gtgaaaggtctttatgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgcc 219
                                                                            ggaatttcacttccatttgattcatgcaatgttgcgcgtacacgatctctgaatccacgt 279
ggtatttttgtaacaacagttgtcatttcgtttcatccattatttgttaccaaagtt 339
                                                GGAATTGAAGTTCAGATGGATTCATGTAATGTTGAACGATCACGGTCCTTAAATCCTCGA 121
                                                                                                                                            GTAAAAGGGCTTTACGATCGCGATGAATGTCGTTCAGATAGTGGTGGACGGCAGGTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
On Oct 30, 1997 this sequence version replaced gi:2160807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Onchocerca volvulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Steven A. Williams
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Filarioidea; Onchocercidae; Onchocerca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     il: genome@smith.edu
primer: pBluescript
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                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 1066 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Wanlewski in the Laboratory of Dr. S. A. Williams.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="XLI-Blue MFF/"
/lab_host="XLI-Blue MFF/"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of 0. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
                                                                                                                                                                                                                                                                                                                                                                                           The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
106 c 138 g 178 t 1 others
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/clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520 cagccagtttatcataaatggacatgcgattctgaaaccgttgatactttctgcgcggtt
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                                                                                                                                                                                                        Contact: Succession Molecular Parasitology
Molecular Parasitology
Smith College Department of Biological Sciences, Clark Science
Department of Biological Sciences, Clark Science
Department of Morthampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA585626 776 bp mRNA EST 30-DEC-1997
SW3D9CA349SK Brugia malayi L3 molting-day 9 larva cDNA
(SAW97MLW-BmL3d9) Brugia malayi cDNA clone SW3D9CA349 5', mRNA
                                                                                                                                      Seq primer: pBluescript SK.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Unpublished (1997)
On May 5, 1995 this sequence version replaced gi:797827
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                                                                                                                                                                                                                                                                                                                                                                                                       Filarioidea; Onchocercidae; Brugia. 1 (bases 1 to 776)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brugia malayi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
                                                                                                                                                                           genome@smith.edu
                                 /clone="SW3D9CA349"
/clone_lib="Brugia malayi L3 molting-day 9 larva cDNA
(SAW97MLW-BmL3d9)"
                                                                                  /organism-"Brugia malayi"
/db_xref="taxon:6279"
'dev_stage="third stage larvae, nine days after infection"
'lab_host="E. coli XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:2393038
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day 9 post-infection,
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1 (bases 1 to 537)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:80
                                                                                                                 Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                          AA668051 20-NOV-1997
SWOV3WCAM02A04SK Onchocerca volvulus molting L3 larva cDNA
(SL9ALW-OvmL3) Onchocerca volvulus cDNA clone SWOV3WCAM02A04 5',
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Pred. No. 8e-
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
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a 102 c 106 g 172 t
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/db_xref="taxon:6282"
/clone="SWOv3MCAM02A04"
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/lab_host="xL1-Blue MRF'"
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TATACGATCAGGCAGGATGCCGAAATGAAGGTGGACGTCAGGTAGCCGGAATTGAAC
                                                                                                                  caataacaatcaattttaatacacgtaatgcattcgaaggacatgtttatgtgaaaggtc 169
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
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On Jan 14, 1998 this sequence version replaced gi:1797124.
Contact: Steven A. Williams
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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SWOVJMCAM12A04SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOVJMCAM12A04 5',
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/db_xref="taxon:6282"
/clone="5MOv3MCAM12A04"
/clone_lib="Onchocerca volvulus molting L3 larva
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Pred. No. 3.5e-72;
"'^matches 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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primer: pBluescript SK.
            //note="Wector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 1056 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of DT. S. A. Williams.
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    The library is available from Dr.
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/lab_host="XL1-Blue MRF'"
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Sara Lustigman (email:
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1 (bases 1 to 531)
Williams,S.A., Lizotte-Waniewski,M., Laney,S., Lustigman,S.,
Hilliams,T., Allen,M., Bowles,L., Geisel,S., Jost,S., Kucaba,
Martin,J., Steptoe,M., Theising,B., White,Y., Wylie,T.,
Chappell,J., Person,B., Gibbons,M., Harvey,N., Pape,D.,
Chamberlain,A., Morales,R., Schurk,R., Ritter,E., Kohn,S.,
                                                                                                                                                                                                                                                                                                                                                                                   AA901444 531 bp mRNA construction on thing L3 larva cDNA SWOV3MCAM03B05 Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVML3) Onchocerca volvulus cDNA clone onch17 5' similar TR:Q93115 Q93115 CUT-1-LIKE CUTICLIN PROTEIN PRECURSOR.;, mRNA
                                                                             Underwood, K. and Marra, M.
Molecular Parasitology OvmL3
Unpublished (1998)
On Jan 19, 1998 this sequence version
Contact: Steven A. Williams
College, Northampton, MA, 01063, USA Tel: 4135853826
                             Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                   Molecular Parasitology
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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                 ctgaaatcacaactgcttttcaaactcaaattgt 443
                                                                              attcgattccggttgacaatggtgtcgaaggtgagccagaaattgaatgtggaccaactt 109
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The library was constructed by Sara Lustigman and Michelle
LlZotte-Wanlewski in the Laboratory of Dr. S.A.Williams. The
Library is available from Dr. Sara Lustigman email
slustigm@nybc.org When requesting this clone from Dr. Lust:
please reference the Williams lab clone id - SWOV3MCAM03B0
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/db_xref="taxon:6282"
/clone="onch17"
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(SL96MLW-OvmL3)"
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                    tatcattggtcagccagtttatcataaatggacatgcgattctgaaaccgttgatacttt 569
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
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/dev_stage="molting L3"
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/clone="SWmL3C0691"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mark.blaxter@ed.ac.uk
The ABI trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/3b6/MB3b6AA4G10T3.html
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Institute of Cell, Animal and
University of Edinburgh
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Brugia malayi
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MB3D6AA4G10T3 Brugia malayi day 6 p
SAW96MLW-BmL3d6 Brugia malayi cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes expressed in day six post-infection,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blaxter, M.L., Waterfall, M., Daub, J.,
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using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 2 x 1085 independent recombinants and average insert size was 900 base pairs. The library was constructed by Michelle Lizotte-Waniewski. The library was constructed by Filaria Genome Project The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email genome@smith.edu."
                                                                                                                                                                                           prepared from third stage larvae of Brugia malayi isolated from the peritoneal cavity of jirds six days after infection. The mRNA was converted to double stranded cDNA
                                                                                                                                                                                                                                                           /dev_stage="third stage larvae, six days after infection" /lab_host="E. coli XLI-Blue" /note="vector: lambdaZapII (UniZap XR); Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a (5' end); Site_2: Xho I (3' end); Brugia malayi is a (1) ymphatic filarial nematode parasite of humans. MRNA was
                                                                                                                                                                                                                                                                                                                                                                                                               /clone="3D6AA4G10"
/clone_11b="Brugia malayi day 6 post-infection third stage
larvae SAW96MLW-BmL3d6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Brugia malayi"
/strain="TRS Labs"
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1 to 354)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:802407.
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 466)
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                                                                                                                                                                                                                                                                                                                                                                                                                   genome@smith.edu
      (SL9bMLW-CVALL),
/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note=""Yector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note=""Yector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Eco RI; Ec
                                                                                                                                                                        /organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SwmL3CO758"
/clone_11b="Onchocerca volvulus
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405277.
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Science Center, S
                                                                                                                          Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
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(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3C02020 5',
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                                                                                                                                                                                                                                      volvulus
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                                                                                                                            Laney, S. and Lustigman, S of Onchocerca volvulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGCTATTCCGGTTGATAACGGTGTAGAAGGTGAACCAGAAATTGAATGTGGTCCAACAT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCCGTTTGATTCCTGTAATGTANCACGTACACGTTCGTTAAATCCACGTGGTATTTTTG
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                       AA625010
                                                                                   SWOV3MCA318SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVmL3) Onchocerca volvulus cDNA clone SWmL3CO318 5', mRNA
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Email: genome@sr
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/clone_lib="Onchocerca volvulus molting L3
(SL96MLW-OvmL3)"
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/db_xref="taxon:6282"
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83.9%;
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Pred. No. 2.1e-60;
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                    aattotaaatgotgatggatgtgotottgataaatatttgotaaataatttggaatatco 683
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GTTCTACCAATGTCAAATTAGTATTACAATTAAAGAACCAAACAGTGAATGTGCACGACC
                                                                                                      ATTATTAAATGCTGATGGTTGTGCTTTGGACAAATATTTGCTCAACAACTTGGAATATCC
                                                                                                                                                                                                                                                                                                                                                    ATTTGCTACCATTGGTCA-CCAGTGTACCATAAATGGACATGTGATTCTGAAACAGTTGA
                                                                                   Contact: Succession Molecular Parasitology
Molecular Parasitology
Smith College Department of Biological Sciences, Clark Science Center,
Department of Biological Sciences, Clark Science Center,
Northampton, MA, 01063, USA
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On May 9, 1995 this sequence version replaced gi:802391.
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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//dev_stage="mol/ing L3"
//lab_host="XL1-Blue MRF'"
//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2 or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is -1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
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1 76 c 88 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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(SL96MLW-OvmL3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 260.4; DB 36; Pred. No. 1e-59;
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Query length: 1161
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Query: US-09-323-427-5
                                            A_Geneseq_36:R29276
A_Geneseq_36:W03474
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                                                                                                                                                                          A_Geneseq_36:W21894
A_Geneseq_36:W63842
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A_Geneseq_36:W13009
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-Q=/cgn2_1/USPTO_Spool/US09323427/runat_14042000_170513_19878/app_query.fasta.1
-Q=/cgn2_1/USPTO_Spool/US09323427/runat_14042000_170513_19878/app_query.fasta.1
-DB=A_Geneseq_36 -QFMT=fastan -SUFFIX=backtrans.rag
-GAPDP=12.000 -GAPEXT=4.000 -MINNATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=4.000 -MINNATCH=0.100 -LOOPCL=0.000
-XGAPEXT=0.000 -GGAPOP=4.500 -QGAPEXT=7.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS-human40.cd1 -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -ALIGN=15 -MODE=LCCAL -OUTFMT=pfs -NORM=ext
-MINLEN=0 -MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36:W13825
36:R06400
36:R06379
36:R06399
36:R74171
36:R76427
36:R10323
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  out_format :
Documentation
                                                                                                                                                                                                    Mouse protease-activated recep; pl10. Recombinant polypeptide S. aureus asparaginyl tRNA syntasparaginyl-tRNA synthetase fro
                                                                                                                                                                                                                                                                                                                                  Type A alpha-amidating enzyme.

B. Sphaericus SLP. Host cell (
Human pl10. Recombinant polype
PtdIns 3-kinase 110 kD cataly)
Human PTP-OB. Protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lambda gt10ch2 encoded C-
Lambda gt10ch101 encoded
Lambda gt10ch201 encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type B alpha-amidating enzyme. Segment of desmosomal cadherin, C-terminal amidation enzyme. cE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE-III (peptidylhydroxyglycine Expression plasmid pUCP1CI799) C-terminal prepro-C-terminal a
                                     Ribosome inactivating protein
Mouse SRY-related protein. Boy
                                                                                        Alpha-Trichosanthin encoded by
                                                                                                         Alpha-facto profibrolase from H. pylori transporter protein, Hydra head activator binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by sequence whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine peptidyl-glycine alpha
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                       BAR1 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast transcription
                                                                                                                                                                                                                                                                                             Human protein tyrosine phospha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oat phytochrome A apoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. difficile toxin A. Fusion | Clostridium difficile toxin A
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E. coli colitose or glucose tra
                                                                                                                                                                                 aureus asparaginyl tRNA syn
  zona
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A_Geneseq_36:R99462
A_Geneseq_36:R97208
A_Geneseq_36:R97210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-465404-A.
08-JAN-1992.
27-MAY-1991;
01-JUN-1990;
10-AUG-1990;
30-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R20112 standard;
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alignment_block:
US-09-323-427-5/rev x R20112
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                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: R20112 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CIBA ) CIBA GEIGY AG.
IWBSAKI Y, Shimoi H, Su:
Kawahara T, Kangawa K;
WPI: 92-010570/02.
N-PSDB; Q20269.
                                                                                                                                                                                                       1015 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                        1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence was deduced from a cDNA insert from pAE-III-202-4 (FERM BP-3172). The vector seas a source for a DNA fragment encoding PHL for the construction of an expression vector for the prepn. of recombinant PHL. The protein may be truncated to comprise only residues 383-706 or 383-713. The PHL catalyses the reaction: R-GlyOH -> R-NH2. It can be used to produce peptides will amidated C-termini, e.g. calcitonin, growth hormone, LH-RH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel DNA encoding peptidyl hydroxy:glycine N-C lyase (PHL) used to prepare PHL which can be used in the amidation of peptide(s) e.g. human calcitonin.
Claim 4; Page 18; 28pp; English.
                                                                                                                                                                                                                                                526 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-1992 (first entry)
AE-III (peptidylhydroxyglycine N-C lyase precursor)
Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                      AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                           ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                         lAlaAspGlyTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP-141678.
JP-210535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP-329911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= AE-III
/note= "including PAM
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Gaps:
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                                                                                .....Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHL domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570
2756
4655
4655
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Human calcium sensor protei
Human kidney calcium sensor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feline ZPB protein. Isolated
                                          871
                                                                                                                                                                                                          966
                                                                                  547
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581 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   628 laValSerTyrAlaPro.....Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 leProHisSerLeuThrMetValProAspGlnGlyGlnLeuCysValAla
                         85 CTCAATGTTTATGGGTTTAAGCATTGCATTGATT...GCTGCCGTCATTA 39
                                                                                   ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVa
                                                                                                                                         GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT
                                                                                                                                                                                                                                                    TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCT
                                                                                                                                                                                                                                                                                                          aGlyValProThrGlnGluLysGlnAsnValValGlnGluSerSerAlaG
                                                                                                                                                                                                                                                                                                                                                           TGATATCAACACCCTTGAA.....ATTAGCGATGATAATCAAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                       GCA.....GAACCGGAGAATATCATT...GATGTACGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alGluLysGlnThrGlnGluLysGlnGlnLys.....GlnLysAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisArgSerValLysLysAlaGlyIleGluValGluGluIleThrGluTh 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyAspAlaHisAlaAsnAlaValTrpLysPheSerProSerLysAlaGlu 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAAT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alGlnGlyPheMetLeuAsnPheSerAsnGlyAsp.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 628
                                                                                                                                                                                             lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .........IleLeuAspThrPheIleProAlaArgLysAsnPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGCTGATGGATGTCTTCATAAATATTTG.....CTAAATAATTT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gly......ValLeuTyrAlaValAsnGlyLysProTyrTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nTrpGlyGluGluThrSerSerAsnValProArgProGlyGlnPheArgI 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...ATTACCATTAAAGAACCAAAT.....AGCGAATGTGTTCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eAspMetProHisAspIleAlaAlaAlaAspAspGlyThrValTyrValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspArgGluAsnGly...ArgIleGlnCysPheHisAlaGluThrGlyAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 829
     ::
     ........GlyTyrSerAlaProV
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                                                                                                                                                                                                                                                                                                          790
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ID p94856
AC p94856;
DT 27-JUN-1990 (first e
DE Expression plasmid pU
KW alpha-amidating; pAX7
OS Synthetic.
PN EP-299790-A.
PD 18-JUN-1988; 306508.
PF 15-JUL-1987; JP-17718
PR 05-DEC-1987; JP-17718
PR 05-DEC-1987; JP-17718
PR 05-DEC-1987; JP-17718
PR 05-DEC-1987; JP-1779/03.
PI WPI; 89-017279/03.
DR N-PSDB; NAY579,
DR N-PSDB; NAY579,
PT Recombinant C termina and their precursors ps Disclosure; 7pp; Engl CC The sequence encodes complete to screen a larger lice to screen a larger lice complete to screen a larger lice compansor sequence says of the plasmid was scree to screen a larger lice complete to screen a larger lice hydrophobic clements sequence 693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-323-427-5/rev x P94856
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.
The sequence encodes a derivative of the mature C-terminal alpha-amidating enzyme from plasmid pXA799.
The plasmid was screened from an E.coli library using plasmid pXA457 to screen a larger library.
Although pXA799 is similar to pXA457 at the N-terminus, it has an are hydrophobic elements suggesting a membrane function.

See also N93060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka S, Matsuo H, Mizuno WPI; 89-017279/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUN-1990 (first entry)
Expression plasmid pUCP1CI799
alpha-amidating; pAX799; alpha
828 AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 779
                                                                                545 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 507 lAlaAspGlyTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               491 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1988; 306508.
17-JUL-1987; JP-177184
05-DEC-1987; JP-306867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840 leAlaIleAlaIlePheIleArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               823 lSerPheValLeuIleIleThrLeuLeuIleIleProIleAlaValLeuI
                                                                                                                                                                                                                                                                                                                                                              AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                      ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 829
                                                                                                                                                                                             nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 545
                                                                                                                                                                                                                                                 Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACCATTTCGTTTAAATTTCGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
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0.945
43.103
                                                                                                                                                                                                                                                                                                                                                                                                               .....Сув
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Gaps: 12
Percent Identity: 21.552
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742

308 725 358 709

807

561

512 916

185 773 226 757 258 692 437 487

664 531 646 631 635 681 612 778 597

675

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alignment_block:
US-09-323-427-5/rev x P94854
                                                                                                                                                                                                                                  alignment_scores:
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                                                                                                                                                                          Percent Similarity:
                                                                            Align seg 1/1 to: P94854 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
                                    1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUN-1990 (first entry)
C-terminal prepro-C-terminal alpha-amidating enzyme alpha-amidating; pAX799; alpha amide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka S, Matsuo H, Mizuno WPI; 89-017279/03.
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; 7pp; English.

Plasmid pXA799 contains a sequence derived from Xenopus laevis.

The plasmid was screened from an E.coli library using plasmid pXA457
                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant C terminal alpha amidating enzymes of xenopus laevis and their precursors dexyribonucleic acid encoding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-1989.
15-JUL-1988; 306508.
17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
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                                                                                                                                                                                                                                                                                                                         to screen a larger library.

Although the gene product is similar to that of pXA457 at the N-terminus, it has an area of hydrophobic elements suggesting a membrane function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          631
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                             See also N93060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; N90791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P94854 standard; protein; 875
CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eGluMetProHisAspIleAlaAlaGlyAspAspGlyThrValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGCTGATGGATGTGCTCTTGATAAATATTTG.....CTAAATAATTT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gly.....ValLeuTyrAlaValAsnGlyLysProTyrTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....MetLeuAsnPheSerAsnGlyAsp.....
                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                             875 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....IleLeuAspThrPheIleProAlaArgLysAsnPh
                                                                                                                                                                       94.50
0.945
43.103
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                                                                                                                                                                       Percent Identity:
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                                                                            875
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12
21.552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    620
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                seq_name: A_Geneseq_36:R73053
                26-APR-1995.
07-SEP-1994; 306587.
08-SEP-1993; JP-257881.
(FURU/) FURUKAWA K.
(SUNR) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1015
                                                                                                                                                                                                           Peptidyl C-terminal alpha-amidating Peptidyl C-terminal alpha-amidating
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   Furukawa
                                                                                                                                                                                                                                              06-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       487 GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT
                                                                                                         EP-649900-A.
                                                                                                                                        peptide
                                                                                                                                                                           Not specified
                                                                                                                                                                                             trichostatin;
                                                                                                                                                                                                                                                                                 R73053 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laValSerTyrAlaPro.....Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 584
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                                                                                                                                                                                                                                                                                                                                                                    \tt eGluMetProHisAspIleAlaAlaGlyAspAspGlyThrValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGCTGATGGATGTCTTCATAAATATTTG.....CTAAATAATTT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGACATGTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....MetLeuAsnPheSerAsnGlyAsp......
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Ohsuye K,
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                                                                                                                        1. .39
/label=
                                                                                                                                          Location/Qualifiers
1. .39
                                                                                                                                                                                                                                                                               Protein; 875
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Sugimura
                                                                                                                    Sig_peptide
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   χ.
                                                                                                                                                                                                           enzyme.
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alignment_block:
US-09-323-427-5/rev x R73053
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing protein prodn. from cultured animal cells - by adding a trichostatin to the medium, effective at low concn. and not injurious to host cells
Disclosure; Page 10-15; 19pp; English.
Disclosure; Page 10-15; 19pp; English.
Jmu-1S cells (i.e. CHO cells expressing a peptidyl C-terminal alphamuls cells (i.e. CHO cells expressing a peptidyl C-terminal alphamuls cenzyme (AB)) were suspended in F-12 medium to which aliquots of trichostatin were added. Cells were cultured for 3 days at 37 deg and then assayed for AE. Without trichostatin, AE productivity was 708 U/ml. At 10, 50, 100 and 200 nM trichostatin, AE productivities were respectively 866, 1897, 1894 and 3359 U/ml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  915
                                                                                                                                                                                                                                                                                                632 laValSerTyrAlaPro.....Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 lAlaAspGlyTyr.....
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N-PSDB; Q87970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
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                                              TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA
                                                                                                                                                TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
                                                                                                                                                                                                Gly.....ValLeuTyrAlaValAsnGlyLysProTyrTy
                                                                                                                                                                                                                                                                                                                                                AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         875 AA;
.MetLeuAsnPheSerAsnGlyAsp.....
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0.945
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                                                                                                 AspSerThrProValGlnGlyPhe
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Percent Identity:
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seq_documentation_block:
ID R88469;
AC R88469;
DT 14-AUG-1996 (first e
PR Paline infectious per
KW vaccine; prevention;
OS Feline infectious per
PN J07327683-A.
PD 19-DEC-1994; 129300.
PF 10-JUN-1994; JP-129300.
PF 10-JUN-1994; JP-129300.
PF 10-JUN-1994; JP-129300.
PR WPI; 96-072341J/08.
DR WPI; 96-072341J/08.
DR WPI; 96-072341J/08.
DR WPI; 96-072341J/08.
DR WPI 196-072341J/08.
DR WPI 196-072341J/08.
DR WPI 196-072341J/08.
DR PDNA encoding feline i
PT Used in a vaccine for
PS Claim 1; Page 14-17;
CC This sequence represect
CC (FIPV-I) spike protei
CC infection. The spike
CC cell with the spike protei
CC that the spike protei
CC that the spike protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-323-427-5/rev x R88469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1029 CGTAATGCATTCGAAGGACATGTTATGTGAAA......GGTCTTTA 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding feline infectious peritonitis I virus spike protein used in a vaccine for prevention and treatment of FIPV-I infection claim 1; Page 14-17; 23pp; Japanese.

This sequence represents the feline infectious peritonitis 1 virus (FIPV-I) spike protein. The FIPV-I spike protein may be used in the production of a vaccine for the prevention and treatment of FIPV-I infection. The spike protein may be produced by transforming a host cell with the spike protein DNA and expressing the sequence such sequence 1464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feline infectious peritonitis 1 virus spike protein. Feline infectious peritonitis 1 virus; FIPV-I; spike protein; vaccine; prevention; treatment.
                                                                                                                                                                                                                                                                                                         789
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10-JUN-1994; JP-129300.
(KITA) KITASATO KENKYUSHO
WPI; 96-072341/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   938 TTTCACTTCCA.....TTTGATTCATGCAAT......GTTGCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        739 LysAsnSerThrThrGlyGluIlePheThrValValProCysAspLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                          772 alAsnGlnThrAspLeuPheGluPheValAsnAsnThrGlnAlaArgArg
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                                                                                                                                                                                                                                                                                                                                                           ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT 854
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TCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG 704
                                                                                                                 AATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTA
                                                                                                                                                                                                                                         TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTAC
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                                               snCys.....ThrSerAlaIleThrTyr 825
                                                                                                                                                                          oGlnPheTyr.....TyrIleThrLysTrpAsnAsnAspThrSerSerA
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Ratio:
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0.508
46.597
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Day of Each
                                                                                                                                          seq_name: A_Geneseq_36:W88310
                                                                                                 _documentation_block:
                                                                                                                                                                                                                                                                                  1040
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26-APR-1999 (first entry) E. coli colitose or glucose transferase.
                                                  W88310 standard; Protein; W88310;
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                                                                                                                                                                                                                                                                                                                            78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hrGlyAsnIleSerIleProLysAsnPheThrValAlaValGlnAlaGlu
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                                                                                                                                                                                       heAlaMetGlnValGlnAlaArgLeuAsnTyrValAlaLeuGln 1070
                                                                                                                                                                                                                                TT......CGTTTAAATTTCGTCCAAATCAGA 6
                                                                                                                                                                                                                                                                                                                        TTTATGGGTTTAAGCATT...GCATTGATTGCTGCCGTCATTATTACCAT 32
                                                                                                                                                                                                                                                                                                                                                                     euProGlyValValAspGlyAsnLysMetSerMetTyrThrAlaSerLeu 1039
                                                                                                                                                                                                                                                                                                                                                                                                                  TIGCIGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAATAC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leGlyLysArgSerAlaValGluAspLeuLeuPheAsnLysValValThr 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT.....GTACGA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sLeuGlyGlyLeuTyrPheAspGlyLeuSerSerLeuLeuProProLysI 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euThrGlnTyrThrSerAlaCysGlnThrIleGluAsnAlaLeuAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r.....TyrValCysAsnGlyAsnThrHisCysLeuLysLeuL 903
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                                                                         374
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alignment_scores:
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Disclosure; Fig 7; 165pp; English.

This is the amino acid sequence of the protein encoded by the wbdM gene of a gene cluster (see x06748) involved in the biosynthesis of the Escherichia coli 0111 0 antigen. The protein shows high homology with TrsE of Yersinia enterocholitica, and is predicted to be a colitose or glucose transferase. The use of nucleic acid molecules derived from particular assembly and transport genes, capaciticularly wbd (transferase), wzx (flippase) and wzy (polymerase) genes, within 0 antigen gene clusters improves the specificity of methods for the detection and identification of 0 antigens, e.g. in testing food- or faecal-derived samples, or samples from patients. The 0 antigen is a major virulence factor of enteropathogenic E. coli strains that cause diarrhoea and haemorrhagic colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: W88310 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-323-427-5/rev x W88310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1998; AU0315.
22-JUL-1997; AU-00816.
01-MAY-1997; AU-00654!
(UNSY) UNIV SYDNEY.
Reeves PR, Wang L;
WPI; 99-059669/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1100 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1009 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli. w09850531-A1. 12-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; X06748.
                                                                                                                                                                                                                                                                                                                                                                                              GTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTT 910
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAACAATCAATTTTAATACACGTAATGCATTCGAAGGAC...... 1010
gLeu.....SerAspPheLeuAlaSerIleThrThrAsnValS
                                         ATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGAT
                                                                                                                                                                                                                                                                                                         GCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGT 860
                                                                                                                                                                                                                                                                                                                                                   ProAspIle.....IleHisSerHisMetPheHisAlaAsn..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuThrGlyIleSerGluValLysProThrGlnAsnIleAsn.....
                                                                                    ThrAlaHisAsnLysAsnGluGlyGlyAsnAlaArgMetPheCysTyrAr
                                                                                                                                ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAG
                                                                                                                                                                       lePheSerArgPheIleArgMetLeuIleProAlaValProLeuIleCys 108
                                                                                                                                                                                                                TGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTG...ATCGTGCAT 813
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Ratio:
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AU-006545
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0.533
46.281
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18
21.763
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seq_name: A_Geneseq_36:W13825
                    28-AUG-1996; U14192.
31-AUG-1995; US-521872.
11-OCT-1995; US-540804.
26-JAN-1996; US-590399.
                                                                                                                                                                                                                                                                                                               .documentation_block:
                                                                                                         04-JUN-1997 (first entry)
Yeast transcription regulatory factor SRBB.
Transcription regulatory factor; suppressor of RNA polymerase SRBB; RNA polymerase II; holoenzyme; SWI/SNF.
Saccharomyces cerevisiae.
W09708301-Al.
06-MAR-1997.
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(WHED)
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                                                                                                                                                                                                                                                                                        3825 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAAT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laGluLysIleAlaGluThrLeuLysIle...AspAspAsnAlaArgLys
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WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                        Protein; 1226 AA
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alignment_block:
US-09-323-427-5/rev x W13825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purified RNA polymerase II holo:enzyme - comprises RNA polymerase II and one or more regulatory proteins, pref. suppressor of RNA polymerase B proteins or SWI/SWF proteins?

Claim 11; Fig 10a-b; 154pp; English.

Rovel yeast SRB (suppressor of RNA polymerase B) proteins SRB4, SRB5, SRB0, SRB9, SRB1 (w13821-28) are transcription regulatory factors that act as positive and negative regulators of RNA polymerase II activity, and are components of the RNA polymerase II activity, and are components of the RNA polymerase II clentify transcription factors involved in RNA polymerase II

C-terminal domain (CTD) function. SRB8 and SRB9 appear to repress CTD activity. Genomic clones (T59904-11) for the SRB appear been obtd. SRBs can be used to treat diseases resulting from alteration or deletion of the SRB gene, pref. by gene transcription alteration or the SRB stabe besided in in vitro transcription of DNA and to identify cpds. that modify gene transcription of DNA and to identify Sequence 1226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: W13825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1148 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1048 AACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGA
                                                                                                                                                                                                                                                     461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         951
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                                                                                                                                                                                                                                                                               GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC
GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA
                                                                                                CTGAAATCACAACTGCTTTTC....AAACTCAAATTGTCCCGATGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      yrAspValLysPheTyrGluIlePheAsnPheAspGlnValValGluIle
                                                                                                                                                  euSerHisLeuCysSerGlyIleLeuSerSerValAsnArgThrValLeu
                                                                                                                                                                                                                                                nLeuSerLysThrProLeuSerIleLysIleMetValAlaGluTrpTyrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGATCTCTGAATCCACGTGGTATTT............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValGlnLeuIleAsnLeuLysIleSerProLeuMetLys.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAAT 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetMetProSerLeuTyrArgLeuLeuAsnIleLeuIleThrTyrGlyIl
                                            LeuLysIlePheLysIlePheCysIleAspLeuGluValPheHisHisPh
                                                                                                                                                                                              TG.....ATAAAACAGTTAGTGCACAGATTGAGGTAT
                                                                                                                                                                                                                                                                                                                                                   ThrGluGlnIleLysMetArgIleLeuSerAsnAspIleThrAsnLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                     .....TTGTAACAACAACTGTTGTCATTCGTTTCATCCATTATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGTCTTTATGATCAAG...AAGGTTGCCCGTAATGAAGGTGGACGT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..SerSerGlyLeuLeuTyrLeuGlnAspSerAsnAspLysPheValHis
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0.468
48.338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
Percent Identity:
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6
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16
20.716
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Seq_AC DT DE KW KW OS PN PP PR PR PR PR PR PR PR
                                                                                                                                                                                                                                                                                                                                  seq_name: A_Geneseq_36:R06400
                26-JUL-1990.
17-JAN-1990, J00042.
17-JAN-1989; JP-005878.
(SUNR ) SUNTORY LTD.
Obsuye K, Kitano K, Tanaka S
                                                                                                                                                                                                                                                                                                 _documentation_block:
                                                                                                                                                                                    R06400;
17-DEC-1990 (first entry)
---- ~+10ch2 encoded C-terminal alpha amidating enzyme.
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                                                                                                                                                                            C-terminal alpha amidating enzyme; human thyroid lambda \mbox{gt10ch2}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       693
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N-PSDB; Q05631
                                                                                                                                         WO9008190-A.
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                          R06400 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                           726 lyLeuGluTyrIleIleArgLeu 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ePheLysTrpIleGluPheIleValTyrHisGlnLeuLeuSerAspIleG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       nLeuIleSerLeuLysLeuLeuThrPheGluValThrGlnAsnValLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAA........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnPheProGluValPheGlnValAsnIleArgPheLeuLeuHis...As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuLysValAspAsnAspLeuArgIleGluLeuGlnSerValTyrAsnAs
                                                                                                                                                                                                                                                                                                                                                                                                                  AATTAGCGATGATAATCAAGCTT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTT.....TACTCAAGAAAAGATCTGCAGAACCGGAGAATA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt snAsnValMetLeuLleuIleAlaThrAsnLeuLysGlnTyrAsnLysPhe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysValTyrSerMetIleAsnAsnSerAsnGlnAlaValGlyGlnThrTrp 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCCAGATCAGTATTACCATTAAAGAACCAA........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pGluLysLeuLysThrGluLysLeuLysAsnAspLysSerGluValLeuL 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hrSerPheMetProPheTrpLysPhePheMetLysAsnPheProPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eIleTyrLysLysValLeuLysGluLysAspValProAlaTyrAsnValT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerGlnPhe...IleAsnAspHisIleLeuPheThrLysThrPheIlePh 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              luSerLeuGluAlaLeuMetAspIleLeuLeuCysTyrGlnLysLeuPhe 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTGCTA.....TCATTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....TCATTGATGTACGAACTGATATCAACACCCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nSerGluIleIleAspThrAsnThrSerLysGlnPheGlnLysAlaArgA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...ATAGCGAATGTTCGACCACAATGTTCAG.....AACCACAAGGA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....CTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..... AACCTGCTGCAGCTGCGCAACTTC
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alignment_block:
US-09-323-427-5/rev x R06400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA
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CDNA libraries were prepared from human thyroid gland poly(A) RNA in lambda gt11 and gt10. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gt10 library, including gt10chT2.

Restriction analysis indicated that gt10chT2 encoded a different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amidated peptides from thei
See also Q05630 and Q05632.
Sequence 776 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The enzyme is useful for prodn. of physiologically active alpha-
amidated peptides from their C-glycyl precursors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type of enzyme to one of the other two clones. The DNA can be inserted into vectors for expression in E.coli or (more efficiently)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coding sequences
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CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT 526
                                                                                                                                                                                                                                                                                                                                                                                                           AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCGTGCATAT...CGAGTACAATGCTTTTACATGGAAGCTGATAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nTrpGlyGluGluSerSerGlySerSerProLeuProGlyGlnPheThrV
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                                                                                                                                                                                                                                                                                                                                                         eValArgGluIleLysHisSerSerPheGlyArgAsnValPheAlaIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt AspArgGluAsnGlyArgIleGlnCysPheLysThrAspThrLysGluPh}
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                                                                                              ATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.....ACTG-861
                                                                                                                                                                                                        ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA 626
                                                                                                                                                                                                                                                       erTyrIlePro.....
                                                                                                                                                                                                                                                                                                       AAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA 676
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                                               .....AspGlnGluProValGlnGlyPhe......
                                                                                                                                                 .....GlyLeuLeuPheAlaValAsnGlyLysProHisPheGly..
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0.592
45.652
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seq_name: A_Geneseq_36:R06379
                                                                             Disclosure: pp: English.

Disclosure: pp: English.

CDNA libraries were prepared from human thyroid gland poly(A) RNA cDNA libraries were prepared from busing probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gt10 library, including gt10ch101.

Restriction analysis indicated that gt10ch7101 encodes a different type of enzyme to one of the other two clones. The DNA can be the into vectors for expression in E.coli or (more efficiently)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .documentation_block:
                                                                                                                                                                                                                                                                                                                     (SUNR) SUNTORY LTD.
Ohsuye K, Kitano K, Tanaka
WPI; 90-254034/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-terminal alpha amidating enzyme; human thyroid gla lambda gt10ch101.
                   The enzymes are useful for prodn. of pamidated peptides from their C-glycyl See also Q05630 and Q05631.
                                                                                                                                                                                                                                               coding sequences.
                                                                                                                                                                                                                                                              C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
                                                                                                                                                                                                                                                                                                       N-PSDB; Q05632
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17-JAN-1989; JP-005878.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9008190-A.
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Lambda gt10ch101 encoded C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R06379 standard; protein; 866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT
                                                                         in animal cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etGlnGluLysGlnLysLeuIleLysGluProGlySerGlyValProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACTCAAGAAAAGATCT.....GCAGAACCGGAGAATATCATTGATGTA
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                                                    physiologically active alpha
                                    precursors
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alignment_scores:

Quality:

87.00

Length:

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alignment_block:
US-09-323-427-5/rev x R06379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                611 eValArgGluIleLysHisSerSerPheGlyArgAsnValPheAlaIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           561 nTrpGlyGluGluSerSerGlySerSerProLeuProGlyGlnPheThrV
                                                  ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
TAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
                                                                                                                                                                                                           CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT
                                                                                                                                                                                                                                                                                                           AGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATCGTGCATAT...CGAGTACAATGCTTTTACATGGAAGCTGATAAAACC
                                                                                                     AGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT
                                                                                                                                                     hrAsnThrValTrpLysPheThrLeuThrGluLysLeuGluHisArgSer
                                                                                                                                                                                                                                                           sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT
                                                                                                                                                                                                                                                                                                                                                                                                                    GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alProHisSerLeuAlaLeuValProLeuLeuGlyGlnLeuCysValAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                              .....LysProValArgLysHisPheAspMetProHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....ValMetAsnPheSerAsnGlyGluIleIleAspIlePhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGACATGCGATTCTGAAAACCGTTGATACTTTCTGCGCGGGTTGTCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspArgGluAsnGlyArgIleGlnCysPheLysThrAspThrLysGluPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TT.....GTCATTTCGTTTCATCCATTATTT.....GTTACCAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.....ACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .GlyAlaIleTyrValSerAspGlyTyr.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....GlyLeuLeuPheAlaValAsnGlyLysProHisPheGly..
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Percent Identity: 18.944
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alignment_scores:
    Quality:
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                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                            US-09-323-427-5/rev x R06399
                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                          1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                    1015 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; pp; English.

CDNA libraries were prepared from human thyroid gland poly(A) RNA in lambda gtl1 and gtl0. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gtl0 library, including gtl0chT201.

Restriction analysis indicated that gtl0chT201 encodes a different type of enzyme to the other two clones. The DNA can be inserted type of enzyme to the other two clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lambda gt10ch201 encoded C-terminal alpha amidating enzyme. C-terminal alpha amidating enzyme; human thyroid gland; lambda gt10ch201.
                                                                                                                                   631 CysGlnProThrAspValAlaValAspProGlyThr.....
                                                                                                                                                                                                                                                                                                                                                                                                          This enzyme is useful for prodn. of physiologically active alphamidated peptides from their C-glycyl precursors. See also Q05631 and Q05632.

Sequence 974 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUNR ) SUNTORY LTD.
Ohsuye K, Kitano K, Tanaka
WPI; 90-254034/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
WO9008190-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               animal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequences.
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17-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R06399 standard; protein; 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AGTTGATTTACGTC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              into vectors for expression in E.coli or (more efficiently) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACTCAAGAAAAGATCT.....GCAGAACCGGAGAATATCATTGATGTA 232
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                               ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
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                                                                   .GlyAlaIleTyrValSerAspGlyTyr.
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0.592
45.652
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Percent Identity: 18.944
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652
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915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685 alProHisSerLeuAlaLeuValProLeuLeuGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                          ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT}
                                                 AGTTGATTTACGTC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC
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leAlaIlePheIle 887
                                                                                                          .ValLeuIleThrThrLeuLeuValIleProValValValLeuLeuAlaI
                                                                                                                                                              CGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCC
                                                                                                                                                                                                                     etGlnGluLysGlnLysLeuIleLysGluProGlySerGlyValProVal
                                                                                                                                                                                                                                                                         TACTCAAGAAAAGATCT.....GCAGAACCGGAGAATATCATTGATGTA
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                                                                                                                                                                                                                                                                                                                                                                                      TAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hrAsnThrValTrpLysPheThrLeuThrGluLysLeuGluHisArgSer
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seq_documentation_block:
ID R74171 standard; Protein;
AC R74171;

3038 AA

seq_name: A_Geneseq_36:R74171

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
                                                                                                                                                                     alignment_block:
US-09-323-427-5/rev x R74171
                                                                                                                                                                                                                                                                                                                            PT Novel DNA encoding triol poly-ketide synthase - used to isolate and pridentify homologues of triol poly-ketide synthase, and in the treatment of hyper-cholesterolaemia profile in the treatment profile in the profile in the profile in the first profile in the profile in translation of the introns from the DNA caseguence and translation of the 9114 nt ORF results in a protein of 3038 AAs (R74171) with a mol. wt. of 269,090 caltons. Inspection of the TPKS AA sequence for active calter residues and motifs known to be associated with a colline in the identification of candidates for expected cresulted in the identification of candidates for expected collines (see FT). Except for the presence of a methyl transferase, the present in FAS, the succession of activities on the control of the present in FAS, the succession of activities on the present in FAS, the succession of activities on the control of the present in FAS, the succession of activities on the control of the present in FAS, the succession of activities on the control of the present in FAS, the succession of activities on the control of the present in FAS.
                                                                                                                                     Align seg 1/1 to: R74171 from: 1
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28-0CT-1994; U12423.

22-NOV-1993; US-148132.

(MERI ) MERCK & CO INC.

Conder MJ, Davis CR, H

Reeves CD, Vinci VA;
                                                                                      1146 ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGA 1097
                               1096 CAATGGTGTCGAAGGTGAGCCAGAAATTGAATGT.....GGACCAACTT 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_difference 282. .288
/label= misc feature
misc_difference 1450. .1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                             TPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 95-193816/25.
N-PSDB; Q92323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_difference
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Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-1996 (first entry)
Aspergillus terreus triol polyketide synthase.
Triol polyketide synthase; TPKS; HMG-COA reductase inhibitor;
hypercholesterolaemia; LDL- cholesterol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                  ValAlaPheGlnThrValIleGlyAla.....TyrSerSerPro....
.....GlyAspArgArgLeuArgCysLeuTyrValProThrH 1200
                                                                                                                                                                                                                                                                                                                                                            protein is the same
                                                                                                                                                                                                                                                                                                                            3038 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               terreus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= misc !
e 1603. .1612
/label= misc !
e 2521. .2535
/label= misc !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= keto reductase motif 2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- dehydratase motif
1446. 1450
/label- methyl transferase motif
1932. 1937
/label- enoyl reductase motif
2164. 2169
                                                                                                                                                                                                                        87.00
0.481
38.347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label - keto-acyl synthase motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label acyl carrier protein motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetyl/malonyl transferase motif
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                                                                                                                                                                                                                      Length: 472
Gaps: 24
Percent Identity: 19.703
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1448		1446
330	GATTCGG	379
1445	IleLeuGluIle	1442
380	. ij	429
1441	CAACAGATTTAATIGCTIGGCCAAGAAGCTCACGTATACAAATATIGCGGAT ::: :::	1426
4. (ThrGluPheTyrThrAsnThrLeuSerPheGlyProAlaLeuHj	1409
480	AATATTTGCTAAATAATTTGGAA	511
1409	rgSe::	1394
512	CGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCT	558
1393	roHisValArgLeuValGlnArgValGlyGlnHisLeuLeuProThrVal	1377
559		559
1377	ThrGluAlaGlnIleGluHisLeuC	1360
559	TACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGA	601
1360	HisLeuTrpTyrAspProGlyTrpGluAs	1351
602	TCAGCCAGTTTATCATAAATG	651
1350	GlnValLeuAlaSerAlaLysGluGlyArg	1341
652	ATTTTGGATGGTGGACCAACCGGTCA	701
1340		1326
702	CTTTTCAAACTCAAAT	742
w		1313
743	ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC	792
793 1312	AAGTTGATCGTGCATATCGAGTACAATGCTTTTAC	827 1296
1296	euThrProAspSerLeuLeuAspAsnProGluTyrTrpAlaTh	1279
828	GTAACAACTGTTGTCATTTGGTTTCATCCATTATTTGTTACCA	873
1279	ProProAspAlaSerThrAspHisAlaMetPheAlaArgTrpSerTrpGl	1263
874	TTGCGCGTACACGATCTCTGAATCCACGTGGTATTTT	921
1262	ysPro	1247
922	ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGA	968
1246	pIl	1233
969	AAAGGTCTTTATGATCAAGA	1009
1233	::: ysGluLysValAlaPheAsnThrIle	1217
1010	ACAATCAATTTTAATACACGTAATGCAT	1047
1216	· ;;; isValAspArgIleThrLeuValProSerLeuCysLeuAlaThrAlaGlu	1200
1048	CAATA	1052

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alignment_block:
                                                                                                alignment_scores:
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                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1527
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                                                                                                                                                        Prodn. of alpha amidating enzyme - using prokaryotic or eukaryotic expression vectors having transcriptional promoter Claim 3; page 19; 24pp; English.

The corrsp. DNA sequence hybridises, under stringent conditions, with a DNA sequence (I) which encodes an alpha amidating enzyme (AEE) and is foreign to the host cell into which it is transformed. (I) is connected to a promoter and is contained in an expression vector. The AEE encoded is used as a catalyst in the conversion of a peptidyl substrate to a corresp. peptidyl amide. This can be used for making a protein biologically active, e.g. calcitonin or growth hormone releasing factor. See also 005637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1463 GlyPheAsnSerTyrThrTyrThrAspIleSerThrGlyPhePheGluGl 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1990; 301034.
06-FEB-1989; US-307366.
06-FEB-1989; US-307366.
(UNIG-) UNIGENE LAB INC.
Betelsen AH, Mehta NM, Beaudry GA;
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 90-248308/33.
N-PSDB; Q05636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-382403-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha amidating enzyme.
Alpha amidating enzyme; peptidyl amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-1990 (first entry)
Protein encoded by sequence which hybridises with DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R06427 standard; protein; 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrAspLeuIleIleAlaSerAsnValLeuHisAlaThrProAsp..... 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gCysThrGluProPhe 1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheIlePheGlyLeuPheAlaAspTrpTrpAlaGlyValAspAspGlyAr 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lyGlnMetValIleLeuGluIleThrHisLysGluHisThrArgLeuGly 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....LeuGluLysThrMetAlaHisAlaArgSerLeuLeuLysProGlyG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euAspIleArgArgSerProAlaGluGlnGlyPheGluPro...HisAla 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTTTGCCAGTTGATTTACGTCAC...CGTGCACTTCTGCAACATAATG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .........CGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATC 241
                                                        Quality:
Ratio:
                                   86.50
0.588
43.363
                               Length: 339
Gaps: 14
Percent Identity: 17.994
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Align seg 1/1 to: R06427
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                                              836 lGluProLysValGluAsnLysProThrSerSerGluLeuGln.....
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332 GAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              688 alProHisSerLeuAlaLeuValProHisLeuAspGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                    sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nTrpGlyGluGluSerSerGlySerSerProArgProGlyGlnPheSerV
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                                                                                                                                                          ValLysLysAlaGlyIleGluValGlnGluIleLysAlaGluAlaValVa
                                                                                                                                                                                                               ....CAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTT..
                                                                                                                                                                                                                                                                   hrAsnThrValTrpLysPheThrLeuThrGluLysMetGluHisArgSer
                                                                                                                                                                                                                                                                                                                     .....AAATATGCGGATCGATCACAGCTTTTCTATCAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                         AGATTTAATGGCTGGCCAAGAAGCTCACGTATAC........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....ValMetAsnPheSerSerGlyGluIleIleAspValPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AspGlnGluProValGlnGlyPhe......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....GlyPheLeuPheAlaValAsnGlyLysProTyrPheGly..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATCGTGCATAT...CGAGTACAATGCTTTTACATGGAAGCTGATAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC
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                                                                                                      ....; CGACCACAATGTTCAGAACCACAAGGATTCG
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283
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GINPYOTHYABPVALALAVALGII ACATGTTTATGTGAAAGGTCTTTJ
65 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1
Align seg 1/1 to: R10323 from: 1 to: 944
alignment_block: US-09-323-427-5/rev x R10323
alignment_scores: Quality: 86.50 Ratio: 0.588 Percent Similarity: 43.363 Percent Identity: 17.994
ences of Tellon of a B cDNA. ence 944
recombinant DNA expression s A stop codon can be placed u pref. between posns. 2340 an
amidating anzyme (AE) useful for post translational modifice of other recombinant polypeptides such as calcitonin. The se includes a membrane spanning domain which may be undesirable
be divided into distinct types, the sequence below being encode Type B. (Type A is given in R10322). The sequence can be insertinto expression vectors for the prodn. of recombinant alpha-
Disclosure; rage /; 52pp; English. The sequence was derived from DNA isolated from lil from RNA extracted from rat medullary thyroid carc derived cell lines such as IVI 10028. The cDNAs e.
PT or euraryotic hosts contg. a recombinant expression vector contg. PT the corresp. DNA sequence.
WPI: 91-02433/04. WPI: 91-02433/04. N-PSDB: Q10278.
Of FEB- (UNIG-)
AU9049043-A. 29-NOV-1990.
<pre>seq_documentation_block: ID R10323 standard; Protein; 944 AA. AC R10323;</pre>
seq_name: A_Geneseq_36:R10323
182 CAGTTGATTTACGTC 168 ::::::::::::::::::::::::::::::::::::
232 ACGAACTGATATCAACACCCTTGAAATTAAGCGATGATAATCAAGCTTTGC 183 ::: ::: ::::::::: :::: 868 1.ValLeuIleThrThrLeuLeuVallleProValLeuValLeuLeuAla 884
282 CTTCGTTTACTCAAGAAAGATCTGCAGAACCGGAGAATATCATTGATGT 233 :::::: ::: ::: ::: 852 MetGlnGluLysGlnLysLeuSerThrGluProGlySerGlyValSerVa 868
851Lys 851

	CAGTTGATTTACGTC 168	182
183 884	ACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGC	232 868
	tGlnGluLysGlnLysLeuSerThrGluProGlySerGlyValSer	Ü
233	TCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGA	282
851	ххд	851
283	GAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCCTGCTGCAGCTGCGCAA	332
850	LysValGlu	836
333	CGACCACAATGTTCAGAACCAC	363
836	ysLys <i>t</i>	820
364	ATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGT	405
819	ThrValTr	803
406	AAATATGCGGATCGATCACAGCTTTTCTATCA	441
803	.laSerGluAspGlyThrValTyrIleGlyAspA	786
442	ATTTAATGGCTGGCCAAGAAGCTCACGTATAC	475
786	LysProValArgLysHisPheAspMetProHi	776
476	TGGATGTGCTCTTGATAATATTTGCTAAATAATTTGGAATATCC	525
775	etAsnPheSerSerGlyGluIleIleAspVal	763
526	CTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAA	575
762	AspGinGluProValGinGlyPhe	755
576	TGGACATGCGATTCTGAAAACCGTTGATACTTTCTGCC	625
754	GlyPheLeuPheAlaValAsnGlyLysProTyrPheGly	742
626	CAATTTGCTATCATTGGTCAGCCAGTTTATCAT	675
741	erTyrIlePro	738
676	AATTGTCCC	725
738	 EValargGluIleLysHisAlaSerPheGlyArgAsnValPheAlaIleS	721
726	TTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACT	775
721	::::	0
776	TCGTGCATATCGAGTACAATGCTTTTACATGGAAGCT	822
704	HisSerLeuAlaLeuValPr	688
823	TTCGTTTCATCCATTATTTGTTACCAAAGT	864
889	$y { t GluGluSerSerGlySerSerProArgPro}$	671
865		865
671	:::::::: eValGlnPheSerProSerGlyI	656
866	TGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAAC	915
655		655
916	ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC	965

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alignment_block:
US-09-323-427-5/rev x W13009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes, we useful for diagnosis and treatment of carcinoma micrometastases SC Llaim 7; Page 5; 8pp; German.

The present sequence is a segment of the desmosomal cadherin (DC), desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) and directed against epitopes of the present sequence can be used to directed against epitopes of the present sequence can be used to diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods and cas a therapeutic to deliver agents, e.g. other Ab or toxins, to metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Segment of desmosomal cadherin, desmoglein Dsg2.

Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial; carcinoma; desmosome; antibody; epitope; diagnosis; detection; micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Franke WW, Schaefe WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-1995; 031033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE19531033-A1.
27-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W13009 standard; protein;
                 TTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT.....
                                                                                                                                                                                   AAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCA 950
                                                                                                                                                                                                                            snValLysGluGlyIleHisPheLysSerSerValIleSerIleTyrVal 348
                                                                                                                                                                                                                                                                 ATGCATTCGAAGGA......CATGTTTATGTG 1000
                                                                                                                                                                                                                                                                                                                                                                                               LeuAspPheSerValIleValAlaAsnLysAlaAlaPheHisAspSerIl
                                                                                                   AGTTGCCGGAATTTCACTTCCATTTGATTCATGCAAT.....
                                                                                                                                                                                                                                                                                                             eArgSerLysTyrLysProThrProIleProIleLysValLysValLysA 332
                                                                                                                                                                                                                                                                                                                                                      T.....GAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTA 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAAT 1070
                                                        nIleIleGlyAsnPheGlnAlaPheAspGluAspThrGlyLeuProAlaH
                                                                                                                                          SerGluSerMetAsp......ArgSerSerLysGly.....Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: W13009 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              560 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schaefer S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.50
0.822
51.232
Gaps:
Percent Identity:
Ξ
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6
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12
25.616
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                                                                                                     912
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seq_name: A_Geneseq_36:R20026
                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                  J03262484-A.
22-NOV-1991.
14-MAR-1990; (
                                                                                                                                                           Claim 1; Fig 1; 18pp; Japanese.

The sequence was deduced from the DNA sequence determined from clone isolated from a library prepd. from mRNA extracted from horse atrium tissue. The sequence is one of four similar ones provided which all have the same sequence up to residue 809 at which point they diverge, having different C-termini. The different termini are created by deletions in the last portion
                                                                                                                                                                                                                                                                                                        \ensuremath{\text{N-PSDB}}\xspace , \ensuremath{\text{Q20198}}\xspace . coding for peptide C terminal amidation enzyme
                                                                                                        DNA (see feature table).
See also R20025-28.
Sequence 973 AA;
                                                                                                                                                                                                                                                                                           obtd. from horse
                                                                                                                                                                                                                                                                                                                                              14-MAR-1990; JP-063306.
(SHIS ) SHISEIDO KK.
WPI; 92-012701/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493 GluLysTrp 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     630 CATAAATGG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 snSerGlyProPheSerPheSerValIleAspLysProProGlyMetAla 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 IleAsnAspAsnCysProThrLeuIleGluProValGlnThrIleCysHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equus caballus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-terminal amidation enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R20026 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         674 CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCA.....GTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459 sAspAlaGluTyrValAsnValThrAlaGluAspLeuAspGlyHisProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 spTyrProArgLysThrIleThrGlyThrValLeuIleAsnValGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T.....TATGAAATTTTGGATGGTGGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gTyrValGlnAsnGlyThrTyrThrValLysIleValAlaIleSerGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerValThrSerGluIleLysLeuAlaLysLeuProAspPheGluSerAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG...CCAGTATGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTT.....GATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AT....ATTGAGGTATCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is \texttt{AlaArgTyrValLysLeuGluAspArgAspAsnTrpIleSerValAsp}
                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                       063306.
85.00
0.582
43.976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               895
                                                                                                                                                                                                                                                                                                                                                                                                                                                            deleted in R20027 and R20028'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
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alignment_block: US-09-323-427-5/rev x R20026

Percent Similarity:

Percent Identity:

14 18.072

Ratio:

Align seg 1/1 to: R20026 from:

6: 973

065	⋗	1016
630	CysGlnProThrAspValAlaValAspProAsnThr	41
015	GACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGT	99(
642	r:::::: ::: r: lePheValSerAspGlyTyr	50
965	${ t STGGACGTCAAGTTGCCGGAATTTCACTTCCATTTG} I$	16
651		51
· -	GCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC	0
ū	.SerArgIleValGlnPheSerProThrGlyArgPheIleThrGl	
865		865
667	${\tt rpGlyGluGluSerSerGluSerAsnProLysProGlyGlnFire}$	84
9	ACTGTTGTCATTCGTTTCATCCATTATTTGTTACCAAAGTT	123
684	HisSerLeuAlaLeuValProHisLeuGlyGlnLeuCysValAl	00
822	TCGAGTACAATGCTTTTACATGGAAGCTGATAAAAC	776
701	gGluAsnGlyArgIleGlnCysPheLysThrAspThrLy	17
775	TTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAA	26
717	ArgGluIleLysHisAlaSerPheGlyArgAsnValPheAlaIl	34
725	AATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGC	76
734	ePro	37
675	GTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCAT	526
738	sProTyrPh	50
625	ACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCA	76
751	7	58
575	TTTGTCGATGATGGTAACGGTGATACTGTGGAAATT	26
759	PheSerSerGlyGluIleIleAspVal	71
525	ATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAAATATCCAAC	476
772	Lys!	82
475	ATTTAATGGCTGGCCAAGAAGCTCACGTATAC	442
782	SASPIleThrAlaSerGluAspGlyThrValTyrValGlyAspAlaHisT 7	99
441	TCGATCACAGCTTTTCTATCAATGC	406
799	rAsnThrValTrpLysPheThrSerThrGluArgValGluHisArg	814
405	CAAATAGCGAATGTGTTCGACC!	56
815	SerValLysLysAlaGlyIleGluVal	127
355	TGTTCAGAACCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCGCAG	306
827	erGlu	139
305	CTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT	59
839	rSerGlu	55
258	GATATC!	12

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78.50 78.50 114.96

128.39 128.39

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Database length: 13297546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query length: 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM of: US-09-323-427-5 to: Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -Q-/G972_1/USP70_Spool/US9323427/runat_14042000_170513_19887/app_query.fasta.1
-QB-/G972_1/USP70_Spool/US9323427/runat_14042000_170513_19887/app_query.fasta.1
-DB-Issued_Patents_AA -OPMT=fastan -SUFFIX=backtrans.rai
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-LOOPEXT=0.000 -QGAPDEXT=4.500 -QSAPEXT=0.050 -XGAPOP=10.000
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-THR_SCORE-PCT -ALICN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext
-MINLEN=0 -MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3
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2_6/ptodata/1/1aa/5A_COMB.pep:US-08-325-071-61
2_6/ptodata/1/1aa/5A_COMB.pep:US-08-325-071-61
2_6/ptodata/1/1aa/5A_COMB.pep:US-08-325-071-63
2_6/ptodata/1/1aa/5A_COMB.pep:US-08-325-071-63
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    Quality:
    Ratio:
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US-09-323-427-5/rev
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                                                                                                                                                                                                                 Percent Similarity:
                                                                           Align seg 1/1 to: US-07-707-367-2 from: 1 to: 935
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1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: C.L. 7 Skyline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-07-707-367-2
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FILING DATE: 19910530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 141678/90
FILING DATE: 01-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         TELEFAX: (919)541-868
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/707,367
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 3
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (914)785-7120
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 10-AUG-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                            Villamizar, JoAnn
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Nishikawa, Yoshiki
Kawahara, Takashi
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Gaps: 18
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                                          GCA.....GAACCGGAGAATATCATT...GATGTACGAAC 227
                                                                                              alGluLysGlnThrGlnGluLysGlnGlnLys.....GlnLysAsnSer
                                                                                                                                           CAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT 259
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AlaGlyValSerThrGlnGluLysGlnAsnValValGlnGluIleAsnAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                              FILING DATE: 02-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                      APPLICATION NUMBER: FILING DATE: 24-APR-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                           APPLICATION NUMBER: JP 1-181933 FILING DATE: 31-OCT-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 1-209687 FILING DATE: 15-AUG-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL THILE OF INVENTION: AMIDATION, AND METHOD OF PREPARING NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    840
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                                                                                                                                                   FILING DATE: 26-MAR-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20036-8218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
NAME: Player, Willi
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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OKAMOTO, HİROShİ
KISHIMOTO, JİRO
IFUKU, Ohjİ
KATO, Ichiro
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TAJIMA, Masahiro
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                                                                                                                  24-APR-1990
                                                                                                                                                                           26-MAR-1990
                      William
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                                                                                                                                     JP 2-106412
                                                                            JP 2-205475
                                                                                                                                                                                               JP 2-76331
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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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US-09-323-427-5/rev x US-08-070-301-16
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 989 amino acids
amino acid
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ORIGINAL SOURCE:
                                                                                                                                                            751
                                                                                                                                                                                                                                                                                                                                                                              778 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
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                                                              762 rGly......AspSerThrProValGlnGlyPhe.....
                                                                                                           631 TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
                                                                                                                                                                                                   681 GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 632
                                                                                                                                                                                                                                             744 laValSerTyrAlaPro.....Gly
                                                                                                                                                                                                                                                                                            731 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 682
                                                                                                                                                                                                                                                                                                                                      728 uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     696 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                       581 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 532
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TOPOLOGY: li
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Length:
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12
21.552
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alignment_block:
US-09-323-427-5 x US-08-477-451-8
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CORRESPONDENCE ADDRESS:
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745 IleValPheCysArgIlePheGluLeuValTyrArgLeuLeuIleAlaLy 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3200 amino aci
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TITLE OF INVENTION: Helicobacter Pylori Cagi Region
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                                       203 CTAATTTCAAGGGTGTTGATATC....AGTTCGTACATCAATGATATT 246
                                                                              761 sLysThrCys......PheSerPheTyrArgLeuIleGluIleV 774
                                                                                                                      153 GCAGAAGTGCACGGTGACGTAAATCAACTGGCAAAGCTTGATTATCATCG
                                                                                                                                                                                                    112 ATTTTGTACTGCAGCAAGTAT.....TACAGGTTGTCCATTATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
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TELEPHONE: 510-655-3542
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0.603
43.360
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1037 AAATTGATTGTTATTGAAGTTGGTCCACATTCAAT...TTCTGGCTCACC 1083
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                                                                                                                                                           CATAAAGACCTTTCACATAAACATGTCCTTCGAATGCATTACGTGTATTA 1036
                                                                                                                                                                                                                                                                 AATTCCGGCAACTTGACGTCCACCTTCATCATTACGGCAACCTTCTTGAT 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTGAGCTTCTTGGCCAGCCATTAAATCTGTTGGATATTCCAAATTATTT 496
                                                                                                                                                                                                                                                                                                                  heLysValAlaPheCysLeuArgTyrLeuAlaGluIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrArgLeu....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGTTTTGCTGCGGCACCACCTGTTTTAACAGCTCCGAATCCTTGTGGT
                                                                                                                                                                                                                                                                                                                                                                      GGATTCAGAGATCGTGTACGCGCAACATTGCATGAATCAAATGGAAGTGA
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...PheAsnPheAsnProPheTrpIle...
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                                                                                                          ..SerCysIleL
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alignment_block:
US-09-323-427-5/rev x US-07-906-349A-6
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                                                                                                                                                                                               Align seg 1/1 to: US-07-906-349A-6
                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPUTER: DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                573 ThrThrAlaAlaAlaThrCysAlaCysThrGlyCysThrGlyCysThrCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/906,349A
FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnik, Edward Y.
APPLICANT: Margolis, Benjamin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 18-JA
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STATE: D.C.
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ZIP: 20004
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AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 197
                                 sCysThrCysThrThrCysCysCysCysThrCysCysThrThr....
                                                                            CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG
                                                                                                                                                         ACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG
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Ratio:
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     801 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Benjamin L.
A NOVEL EXPRESSION-CLONING METHOD FOR LICENTIFYING TARGET PROTEINS FOR EUKAR
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                                                                                                                                                                                                                                                                                                 Percent Identity: 28.571
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                                       604
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49.669

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alignment_scores:
                                                                                           ; NAME/KEY:
; NAME/KEY:
US-08-415-751-35
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                                                                                                                                                                                                                                                                       TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Cry
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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SOFTWARE: Wordperfact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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Quality:
Ratio:
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: California
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                                                                                                                                                                                                                                                                                                                                                                                                                              Hana Dolezalova
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NELSON, RICHARD, C.
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                                                                                                            Positions coded by nonsense codons are identified as Xaa.
                                                                                                                                                                Cryptosporidium parvum
                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                        (415) 324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette - 3.5 inch, 1.44 Kb storage
                                                                                                                                                                                                     peptide
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                                                                                                                                                                                                                                                                                                                                                                                                           30,518
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Length:
Gaps:
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alignment_block: us-09-323-427-5/rev \times us-08-415-751-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 67, Application US/08325071 Patent No. 5587311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                           APPLICANT: RIDING, G
APPLICANT: RAND, Kei
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 AAAACCTGCTGCAGCTGCGCAAC.....TTC
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 uCysCysCysGlyCysCysSerLysIleTrpAspAsnCysCysCysSerL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 GCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACA.... 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 GTTTACTCAAGAAAAGAT.....CTGCAGAACCGGAGAATATCATTGAT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 AATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 SerAsnLeuLeuGlnHisSerArgArgHisPhePheGluArgLeuGl
                                                                              COUNTRY: USA
ZIP: 20007-5109
                                                                                                               STREET: 3000 K St. CITY: Washington,
                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuGluSerGlnIleAspPheLysLeuGlnAsnArgLeu.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......CTGCATGTCACCATTTGGCTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....LeuValGlu******LeuGlnLeuArgLeuValValLeuLeu* 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yMetArgAsn***ProHisArgGluLeuLeuHisGlüLeuValValLysG
                                                                                                                         E: Foley & Lardner 3000 K Street, N.W. ashington, D.C.
                                                                                                                                                                                                                                                                                           RAND, Keith No. 5587311man
                                                                                                                                                                                                                                                                                                                                           KEMP, David Harold
SRISKANTHA, Alagacone
                                                                                                                                                                                                                                                                                                                                                                                           WILLADSEN,
                                                                                                                                                                                                                                                                                                                                                                                                                  JOHNSON, Law Anthony York
                                                                                                                                                                                                                         DNA Encoding A Cell Membrane
Glycoprotein Of A Tick Gut
71
                                                                                                                                                                                                                                                                                                                                                                                                Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.828
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alignment_block:
US-09-323-427-5/rev x US-08-325-071-67
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-325-071-67
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APPLICATION UNMER: AU PI2570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE_DOCKET NUMBER: 60042/1
TELECOMMUNICATION INFORMATION:
TELEPAN: 202 672 5300
TELEPAN: 202 672 5399
TELEX: 904136
INFORMATION FOR SED ID NO: 67:
SEDIFICE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION UNMBER: US/08/325,071
APPLICATION UNMBER: US/08/325,071
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/062,109
ETILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/926,368
ETILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/242,196
ETILING DATE: 06-UUL-1988
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/AU87/00401
APPLICATION UNMBER: PCT/AU87/00401
APPLICATION UNMBER: APPLICATION DATA:
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APPLICATION UNMBER: APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1001 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
TOPOLOGY: linear
200 yProAspGlyGlnCysLysAsnAlaCysArgThrLysGluAlaGlyPheV 217
                                                                                      868 ......AACAACTGTTGTCAT......TTCG 850
                                                                                                                                                                                     187 ProProAlaAspSer.
                                                                                                                                                                                                                                                                           901 ACGATCTCTGAATCCACGTGGTATTTTTGTAAC.........
                                                                                                                                                                                                                                                                                                                                                             173 rgCysCysGlnGlyTrpAsnThr.....AlaAsnCysSerAlaAla 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 951 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||::: |||||||
147 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.00
0.612
40.947
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Percent Identity: 21.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60042/111 BIAU
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250	GAACCG	
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401	ysTyrVa	
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375	erIleGlyLysGluV	
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360	SCysLysArgTyrGl	
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484 350		
334	20 pLysSerArgLysProGlyProAsnValAsnIleAsnGluC	
519	ATACTGTGGAAATTCTAAATGCTGATGGAT	
320	rMetAsnArgGlnSerCysTyrCysProTr	
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303	cAspCysValAspLysLysCysHisGluGlu	
571	GAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC	
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266	:: ::: 250 erTyrThrValSerCysThrValGlnLysGlnThrCysArgProThr	
712	758 AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG	
250	roSerGlySerThrValAlaGluAspGlyIleThrCysLysSerII	
759	CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	
800	849 TTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG ::: :::::: ::: ::: 217 alCysLysHisGlyCys.ArgSerThrAspLysAlaTyrGluCysThrCy	

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; Sequence 61, Application US/08325071
; Patent No. 5587311

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-325-071-61
                                            alignment_block:
US-09-323-427-5/rev x US-08-325-071-61
Align seg 1/1 to: US-08-325-071-61 from: 1 to: 549
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION UNMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION UNMBER: US 07/926,368
FILING DATE: 06-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/242,196
FILING DATE: 06-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/242,196
FILING DATE: 06-JUL-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION UMBER: PCT/AU87/00401
APPLICATION UMBER: APPLICATION DATA:
APPLICATION UMBER: AU PI4912
APPLICATION UMBER: AU PI4912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION UMBER: AU PI2570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION UMBER: AU PH9196
APPLICATION UMBER: AU PH9196
APPLICATION UMBER: 27-NOV-1986
APPLICATION UMBER: 29,768
REGISTRATION UMBER: 29,768
REGISTRATION UMBER: 60042/111
B. REFERENCE/DOCKET NUMBER: 60042/111
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: COBON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WILLADSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Wa
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MOORE, Joanna Terry
JOHNSON, Law Anthony York
                                                                                                                           89.00
0.614
40.390
                                                                                                                      Length: 359
Gaps: 22
Percent Identity: 22.284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60042/111 BIAU
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519	ACTGTGGAAATTCTAAATGCTGATGG	555
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185	 ysArgProTh	169
712	GGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTC	758
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759	·····TTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATT	799
152	sGluHisGlyCys.ArgSerThrAlaLysAlaTyrGluCysT	136
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TELEPHONE:

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27 NOV-1986
ATTORNEY_AGENT INFORMATION:
NAME: BENT, Stephen A,
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrar
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: AU PI4912 FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/AU87/00401 FILING DATE: 27-NOV-1987
                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                             APPLICATION NUMBER: AU PI2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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5587311 ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILLADSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOHNSON, Law Anthony York
                                                                                                                                                                                                     19-JUN-1987
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                          60042/111 BIAU
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-325-071-63
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US-09-323-427-5/rev x US-08-325-071-63
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    Quality:
    Ratio:
Percent Similarity:
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1001 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 163
320 pLysSerArgLysProGlyProAsnVal.....AsnIleAsnGlyC 334
                                                                                                                                                                                                                                               620 CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC 571
                                                                                                                                                                                                                                                                                                                                               670 TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA 621
                                                                                                                                                                                                                                                                                                                                                                                             267 GluAspCysArgValHisLysGlyThrValLeuCysGluCysProTrpAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             951 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 sGluLysAsnLeuLeuGlnArgAsp......SerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 erHisThrValSerCysThrAlaGluGlnLysGlnThrCysArgProThr 266
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                                             .....AACGGTGATACTGTGGAAATTCTAAATGCTGATGGAT 519
                                                                                               PheMetAspCysGlyValTyrMetAsnArgGlnSerCysTyrCysProTr 320
                                                                                                                                               TTTGTCGATGATGGT.....
                                                                                                                                                                                               AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTC...CCGATG
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORM
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
APPLICATION NUMBER: US/08/450,332 FILING DATE: 25-MAY-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: CARTY, CHRISTINE E. REGISTRATION NUMBER: 36,099 REFERENCE/DOCKET NUMBER: 19076CA TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HENDRICKSON, LEE E.
APPLICANT: RAMBOSEK, JOHN
TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401
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CITY: F
                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 07065-0907
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STREET: 126 E. LINCOLN AVENUE, P.O. Box 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONDER, MICHAEL J. MCADA, PHYLLIS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VINCI, VICTOR A.
                                                                                                                                                                                                             Version
                                                                                                                                                                                                                  #
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alignment_block:
US-09-323-427-5/rev x US-08-450-332-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 3038 amino aci
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1341 .....GlnValLeuAlaSerAlaLysGluGlyArg......
                                                                                                                                                                                                                                                                                                                                                                                                                1279 yProLeuThrProAspSerLeuLeuAspAsnProGluTyrTrpAlaThrA 1296
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                                                                                                                                                                                                                                                           792 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC 743
                                                                                                                                                                                                                                                                                                                                                             827 AAGTTGATCGT......GCATATCGAGTACAATGCTTTTAC 793
                                                   701 GTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCT 652
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TOPOLOGY: lir
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                                                                                                    nGlnAlaAlaPheHisLeuGlnLysGlnIleGluTrpLeuGlu.....
                                                                                                                                                                                                                                                                                                            laGlnAspLysGluAlaIleProIleIleGluArgIleValTyrPheTyr 1312
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linear
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Percent Identity: 19.703
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seq_documentation_block:
; Sequence 2, Application US/08637640
; Patent No. 5849541
                                                                                                                             seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-637-640-2
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1575 gCysThrGluProPhe 1580
                                                                                                                                                                                                                                                                                                                      1559 PheIlePheGlyLeuPheAlaAspTrpTrpAlaGlyValAspAspGlyAr 1575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429 CGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC 380
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                                                                                                                                                                                                                                                          CTGCATGTCACCATTT 91
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alignment_block:
US-09-323-427-5/rev x US-08-637-640-2
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US-08-637-640-2
                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-637-640-2 from: 1 to: 3038
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APPLICANT: VINCI, VICTOR A.

APPLICANT: CONDER, MICHAEL J.

APPLICANT: MCADA, PHYLLIS C.

APPLICANT: MCADA, PHYLLIS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/148,132
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 908-594-4720 INFORMATION FOR SEQ ID NO:
                                                       1200 isValAspArgIleThrLeuValProSerLeuCysLeuAlaThrAlaGlu 1216
                                                                                                                                                                 1096 CAATGGTGTCGAAGGTGAGCCAGAAATTGAATGT......GGACCAACTT 1053
                                                                                                                                                                                                                           1175 ValAlaPheGlnThrValIleGlyAla.....TyrSerSerPro..... 1187
                                                                                                                                                                                                                                                                   1146 ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGA 1097
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APPLICATION NUMBER: US/08/637,641
FILING DATE: 23-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3038 amino aci
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TITLE OF INVENTION: DAA ENCODING TRIOL POLYKETIDE SYNTHASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CHRISTINE E. CARTY
STREET: P.O. BOX 2000; 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
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STRANDEDNESS: sir
TOPOLOGY: linear
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ZIP: 07065
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                     .....ACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 1010
                                                                                                                                      .....GlyAspArgArgLeuArgCysLeuTyrValProThrH 1200
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38.347
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2:
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Gaps: 24
Percent Identity: 19.703
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#1.25
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1479	leSerThrGlyPhePheGluGl	1463
280		٠ œ
280 1462	GTTAAAACAGGTGGTGCCGCAGCAAAACCTGCGCAGCTGCGGCAACTT ThrGlyGlyAlaThrLysTyrValLeuAlaThrProGlnLeu	329 1449
330 1448	CGACCACAATGTTCAGAACCACAAGGATTCGGAG glyalagly.	379 1446
1445	euGluIle	4
380	AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC	429
430 1441	CAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGGAT::: ::: :::	479 1426
480 1426		511 1409
512 1409	TAAATGCTGATGGATGTGCTCT ::: euAspHisAspGlyLeuLe	558 1394
1393	alGlyGlnHisLeuLeuProThrVal	1377
559		559
559 1377	ATGAT ::::: snSerTyrHisP	601 1360
602 1360	ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT	651 1351
1350	GlnValLeuAlaSerAlaLysGluGlyArg	
n w	3 .	701
02	CTGGTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCC	74
743 1326	PAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC :::::: ::: ::: ::: ::: ::: ArgSerPheLeuSerGInLeuThrLeuGluGluArgGl	792 1313
793 1312	TTTTAC PheTyr	827 1296
828 1296	<pre>IGTCATTTCGTTTCATCCATTATTTGTTACCA ::::::: LeuLeuAspAsnProGluTyrTrpAlaThrA</pre>	873 1279
874 1279	ATGCAATGTTGCGCGTACACGAGTCTCTGAATCCACGTGGTATTTTT	921 1263
922 1262	GTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGAT ::: ::::: ::: hrLeupheGinValGluAsnIleThrPheLysProPheSer	968 1247
969 1246	GTA	1009 1233
1233	SerGlyCysGluLysValAlaPheAsnThrIleAsnThrTyrAspLysGl	

APPLICATION NUMBER: US/08/540,804 FILING DATE: 11-OCT-1995 CLASSIFICATION: 424 PRIOR APPLICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/521,872 FILING DATE: 21-AUG-1995 PRIOR APPLICATION NUMBER: US 08/218,265 APPLICATION NUMBER: US 08/218,265 FILING DATE: 25-MAR-1994 ATTORNEY/AGENT INFORMATION: NAME: Granahan, Patricial REGISTRATION NUMBER: WHI94-03A2 TELEPOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240 TELEFAX: 617-861-9540 INFORMATION FOR SEO ID NO: 12: SEQUENCE CHARACTERISTICS:	block: lication US/08540804 66 66 66 66 06 68 69 Oleske, Anthony J. hompson, Craig M. NTION: No. 5919666el Factors Whi NTION: Transcription and Methods UENCES: 39 LE ADDRESS: Hamilton, Brook, Smith & Reynold O Militla Drive ngton Sachusetts Sa ABLE FORM: Floppy disk IBM PC compatible YSTEM: PC-DOS/MS-DOS PATEION DATA: CATION DATA:	GCTGCAGTACA : : : : AlaAspTrpTrpAlaGlyValAs 1 580 /laa/5B_COMB.pep:US-08-	280
	hich Modify Gene ds of Use Therefor lds, P.C.	AAAATGGAAT 107 ::::: :spAspGlyAr 1575	PheGluProL 1496 GGAGAATATC 241

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alignment_block:
US-09-323-427-5/rev x US-08-540-804-12
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; MOLECULE TYPE:
US-08-540-804-12
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560 eIleTyrLysLysValLeuLysGluLysAspValProAlaTyrAsnValT 577
                                                                                                                                                                                                                                                                                                          511 ePheLysTrpIleGluPheIleValTyrHisGlnLeuLeuSerAspIleG
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                                                                                                                                                 AGCCAGTTTATCATAAATGGACATGCGATTCTG...AAACCGTTGATA.. 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAAATCACAACTGCTTTTC.....AAACTCAAATTGTCCCGATGCCA 709
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                                                  SerGlnPhe...IleAsnAspHisIleLeuPheThrLysThrPheIlePh
                                                                                                                                                                                                     luSerLeuGluAlaLeuMetAspIleLeuLeuCysTyrGlnLysLeuPhe 544
                                                                                                                                                                                                                                                                                                                                                            GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrGluGlnIleLysMetArgIleLeuSerAsnAspIleThrAsnLeuGl 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTGCTA.....TCATTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                              LeuLysIlePheLysIlePheCysIleAspLeuGluValPheHisHisPh 511
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Ratio:
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amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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47.949
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Gaps: 13
Percent Identity: 19.744
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08218265 Patent No. 5922585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                     APPLICATION NUMBER: US/08/218
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI9
                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Young, Richard A.
APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5922585el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         710 uIleSerLeuLysLeuLeuThrPheGluValThrGlnAsnValLeuGlyL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    644 AsnPheProGluValPheGlnValAsnIleArgPheLeuLeuHisAsnSe
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             627 ysValTyrSerMetIleAsnAsnSerAsnGlnAlaValGlyGlnThrTrp 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...ATAGCGAATGTTCGACCACAATGTT...........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGCGATGATAATCAAGCTT 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....CAGAACCACAAGGATT 335
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                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                    US/08/218,265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brook,
                              WHI94-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith & Reynolds, P.C
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; LENGTH: 1226 amino ac
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-218-265-12
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US-09-323-427-5/rev x US-08-218-265-12
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-218-265-12 from: 1 to: 1226
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TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1148 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT 1099
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                            641 AGCCAGTTTATCATAAATGGACATGCGATTCTG...AAACCGTTGATA.. 597
                                                                                                                                                                                                                    511 ePheLysTrpIleGluPheIleValTyrHisGlnLeuLeuSerAspIleG
                                                                                                                                                                                                                                                                                                                                 495 LeuLysIlePheLysIlePheCysIleAspLeuGluValPheHisHisPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 nLeuSerLysThrProLeuSerIleLysIleMetValAlaGluTrpTyrL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416
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        545
                                                                                                            528 luSerLeuGluAlaLeuMetAspIleLeuLeuCysTyrGlnLysLeuPhe
                                                                                                                                                                                                                                                                       708 GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA 659
                                                                                                                                                                                                                                                                                                                                                                   752 CTGAAATCACAACTGCTTTTC.....AAACTCAAATTGTCCCGATGCCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           834 GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             951 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 902
                                                                                                                                                          ATTTGCTA.....TCATTGGTC 642
SerGlnPhe...IleAsnAspHisIleLeuPheThrLysThrPheIlePh 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                 euSerHisLeuCysSerGlyIleLeuSerSerValAsnArgThrValLeu 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....TTGTCATTTCGTTTCATCCATTATTT
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0.457
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Gaps: 13
Percent Identity: 19.744
                                                                                                            544
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	APPLICATION NUMBER: UFILING DATE: 07-JUN-1	
	ARE: PatentIn Relea APPLICATION DATA:	
	PE: Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DC	
	P: 94104 UTER READABI	
	TRY:	
	REET: 220 MONTGOMERY STREET, TY: SAN FRANCISCO	
	OF SEQUENCES: 32 ONDENCE ADDRESS: SSEE: MEDIEN & CARROLL II	
AND	OF INVENT	
	PPLICANT: FIRCA, JOSEPH R. PPLICANT: STAFFORD, DOUGLAS C.	
	LICANT: THALLEY, BRUCE LICANT: PADHYE, NISHA	••••
	eq_documentation_block: Sequence 6, Application US/08480604A Patent No. 5736139 GENERAL INFORMATION: APPLICANT: KINK, TOHN A.	0
	seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-480-604A-6	ξ.
	::: 27 euGluTyrIleIleArgLeu 73	
	205 TAGCGATGATAATCAAGCTT 186	
727	710 uIleSerLeuLysLeuThrPheGluValThrGlnAsnValLeuGlyL	
206	AACT	
710	Ė	
243	AAGAAAAGATCTGCAGAACCG	
693	77 snValm	
ò.	34 CCC3CCTCTTCTTAAAC	
677	60 rGluIleIleAspThrAsnThrSerLysGlnPheGlnLysAlaArgAs	
335	CAGAACC	
351	377ATAGCGAATGTGTTCGACCACAATGTT	
643	ysValTyrSerMetIleAsnAsnSerAs	
378	09 ATGCCAGATCAGTATTACCATT	
627	610 pGluLysLeuLysThrGluLysLeuLysAsnAspLysSerGluValLeuL	
410	AGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTAT	
610	594 LeuLysValAspAsnAspLeuArgIleGluLeuGlnSerValTyrAsnAs	
460	509 ATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC	
593	::: ::: hrSerPheMetProPheTrpLysPhePheMetLys	
510	TGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	
577	60 elleTyrLysLysV	
560	.CTTTCTGCGCGGTTGTCCATTCCTGC	

CLASSIFICATION:

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alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: 1; MOLECULE TYPE: US-08-480-604A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-480-604A-6 from: 1 to: 2710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
  264 uAlaAlaAlaSerAspIleVal.
                                      333 GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 284
                                                                                                                         383 AACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTC 334
                                                                                                                                                                 232
                                                                                                                                                                                                       433 GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG 384
                                                                                                                                                                                                                                                  230
                                                                                                                                                                                                                                                                                          483 TATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC 434
                                                                                                                                                                                                                                                                                                                               533 TAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAA 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        583 TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 TyrTyrLysSerGlnIleAsnLysProThrValProThrIleAspAspIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633 TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 02-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/405,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/422,711
                                                                                GlnGluLeuLeuAsnIleTyrSerGlnGluLeuLeuAsnArgGlyAsnLe
                                                                                                                                                               snSerAsnHisGlyIleAspIleArgAlaAsnSerLeuPhe...ThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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02-DEC-1993
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Percent Identity: 22.449
....ArgLeuLeuAlaLeuLysA 278
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; MOLECULE TYPE: US-08-405-496A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-405-496A-6
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                                                                                                                           TELEFAX: (415) 397-83:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/329,154 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                             FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 PheLysLeuIleIleGluSerLysSerGluLysSer 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WILLIAMS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 16-MAF CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                        TOPOLOGY:
                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/429,791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..TACGTCACCGTGCACTTC.....TGCAACATAATGGACAAC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pGluMetIleLysLeuGluAlaIleMetLysTyrLysLysTyrIleAsnA 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspLeuPheLysThrIleSerArgProSerSerIleGlyLeuAspArgTr 311
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                                                          amino acid
                                                                                                                                                                                                                                                         INGOLIA, DIANE E
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                                                                                   2710 amino acids
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                                                                                                                                                                        (415) 705-8410
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16-MAR-1995
                                                                                                                                                      397-8338
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seq_documentation_block:
    Sequence 65, Application US/08325071
    Patent No. 5587311
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Quality:
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US-09-323-427-5/rev x US-08-405-496A-6
                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-325-071-65
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                                                                                                                                                                                                    Patent No.
                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                            APPLICANT:
APPLICANT:
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                                                 APPLICANT:
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                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 yrAsnArgAspGluThrValLeuGluSerTyrArgThrAsnSerLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 TAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAA 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 TATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC 534
                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt snPheGlyGlyValTyrLeuAspValAspMetLeuProGlyIleHisSer}
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                                                                                                                                    COBON, Stewart Gary MOORE, Joanna Terry
KEMP, David Harold
SRISKANTHA, Alagacone
RIDING, George Alfred
RAND, Keith No. 558731lman
                                                                                       WILLADSEN, Peter
                                                                                                               JOHNSON, Law Anthony York
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Gaps: 9
Percent Identity: 22.449
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alignment_scores:
    Quality:
    Ratio:
                                                                                                                                                               alignment_block:
US-09-323-427-5/rev x US-08-325-071-65
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                                                                                                                                  Align seg 1/1 to: US-08-325-071-65
                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                           1024 TGCATTCGAAGGACATGT.....TTATG 1002
                               1001 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 133
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/242,196
FILING DATE: 06-UUL-1988
PRIOR APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
133 sGluLysAsnLeuLeuGlnArgAsp...
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-OCT-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 2v2
TELEFAX: 904136
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                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: AU P
FILING DATE: 19-JUN-1987
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                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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14-OCT-1993
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Glycoprotein Of A Tick Gut
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04	etTyrProLysLeuLeuIleLysLysAsnSerAlaThrGluIleGluGlu 4	388
50	GAACCG 2	276
88	 	371
77	ACTTCGT 2	283
171	::: :::	357
84	GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 2	333
5 34 5 4	AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC 3 ::: ::: :::::: AsnCvarthrG1 hAsp	383
45	uAspArgValLeuGluAlaIleArgThrSerIleGlyLysGluV 3	330
84	GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG 3	<u> </u>
30	PheAspSerAspHisCysLysArgTyrGl 3	321
2 6	ysLeuLeuAsnGLuTyrTyrTyrTnrvaLserPneTnrPnAsnLleser	304
8 4	GTGCTCTTGATAAATATTTGCTAAATAATTTGGAA 4	518
19	PLYSSerargLysProGlyProAsnValASnIleAsnGluC	555 290
90	PheMetAspCysGlyValTyrMetAsnArgGlnSerCysTyrCysProTr 2	274
56	TTTGTCGATGATGGT 5	570
73	ysCysIleSerAspCysValAspLysLysCysHisGluGlu 2	260
71	CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC 5	N
21	TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA 6 : ::::: ::: nGlnHisLeuValGlyAsp	570 253
53	GluAspCysArgValGlnLysGlyThrValLeuCysGluCysProTrpAs 2	237
71	CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGG 6	111
36	erTyrThrValSerCysThrValGluGlnLysGlnThrCysArgProThr 2	20
12	AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG 7	58
59	TTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG 7 ::: ::: : SerGlySerThrValAlaGluAspGlyIleThrCysLysSerIleS 2	99
203	CCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG E ::	.87
87	roAspGlyGlnCysLysAsnAlaCysArgThrLysGluAlaGlyPheV J	.70
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70	ProProAlaAspSerTyrCysSerProGlySerProLysGl 17	57
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pir2:A49772
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-Q-/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19903/app_query.fasta.
-Q-/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19903/app_query.fasta.
-DB-PIR_62 -QFMT-fastan -SUFFIX-backtrans.rpr -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT=0.000
-QGAPEXT=4.000 -GAPEXT=-0.050 -XGAPOP-10.000 -XGAPEXT=0.500
-GAPOP=6.000 -GAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-DELOP-6.000 -GAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
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2:S72278
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               calsequestrin precursor, cardia hypothetical protein F46Gll 2 NADH dehydrogenase (ubiquinone)
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seq_documentation_block:
cuticle protein cut-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
C;Accession: A49772
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A:Title: cut-1 a Caenorhabditis elegans gene coding A;Reference number: A49772; MUID:91323673
A;Accession: A49772
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                   CTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATT
                                                                                                         GGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAA 741
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21s rRNA intron protein - Em
23s rRNA intron protein - Ne
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                                   coding
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                                                                               09-Sep-1997
                                    specific
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US-09-323-427-5/rev
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A;Cross-references: EMBL:M55997; NID:g156271; PID:g156272 C;Genetics: A;Gene: CUT-1 A;Introns: 245/3

Percent Identity: Length: Gaps: 302 5 60.596

CysPheTyrMetGluSerAspLysThrValSerThrGlnIleGluValSe 22

801 TGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATC 601 TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG 751 TGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCC 701 GTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCT AAGATCT...GCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA TCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGA GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT rAspThrPheCysAlaValValHisSerCysThrValAspAspGlyAsnG ThrIleGlyGlnGlnValTyrHisLysTrpThrCysAspSerGluThrTh ProAlaValProArgAlaThrLeuAlaGlnLeuArgLeuLeuArgLysLy GCGCAACTTCGTTTACTC...AAGAA rovalGlyAlaAlaProvalAlaAlaProvalAlaAlaAlaAlaAlaAla aHisAlaAlaAlaAlaProGlnAlaGlyValGluValGlnAlaAlaP ACCTGCTGCAGCT..... TCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGT aHisValTyrLysTyrAlaAspArgSerGlnLeuPheTyrGlnCysGlnI lyAspThrValGlnIleLeuAsnGluGluGlyCysAlaLeuAspLysPhe ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT rAspLeuThrThrAlaPheGlnThrGlnValValProMetProValCysL 189 402 219 222 266 205 289 289 155 352 122 452 105 502 89 552 72 55 39 702

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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N;Alternate names: peptidylhydroxyglycine N-C lyase
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: S17855
C;Accession: S17855
Eur. J. Biochem. 201, 551-559, 1991
A;Title: Purification and cDNA cloning of Xenopus laevis skin peptidylhydroxyglycine N-C A;Accession: S17855; MUID:92037609
A;Reference number: S17855; MUID:92037609
A;Accession: S17855
A;Accession: S17855; MUID:92037609
A;Accession: S17855; MUID:92037609
A;Accession: S17855; MUID:92037609
A;Accession: S17855; MUID:92037609
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A;Accession: S17855; MUID:92037609
A;Accession: S17855; MUID:92037609
A;Accession: S17855; MUID:92037609
A;Accession: S17855; MUID:92037609
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US-09-323-427-5/rev x S17855
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C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolog
C;Keywords: oxidoreductase
F;131-342/Domain: peptidylglycine monooxygenase I homology <PGM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 542
                                                           563 nTrpGlyGluGluThrSerSerAsnValProArgProGlyGlnPheArg1 580
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                                                                                                                                                                                  AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA..... 871
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....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 829
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0.541
47.315
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Gaps: 18
Percent Identity: 19.437
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	38 TTACCATTTCGTTTAAATTTCGT 16	
39 840	85 CTCAATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTA ::::::::::::::::::::::::::::::::	
86 823	5 GTAATACTTGCTGCAGTACAAAATG ::: 7 ValSerThrGlnGluLysGlnSerV	
136 806	5 TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACAC ::::::::::::: ::: 0 lyValSerThrGlnGluLysGlnSerValValGlnGl	
186 790	226 TGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTT : ::	
227 773	258 GCAGAACCGGAGAATATCATTGATGTACGAAC	
259 756	308 CAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT ::	
309 742	358 ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCG ::: :::	
359 725	TAAAGAACCAAAT: ::::::::::::::::::::::::::::::	
397 708	GCGGATCGATCACAGCTTTTCTAT ::::::: ::: AspAlaHisAlaAsnAlaValTrp	
438 692	487 GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAAT ::::	
488 675	AATGCTGATGGATGTGCTCTTGATAAATATTTGCT	
532 663	TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTO	
582 652	31 TCATAAATGGACATGCGA	
632 646	GTCAACCAGTTCAATTTGCTATCATTGGTC :: :: : ValLeuTyrAlaValAsnGlyL	
682 634	731 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT :::::: :: 628 laValSerTyrAlaProGly	
732 628	778 AACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTC :	
779 612	828 AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA ::::::::::::: ::: ::: :::	
596	580 leProHisSerLeuThrMetValProAspGlnGlyGlnLeuCysValAla	

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A; Molecule type: mRNA
A; Residues: 1-843 <JUS>
A; Cross-references: GB:M64108; NID:g340081; PI
C; Superfamily: collagen alpha 1(XIV) chain; fi
C; Keywords: glycoprotein
F:165-246/Domain: fibronectin type III repeat
F:255-338/Domain: fibronectin type III repeat
F:347-427/Domain: fibronectin type III repeat
F:436-520/Domain: fibronectin type III repeat
F:436-520/Domain: fibronectin type III repeat
F:437-632/Domain: fibronectin type III repeat
F:437-832/Domain: fibronectin type III repeat
F:438-520/Domain: fibronectin type III repeat
F:438-520/Domain: fibronectin type III repeat
F:438-520/Domain: fibronectin type III repeat
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    Quality:
    Ratio:
    Percent Similarity:
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R;Just, M.; Herbst, H.; Hummel, M.; Duerkop, H.; Tripier, D.; Stein, H.; Schuppan, D. J. Biol. Chem. 266, 17326-17332, 1991
J. Biol. Chem. 266, 17326-17332, 1991
A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular A;Reference number: A40970; MUID:91373351
A;Accession: A40970
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C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1022 CATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              840
                                                                                                             389 uIleAsnGluValGluValAspProIleThrThrPheProLeuLysGlyL
                                                                                                                                                                                                                                                                                      822 GATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               352
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                                                     TTGTCCCGATG.....CCAGTATGCCGTTATGAAATTTTGGATGGT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACTTCAATAACAATCAATTTT.....AATACACGTAATG 1023
euThrProLeuThrGluTyrThrIleAlaIlePheSerIleTyrAspGlu
                                                                                                                                                                        TAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAA 723
                                                                                                                                                                                                                                 IleAsnGlyTyrArgIle.....ValTyrAsnAsnAlaAspGlyThrGl
                                                                                                                                                                                                                                                                                                                                                                                                       TAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            gAsnLeuArgIleSerAsnValGlySerAsnSerAlaArg......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: A40970
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Percent Identity:
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homology <FN3E>
homology <FN3F>
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homology <FN3B>
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22.222
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A;Molecule type: mRNA
A;ResIdues: 1-13288 <CGK>
A;ResIdues: 1-13288 <CGK>
A;Cross-references: EMBL:AF005273; NID:g2581863; PID:g2581864
R;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
J. Biol. Chem. 266, 9678-9886, 1991
A;Title: Porcine submaxillary mucin contains a cystine-rich, carboxyl-terminal
A;Reference number: A40009; MUID:91236743
A;Accession: A40009
A;Molecule type: mRNA
A;Residues: 12139-12167,'T',12169-13288 <EC3>
A;Cross-references: GB:M61883; NID:9454837; PID:9
R;Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.;
J. Biol. Chem. 263, 1081-1088, 1988
                                                                                                                                                                                                                                                                                                                                                                                                     R;Eckhardt, A.E.; Timpte, C.S.; DeLuca, A.W.; Hill, R.L. J. Biol. Chem. 272, 33204-33210, 1997
A;Title: The complete cDNA sequence and structural polymorphism A;Reference number: Z14839; MUID:98070526
A;Accession: T03099
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
C;Accession: T03099; A40009; A28528; B29789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mucin, submaxillary - pig
N;Alternate names: apomucin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 CAACAGATTTAATGGCT..........GGCCAAGAAGCTCACGTATAC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCGGAGAATATCATTGATG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCTGCAGCTGCGC...AACTTCGTTTACTCAAGAAAAGATCTGCAGA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hrIleValPro...ThrThrSerValThrSerValPheGlnThrGlyIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgAsn.....LeuValValGlyAspGluTh
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                                                                  PID:g164374
                                     Hill,
                                     R.L.
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Porcine submaxillary gland apomucin contains tandemly repeated, identical

domain

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alignment_scores:
Quality:
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C;Keywords: tandem repeat
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A; Residues: 12139-12167, 'T', 12169-12641 <TIM>
A; Cross-references: GB:J03512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13124 AspThrCysCysGluIle......GlyHisCysGluLysArgThrCy 13137
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| sThrCysThrGluAlaLysThrValAspCysLysProLysGluCysProS 13107
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                                                                                 s...GlnAsnThrGlyPheThrAlaValValGlnAsnCysProLysGlnT 13178
                                                                                                                                    TTCAGAACCACAAGGATTCGGAGCTGTTAA......AACA 319
                                                                                                                                                                                         ValGlySerSerPheAspAspProAsnAsnProCysValThrTyrSerCy 13162
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Gaps: 12
Percent Identity: 23,982
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A; Residues: 1-875 < OHS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13211 rAsnGlyCysThr
584 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
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Ratio:
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A;Cross-references: GB:M20191
A;Cross-references: GB:M20191
C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of p C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of p C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of p le and dismutates to glyoxylate and the corresponding desglycine peptide alpha-amide. C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase II peptidylglycine monooxygenase; oxidoreductase; transmembrane protein F;1-24/Domain: signal sequence #status predicted <SIG>F;40-385/Product: peptidylglycine monooxygenase II #status predicted <MAT>F;40-385/Product: peptidylglycine monooxygenase II #status predicted <MAT>F;133-344/Domain: peptidylglycine monooxygenase II homology <PGM>F;164-787/Domain: transmembrane #status predicted <TMN>F;365,662,743/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidylglycine monooxygenase (EC 1.14.17.3) II precursor - African clawed frog N;Alternate names: C-terminal alpha-amidating enzyme II (AE-II); peptidyl alpha-amida C;Species: Xenopus laevis (African clawed frog) C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Jun-1997 C;Accession: A27715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Ohsuye, K.; Kitano, K.; Wada, Y.; Fuchimura, K.; Tanaka, S.; Mizuno, K.; Matsuo, H. Biochem. Biophys. Res. Commun. 150, 1275-1281, 1988
A;Title: Cloning of cDNA encoding a new peptide C-terminal alpha-amidating enzyme hav A;Reference number: A27715; MUID:88134244
A;Accession: A27715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-323-427-5/rev x URXLA2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               530 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 lAlaAspGlyTyr.....
                                                                                  nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 584
....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
                                                                                                                                                                                                                                                       Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl 567
                                                                                                                                                                                                                                                                                                                                 AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 916
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0.945
43.103
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21.552
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                                                                                                                                                                     871
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seq_documentation_block:
hypothetical protein D1044.3 - Caenorhabditis elegans
c)Species: Caenorhabditis elegans
c)Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
c;Accession: T15881
R;Pauley, A.
                                                                                                                                                                                                                                    alignment_block:
US-09-323-427-5/rev x T15881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;MoLecule type: DNA
A;Residues: 1-1895 <PAU>
A;Residues: 1-1895 <PAU>
A;Cross-references: EMBL:U00065; NID:g495681; PID:g495684; PIDN:AAA50735.1;
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, June 1994
A;Description: The sequence of C. elegans cosmid D1044.
A;Reference number: Z18423
A;Accession: T15881
                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:D1044.3
A;Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:T15881
                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
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                                                                                                        1149 GlnCysIleAspAsnSerValCysMetAsnGlnMetCysThrCysAsnAs
                                                              866 CAAC......TGTTGTCATTTCGTTTCATCCATTATTT
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                                                                                                                              CAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAA 867
                   nAsnTyrArgLeuValTyrGlyTyrCysValProIleThrSerSerIleC
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0.940
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Percent Identity:
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                   alignment_block:
                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-610 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:C70126
US-09-323-427-5/rev x C70126
                                                           Percent Similarity:
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                                                                                 Quality:
Ratio:
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A;Cross-references: GB:AE001131; GB:AE000783; NID:g2688098; A;Experimental source: strain B31
                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown;
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SerGlnCysValGlySerGlnGlnCysLeuSerAsnSerGlnCysIleSe 1323
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  93.50
0.519
46.272
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Identity:
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    22
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23
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                                                                                                                                          PID:g2688099; TIGR:BB0211
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B ~ 5

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Align seg 1/1
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                                                                                                                                                                                                                                                           283 CysTyrLeuPheLeuGluIleAsnProGluTyrIleAspPheAsnValHi
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...TTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCA 343
                                                                                                                                                                                                                                                                                                         CTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProIleAspGlnLysAspLeuLeu......GluAlaIleThrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snPheSerLysLysSerLysArgHisIleLysThrPheValAsnArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAA 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCT 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erLeuIleAspArgValGlnAsnValTyrGlyAsnValIleGluAsnAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCACGTGGTATTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etCysLeuLys.....ValLeuGluGluLysIleIleThrHisProGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTA 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InProAlaIleAsnGlyThrIleValAspValThrLysIlePheHisAsn 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uSerTyrGlnIleGluValGluAsnGlyIleGluLysCysPheLysLysG
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                                                                                                                                                            sPro......GlnLysLysGluValArgPheTyrAsn......
                                                                                                                                                                                                             ACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCG 428
                                                                                                                                                                                                                                                                                                                                                                                                    TTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysPhe.....ArgValle
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                                                                                                                                                                                                                                                                                                                                                .....GlyAsnPheProIle 282
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                                                                    .....LeuProPheLeuPheLys 315
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C;Accession: T11616
R;Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V. submitted to the EMBL Data Library, October 1995
A;Reference number: Z17300
A;Accession: T11616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) - fission yeast (Sc C;Species: Schizosaccharomyces pombe C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-323-427-5/rev x Tl1616
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Quality:
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A; Residues: 1-2244 <BAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: IL
A; Note: SPAC22G7.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:254328; NID:g1009451; PID:g1009456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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Percent Similarity:
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1039 AlaValArgThrLeuArgAspArgGlyVal.....LysThrIleMe
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                       CGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGT 857
                                                                                                                                                                                                                       TyrThrThrTyrAsnAlaValGluHisAspIleHisPhe...... 1011
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                                                                                     GACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCG 907
                                                                                                                                                                               ......AsnAspLysGlyValMetValLeuGlySerG
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Gaps: 17
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m J}T_{
m 1118}
                                                                   114 AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGT 70
                                                                                                                                                                                                       164 GTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 AGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACAC 215
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                                                                                                                                    rgAla.....SerArgSerPheProPheValSerLysValIle...
                                                                                                                                                                                                                                                                           eGlnPheIleAlaLysAspAsnGluIleLysValIleGluCysAsnValA
                                                                                                                                                                                                                                                                                                                                               CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACC 165
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| pLeuHisSerTyrLeuGlnGlnAlaValAlaIleAsnLysAspHisProV 1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....GCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerTyrValLeuSerGlyAlaAlaMetAsnThrValTyrSerGlnSerAs 1187
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R;Bhargava, A.K.; Woitach, J.T.; Davidson, E.A.; Bhavanandan, V.P. Proc. Natl. Acad. Sci. U.S.A. 87, 6798-6802; 1990
A;Title: Cloning and CDNA sequence of a bovine submaxillary gland mucin-like A;Reference number: A36054; MUID:90370871
A;Accession: A36054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 10-Sep-1997
C;Accession: A36054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-323-427-5/rev x A36054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-563 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mucin homolog - bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:A36054
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Ratio: 0.612
Percent Similarity: 42.609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: A36054 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1101 GTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTC 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1051 AATAACAATCAATTTTAATACACGT...AATGCATTCGAAGGACATGTTT 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 IleGlnThrGlyIleThrGlyThrGlySer..........GlyThrThrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 rSerProGlyGlyPheAsnAlaGluAlaThrThrPheLysGluHisValA 222
644 GTCAGCCAGTTTATCATAAATGGACATGC...GATTCTGAAAACCGTTGAT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 854 TTTCGTTTCATCCATTATTTGTTACC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         904 TACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCA 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          954 CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCG 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 rThrSerLysSerAsnArgIleThrThrSerSerArgIlePro.....T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 LysGluAlaSerGluThrThrThrGlyProGlyIleSerThrThrGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 alserGlyArgValThrGlyValSerGluSerSerProGlyThrSer 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 rSerThrGlyValGlyArgGln.....ThrSerThrAlaValV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 rgThrThrGluThrArgIleLeuSerGlyThrThrArgGlyArgSerGly 238
                                                                                                                                                                                       LysThrGlyCysThrThrSerLeuProProProProAlaCysTyr....
                                                                                                                                                                                                                                                                                                                         yrProGluThrThrValValAlaThrGlyGluGlnGlu...ThrGluThr 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGA
                                                                                                                                                                                                                                                                                                                                                                                             ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGA 955
                                                             .....GlyProLeuGlyGluLysLysSerProGlyAspIleT
                                                                                                                              AATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....AAAGTTGATCGTGCATATCGAGTACAATGCTTTT 795
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Gaps: 18
Percent Identity: 20.290
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R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyl
J. Mol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fa
A;Reference number: S72277; MUID:96346169
A;Accession: S72278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
seq_documentation_block:
ATP-dependent Clp proteinase (EC 3.4.21.-) homolog - Plasmodium falciparum plastid C:Species: plastid Plasmodium falciparum
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
C:Accession: S72278; S78483
                                                                                                                                                                                                                             A:Cross-references: EMBL:X95276; NID:g1171591; PID:e220210; PID:g1171612 C:Genetics:
                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A:Reference number: S78483
A:Accession: S78483
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-765 <WIL>
                                                                      alignment_scores:
                                                                                                                                                                                                          A;Gene: clpC
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-95,'N',96-765 <WIW>
                                                                                                                                                                                                                                                                                                                                                                                           R; Wilson,
                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: X95276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: pir2:S72278
    Ratio:
Percent Similarity:
                                                                                                                                   Note: this apparently degenerate plastid is referred to as the apicoplast; Reywords: hydrolase; plastid; serine proteinase
                                                                                                                                                                                Genome: plastid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 TCTGCAGAACCGGAGAATATCATTGATGTACGAAC 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rAspSerThrLysCysCys.......TyrThrCysLysProT 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTT 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laTyrCysGluProArgThrCysLeuPheAsnAsnAsnAspTyr.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....AGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....ArgLeuValLysPheLysAspAsnAspThrCysCysGluIleA 401
  90.00
0.720
55.556
  Length: 225
Gaps: 20
Percent Identity: 27.111
                                                                                                                                                                                                                                                                                                                                                                   January 1996
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R:Latreille, P. submitted to the EMBL Data Library, May 1994 A;Description: The sequence of S. cerevisiae A;Reference number: $46691
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US-09-323-427-5/rev x S72278
                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                        seq_name: pir2:S48944
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hypothetical protein YHR102w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change C;Accession: S48944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508 TAAATATTTGCTAAATAAT...TTGGAATATCCAACAGATTTAATGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               848 TTCATCCATTATTTGTTACCAAAGTTGATC........GTGCATATC..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCACAATGTTCAGAAC......CACAAGGATTCGGAGCTGTTAAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTG 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rIleAsnTyrTyrLysIleAsn.....IleAsnAsnTyrIleIleTyrG 359
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                                                                                                                                                                                                                                                                                                   nHisIleTyrGlyGlnAsn
                                                                                                                                                                                                                                                                                                                                                          AAGAAAAGATCTGCAGAAC
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cosmid 8263
                                                                                                       #text_change
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                                                                                                       24-Sep-1999
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alignment_scores:
Quality:
Ratio:
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A;Cross-references: SGD:S0001144; MIPS:YHR102w
A;Map position: BR
G;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
C;Keywords: ATP; serine/threonine-specific protein kinase
E;21-276/Domain: protein kinase homology <KIN>
E;29-37/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S48944
A;Molecule type: DNA
A;Residues: 1-1080 <LAT>
A;Cross-references: EMBL:U00059; NID:g529116; PIDN:AAB68860.1; PID:g529127; MIPS:YHR102w
C;Genetics:
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US-09-323-427-5/rev x S48944
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  171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 LysValAspIleTrpSerLeuGlyIleThrThrTyrGluIleAlaThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           732 CAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGG
                                                                                                                                                                                                                                   LysSerIleAlaSerAsnAspAsnGluIleLysArgValAsn......
                                                                                                                                                                                                                                                                                                                                                                             CAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAA 301
CGTCACCGTGCACTTCTGCAACATAAT 145
                                                                                                                                                                                                                                                                                 CCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                        ySerIleProGluAsnGluProSerLysProSerGluAlaProLysProS
                                                spTyrIleIleGluAsnAsnIleAsnLeuAspAlaLeuAlaGluAspAsn
                                                                                         AT.....
                                                                                                                                                                                       GGAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCG
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                                                                                                                                         .GluGlyAspValGluMetLysTrpAspPheAspSerLeuSerSerSerA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leLysSerLysProProArgLeuGluAspArgSerTyrSerThrSerLeu
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Percent Identity: 21.531
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R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, I.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: C71618
                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999 C;Accession: C71618
A;Cross-references: GB:AE001386; GB:AE001362; NID:g3845148; PID:g3845151; TIGR:PFB031
A;Experimental source: clone 3D7
                                                                             A; Molecule type: DNA
A; Residues: 1-1712 <GAR>
                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnGluTrpAlaThrAlaGlnHisAsp
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                                                                                                                                                                  translation
                                                                                                                                                                      not shown
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H.

Align seg 1/1 to: C71618 from: 1 US-09-323-427-5/rev x C71618 90.00 0.584 45.161 Percent Identity: . 0 1712 19.941

1102 MetLysLysLysLysThrGlnGluTyrValAspIleGlu.....Th 1116 rValTyrGluTyrValIleGluLysTyrLysArgValHisValLeuTyrL 1133 1166 tGluLysLeuLysLysAsnTyrIleHisCysIleTyrAspIleSerAspL 642 CAGCCAGTTTATC.....ATAAATGGACATGCGATTCTGAAACCGT 742 AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 693 ACGGTGATACTGTGGAAATTCTAAATGCTGATG.....GATGTGCTCTT 511 ATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAA ::: ::::::|||::: TGATACTTTCTGCGCGGTTGTCCATTCCT...GCTTTGTCGATGATGGTA LysTyrSerPheHisLysLeuArgIlePheTyrGluTyrLysIleGluMe 1166 CATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTAC euGlyArgLeuLeuGlnIleValGluLysLeuPheLysLysTyrIleLeu 1149 euLeuLeuLysGluLysSerAlaTyrGlnAsnHisLeuGlyLysAsnTyr 1238 uSerSerPheIleAsnTyrGlnIleLysThrAsnAspMetLeuTyrAsnLPheAsnHisIleIleIleAsnSerTyrGl 1205 TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT ysLeuGluPheLeuIleLysLysLysMetGlnHisTyr...... ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC 743 TC...CACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATC ATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGA 602 1222 843 940

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posterior-group protein tudor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999
C;Accession: A41519; S19019
R;Golumbeski, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E.
Genes Dev. 5, 2060-2070, 1991
alignment_block:
                                                                                                                                                                                          A;Cross-references: FlyBase:FBgn0003891
C;Superfamily: posterior-group protein tudor
                                                                                                                                                                                                                                                                                   A;Cross-references: GB:X62420; NID:g8753; PIDN:CAA44286.1; PID:g8754
                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-2515 <GOL>
                                                                                                                                                                                                                                                                                                                                                               A;Title: tudor, a posterior-group gene of Drosophila melanogaster, encodes A;Reference number: A41519; MUID:92038995 A;Accession: A41519
                                                                                                                      alignment_scores
                                                                                                                                                                                                                                             A;Gene: tud
                                                                                                                                                                                                                                                                      C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:A41519
                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnValIleGluLysAsnValTyrArgLeuValLysLeuIleSerLysIl 1355
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Ratio:
                                             90.00
0.552
44.414
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                                             Percent Identity:
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16
19.074
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1066 ATGTGGACCAACTTCAATAACA.....ATCAATTTTAATACAC 1029
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                                                 2125 rAlaSerProProValValArgLeuThrThrLysAspLysArgSerLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2035 AlaAspAspLeuGluPheTyrArgSerArgIleLeuGluValLeuGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2018 lnProLysThrGluLysAlaAlaValAspAspMetCysValValGlnPhe
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                                                                                                              490 TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA 441
                                                                                                                                                                                                                      540 GAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAA 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       984 CAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTC
440 AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheThrLeuIle...LysProValAlaGlu.....IleCysSerMetGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...ThrHisValGluAsnThrSerArgIleTyrLeuGlnPheSerGluLy 2001
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                                                                                                                                                                                                                                                                                                                                    GCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTG 541
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                                                                                                                                                               .....LysGlyValValAlaValGluPheValAsnLysSe
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hypothetical protein yob! - Bacillus subtilis

C:Species: Bacillus subtilis

C:Species: Bacillus subtilis

C:Species: Drotein yob! - Bacillus subtilis

C:Species: Drotein yob! - Bacillus subtilis

C:Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 24-Sep-1998

C:Accession: H69998

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C:Accession: H69998

C:Accession: S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc

A: Ebrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

A: Ebrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

A: Ebrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

A: Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lavinois, A.; Cogwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Hench, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Zamanoto, H.; Yamanoto, K.; Yasumoto, K.; Yasta, K.; Yoshida, K.; A; Lavinois, A.; Lavinois, A.; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; A; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavinois, A.; Lavi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PID:e1185369; PID:g2634290
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1201 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: H69898 from: 1 to: 1201
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                                                                                                                                                                                                                                                                                                    1100 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 1051
                                               1050 ATAACAATCTTTAATACACGTAATGCATTCGAAGGACATGTTTATGT 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2192 leValLysThrLeuGlnSerLeuLysLysGluLysLeu.....LysLys 2206
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                                                                                                                                                                                                 552 LeuLeuGluLeuGluArgGluLysGlnGluIleArgAlaGlnSerLeuGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 CAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAAT 244
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n.....ValLeuIleThrLysMetAsnSerLysAspValPheSerA 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 193
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Ratio:
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0.511
44.643
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Gaps: 17
Percent Identity: 18.367
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848	· ···············GlnGlnAlaValIleAsnTyrValAsnA	839
359	TGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACC	408
838	ANGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAA :::::: ::: ProAsnIleThrTyrAlaAlaValLysAsnSerAsp	458 827
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459 826	TTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC	502 816
₩	: ::::: ::: rGluThrIleTyrAspPheValValGln	799
503	GGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAAT	552
553 799	ATACTTTCTGCGCGGTTGTCCA ::: ::: LeuLeuLysLeuGlnValLysP	599 783
600 782	CATTGGTCAGCCAGTTTATCAT	649 771
650 771	TATGAAATTTGGATGGTGGACCAACCGGTCAACTTGCTAT :::	758
Ci	TyrAlaAspIleAlaAspIleIleArgMetAsnLysGluSerV	744
700	TTCAAACTCAAATTGTCCCGATGCCAGTATGCC	734
4.	erAsnTyrThrGlnGlnLysLysGluGluTyrLeuSerAspIleLeuT	727
w	AGATTGAGGTATCTGAAATCACAACTGCT	764
N	nSerIleSerSerLysTrpAspAspPheTrpSerPheIleGluLeuArq	710
765		765
710	PheIleAspGlyPheLysGluArgAlaIleAsnLysAlaAlaPheIle	694
765		765
9	<pre>:::::: ::::::::::::::::::::::::::::</pre>	
765	CATGGAAGCTGATAAAACAGTTAGTGCAC	793
794 677	3 CCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTA :::: :::::::::::::::::::::::::::	843 664
664	3 TGAANCCACGTGGTATHTTTGTAACAACAACTGTTGTCATTTCGTTTCAT ::: :: :::: :::: :::::: E LeuValGlyAlaGluPheLysGlnTleGluValLeuAsnPheHisLeuLe	648
. 4	erLeuProTyrSerPheGluLeuAspAsnIleGlyLysIleMetSerL	ν
894	TGTTGCGCGTACACG	913
631	rLeuSerLeuSerAspIleLysPheValPheSerIleLysAsr	614
914		920
614	<pre>::: :::::: TyrIleAspGluMetTyrAsnHisTyrIleThrTyrPheTyrProGluS</pre>	598
921	AAGTTGCCGGAATTTCACTTCCATTTGATT	950
9	:::::: ::: ::: spLysLeuTyrGluLysLysLeuLeuValTyrLeuLeuArgHisG	582
951	O GAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTC	1000

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Swissprot_38:AVM_SWN3-3
Swissprot_38:KBF1_CHICK-
Swissprot_38:FDE_DICDI-
Swissprot_38:PDE_BACST-
Swissprot_38:PDE_BACST-
Swissprot_38:GBF_DICDI-
Swissprot_38:GBF_DICDI-
Swissprot_38:GBF_DICDI-
Swissprot_38:GBF_DICDI-
Swissprot_38:YSO2_CAEEL-
Swissprot_38:YSO2_CAEEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SwissProt_38:CGE1_CHICK
SwissProt_38:PY3_AVESA
SwissProt_38:PYA0E_SCHPO
SwissProt_38:SRB8_YEAST
SwissProt_38:BF3_HUMAN
SwissProt_38:BF11A_MOUSE
SwissProt_38:RPOD_SPIOL
SwissProt_38:RPOD_SPIOL
SwissProt_38:DY4G_CHLRE
SwissProt_38:DY4G_CHLRE
SwissProt_38:CAQC_CANFA
SwissProt_38:CAQC_CANFA
SwissProt_38:CAQC_CANFA
SwissProt_38:CAQC_CANFA
SwissProt_38:CAQC_CANFA
SwissProt_38:DOSM_APILI
SwissProt_38:DOSM_APILI
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SwissProt_38:NRK1_YEAST -
SwissProt_38:TUD_DROME -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query: US-09-323-427-5
Query length: 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SwissProt_38:SSR5_RAT -
SwissProt_38:AMD_HUMAN -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_38:AMD2_XENLA -
SwissProt_38:YLK3_CAEEL -
SwissProt_38:PYR1_SCHPO -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SwissProt_38:APMU_PIG -
SwissProt_38:GALU_PSEAE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Strd
SwissProt_38:CUT1_CAEEL
SwissProt_38:YQH3_CAEEL
SwissProt_38:YAY3_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database sequences: 82229
Database length: 29864866
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363 i p30938 rattus norvegicus (rat)
974 i p19021 homo sapiens (human).
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7 i P49707 gallus gallus (chicke
128 i P06593 avena sativa (oat).

260 i Q10093 schizosaccharomyces.

427 i P25648 saccharomyces cerevi
117 i Q14126 homo sapiens (human).

1025 i O42611 fugu rubbipes (japan).

1068 i P42337 mus muscullus (mouse).

361 i P11704 spinacia oleracea (circi).

361 i P11704 spinacia oleracea (circi).

361 i P11704 spinacia oleracea (circi).
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! P12890 xenopus laevis (afric
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P12637 canis familiaris (dog
P34855 apis mellifera ligust
P21421 plasmodium falciparu
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1 Q09276 caenorhabditis elegan
1 Q10211 schizosaccharomyces r
                                                                                                                  P15305 oncorhynchus mykiss
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i Q048 f3 gallus gallus (chick)
i P22549 dictyostelium discoid
i P77836 bacillus stearothermoj
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P009794 schizosaccharomyces
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    Q10128 caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                noncollagenous component of the cuticle."; Dev. Biol. 146:519-530(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEBASTIANO M., LASSANDRO F., BAZZICALUPO P.; "cut-la Caenorhabditis elegans gene coding for
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                            Hypothetical
TRANSMEM
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KD PROTEIN C43C3.3 IN CHROMOSOME
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TRANSMEM NP_BIND SEQUENCE

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WW; ATP POTENTIAL. POTENTIAL.

rp (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 LysGlyLeuThrAsnPheAsnLeuThrIleProTyrGlySerGluCysAs
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                                                                                                                                                                                                                                      CTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTTG.....
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PheArgThrPheArgPheGlyAsnGlnSerThrValPheValHisCysGl
                                   GCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCA 404
                                                                           ... IleIleAspProLeuAlaAsnValAsnAspGlnIleTyrPheSerLys
                                                                                                                                                    nAsp.....
                                                                                                                                                                                                CGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAAT
                                                                                                                                                                                                                                                                                                                   ysGluCysThrPheSerAspArgGluAspIleSerAlaProAspAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrAspSerGlyLysThrLeuGlnAlaAlaArgGluAsnGluPheValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hrGlyGlyLysProLysPro.....LysValGluMetLeuPheArgSer 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ....IleArgPheSerAspValSerAsnGlyHisGluValIleAlaSerT
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                                                                                                                   ....ACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAA 554
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Gaps: 19
Percent Identity: 22.647
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alignment_block:
US-09-323-427-5/rev x YAY3_SCHPO
                                                                                                                                                                                                                      alignment_scores:
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Percent Similarity:
                                                          1089 GTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATCAA 1040
 1039 TTTTAATACACGTAATGCATTC.....
                                                                                                                                                                                                                                                                   TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPAC4H3.03C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                 Hypothetical protein; Transmembrane TRANSMEM 265 285 POTENT: TRANSMEM 564 584 POTENT:
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Q10211;
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                             36 LeuAspGlySerValGluMetMetCysTrpPro.....As
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SerAsnLeuThrAlaGluArgLeuArgPheArgHisLysArgSer....
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0.554
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Gaps: 23
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                                             TrpIleArgAspSerAlaPheThrIleTyrAlaLeuAlaGlnLeuGlyPh
                                                                                                                                   erLeuProGluAspLeuGlyGlyValArgAsnTrpAspTyrArgPheThr
                                                                                                                                                                                                                                                                                TATTACCATTAAAGAACCAAATAGCGAATGTGTT...CGACCACAATGTT
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                                                                                                                                                                                   CAGAACCACAAGGATTCGGAGCTGTTAAAACA.........
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.CGTTTACTCAAGA
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seq_documentation_block:
ID APMU_PIG
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MEDLINE; 97248516.

MEDLINE; 97248516.

GERKEN T.A., OWENS C.L., PASUMARTHY M.;

GERKEN T.A., OWENS C.L., PASUMARTHY M.;

Determination of the site-specific O-glycosylation pattern of the potential proposed of the submaxillary mucin tandem repeat glycopeptide. Model proposed for the polypeptide; galnac transferase peptide binding site.";

J. Biol. Chem. 272:9709-9719(1997)

-I- FUNCTION: APOMUCIN IS PART OF MUCIN, THE MAJOR GLYCOPROTEIN SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE GLAND. TO ANT CANTTY AND TO PROTECT IT FROM THE EXTERNAL
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Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metaztiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycosylated domain.";
J. Biol Char
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                                                                                                                                                                                                                                                        ECKHARDT A.E., TIMPTE C.S., ABERNETHY J.L., TOUMADJE JOHNSON W.C. JR., HILL R.L.;
"Structural properties of porcine submaxillary gland J. Biol. Chem. 262:11339-11344(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Porcine submaxillary mucin carboxyl-terminal domain in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1989 (Rel. 12, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
APOMUCIN (MUCIN CORE PROTEIN) (FRAGMENT).
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Submitted (DEC-1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q59633;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U03751; AAB01486.1; -. PFAM; PF00483; NTP_transferase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).

-i- CATALYTIC ACTIVITY: UTP + ALPHA-D-GLUCOSE 1-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALU_PSEAE
                                                                  74
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                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                 GGT...TGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACT
                                                                                                                                                                                                                                                                     GTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                   AGAAATTGAATGTGGACCAACTTCAATAACAATC...AATTTTAATACAC
TCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTG
                                                           AsnGlnIleLysGlyThrAspLysGluLysTyrLeuValGlyIleArgLy
                                                                                                                                                                                               ysArgAlaLeuGluAspHisPheAspIleSer.....TyrGluLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitted (DEC-1993) to the EMBL/GenBank/DDBJ databases. FUNCTION: MAY PLAY A ROLE IN STATIONARY PHASE SURVIVAL (BY
                                                                                                                                                                                                                                                                                                                                    uAlaLeuAspAlaGlyLeuAsnGluIleSerIleValThrGlyArgGlyL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuProValValAsnLysProLeuIleGlnTyrGlyVal.....GluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE PROKARYOTIC UDPGP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATTGATGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYROPHOSPHATE + UDP-GLUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SwissProt_38:GALU_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinase; Nucleotidyltransferase.
79 AA; 30939 MW; D967F501 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.00
0.807
50.424
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seq_name: SwissProt_38:AMD2_XENLA
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                  Biochem. Biophys. Res. Commun. 150:1275-1281(1988).
-!- FUNCTION: C-TERMINAL ALPHA-ANLIDATION OF BIOLOGICAL PEPTIDES.
-!- CATALYTIC ACTIVITY: PEPTIDYLGLYCINE + ASCORBATE + O(2) =
PEPTIDYL(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)O.
(THE PRODUCT IS UNSTABLE AND DISMOTATES TO GLYOXYLATE AND THE
CORRESPONDING DESGLYCINE PEPTIDE AMIDE).
                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE II PRECURSOR
(EC 1.14.17.3) (PEPTIDE C-TERMINAL ALPHA-AMIDATING ENZYME II) (AE-II).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
                                                                                                                                                                                                                  OHSUYE K., KITANO K., WADA Y., FUCHIMURA K., TANAKA S., MIZUNO K.,
                                                                                                                                                                                                                                     MEDLINE; 88134244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P12890;
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                                                                                                                                                       enzyme having a putative membrane-spanning domain from
                                                                                                                                                                                                  MATSUO H.
                                                                                                                                                                                                                                                           TISSUE-SKIN;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         Batrachia;
                                                                                                                                                                           "Cloning of cDNA encoding
                                                                                                                                                                                                                                                                                                                  Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMD2_XENLA
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  COFACTOR:
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                                                                                                                                                                                                                                                                                                                                     Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511
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  COPPER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
AND ASCORBATE.
                                                                                                                                                                           a new peptide C-terminal alpha-amidating
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                                                                                                                                                         Xenopus laevis
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alignment_block:
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Percent Similarity:
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M19032; AAA49667.1; --
PIR; AZ7115; URXLA2.
PROSITE; PS00084; CU2_MONOOXYGENASE_1;
PROSITE; PS00085; CU2_MONOOXYGENASE_2;
                                                                                                                                                                                          567
                                                                                                                                                                                                                                                                                                                                                                                 965 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 546
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                                                                                                                                                                                      \verb"nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI"
                                   AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                                              leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                   AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
                                                                        AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE COPPER TYPE II, ASCORBATE-DEPENDENT
                                                                                                                                                   ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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787
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Gaps:
Percent Identity:
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06EEF456 CRC32;
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POLY-ASP.
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Seq_documentation_block:

ID YIM3_CABEL STANDA
AC P41951;

DT 01-NOV-1995 (Rel. 32,
DT 01-NOV-1998 (Rel. 32,
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   Hypothetical protein; T
ATP-binding: EGF-like d
DOMAIN 431 703
NP_BIND 437 445
BINDING 461 461
ACT_SITE 569 569
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00101: PROTEIN_KINASE_DOM; 1.
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Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: STRONG, TO ZC84.1.
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
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01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3
(EC 2.7.1.-).
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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-!- SIMILARITY: CONTAINS ? EGF-LIKE DOMAINS.
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PFAM;
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PROSITE; PS00442; GATASE_TYPE_I; 1.
PROSITE; PS00866; CPSASE_I; 2.
PROSITE; PS00867; CPSASE_2; 2.
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                                                                                                                                                                                                                                                                              PF00289; CPSase_L_chain; 2. PF00744; Dihydrooratase; 1. PF00988; CPSase_sm_chain; 1.
                                                                                                                                                                                                                                                                                                                                                PF00117; GATase; 1. PF00185; OTCace; 1.
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Z54328; CAA91130.1;
P00968; LJDB.
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                  BOUNDARY BETWEEN ENZYMATIC DOMAINS (BY SIMILARITY).
DEFECTIVE DHOASE DOMAIN (BY SIMILARITY).
BOUNDARY BETWEEN ENZYMATIC DOMAINS
  SIMILARITY).
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AND ATCASE) (BY SIMILARITY).

AND ATCASE) (BY SIMILARITY).

CATALYTIC ACTIVITY: 2 ATP + GLUTAMINE + CO(2) + H(2)O = 2 ADP + CATALYTIC ACTIVITY: CARBAMOYL PHOSPHATE + GSPARTATE = CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASSARTATE = CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASSARTATE = CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASSARTATE = CATALANEOUS: GATASE (GLUTAMINE AMIDOTRANSFERASE) AND CPSASE (CARBAMOYL PHOSPHATE SYNTHASE) FORM TOGETHER THE (CARBAMOYL PHOSPHATE SYNTHASE) FORM TOGETHER THE GLUTAMINE-DEPENDENT CPSASE (GD-CPSASE) (EC 6.3.5.5).

CATALANEOUS: IN EUKARYOTES EC 6.3.5.5 IS SYNTHESIZED BY TWO PATHWAY-SPECIFIC (ARGININE AND PYRIMIDINE) UNDER SEPARATE CONTROL.

SIMILARITY: THE CPSASE DOMAIN IS SIMILAR TO OTHER CPASES.

SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-1 GLUTAMINE AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BADCOCK K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH Submilted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THIS PROTEIN IS A "FUSION" PROTEIN ENCODING THREE ENZYMATIC ACTIVITIES OF THE PYRIMIDINE PATHWAY (GATASE, CPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "As in Saccharomyces cerevisiae, aspartate transcarbamoylase is assembled on a multifunctional protein including a dihydroorotase-like cryptic domain in Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                URA1 PROTEIN [INCLUDES: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5); ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3. URA1 OR SPAC22G7.06C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl: Ascomycota; Archiascomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5); ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2)].
                                                                                                                                                                                                                                             Ligase; Transferase; Multifunctional enzyme.
GATASE (GLUTAMINE AMIDOTRANSFERASE)
BOUNDARY BETWEEN ENZYMATIC DOMAINS (BY SIMILARITY).
CPSASE (CARBAMOYL-PHOSPHATE SYNTHASE) (BY SIMILARITY).
                                                                                                                                                                                                     (BY SIMILARITY)
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Percent Similarity:
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                                 .....AspThrValGlyTyrProValLeuValArgPro 1170
                                                             TCGATGATGGTAACGGTGATACTGTG.....GAAATTCTAAATGCTGAT
                                                                                               rPheAspGlu...AlaAspLysPheCys..........
                                                                                                                                                                  MetLeuAspAspIleGlyValAspGlnProLysTrpLysGluLeuThrSe 1151
                                                                                                                                                                                                   CCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATG
                                                                                                                                                                                                                                                                                                                                                                         GluGlnGluSerSerGlyIleIleIleAlaMetGlyGlyGlnThrAl 1101
                                                                                                                                                                                                                                                                                                                                                                                                         GCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATT..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lyValTyrArgIleGlySerSerValGluPheAspTrpCysAlaValArg 1038
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                                                                                                                                  CGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGCTTTG
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GATASE (BY SIMILARITY).

GATASE (BY SIMILARITY).

GIC -> RYF (IN REF. 1).

CAVRA -> LQFAQ (IN REF. 1).

EL -> DV (IN REF. 1).

G -> E (IN REF. 1).

G -> E (IN REF. 1).

G -> E (IN REF. 1).
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seq_documentation_block:
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                                                                                                                                                                                    "Cloning and cDNA sequence of a bowine submaxillary gland mucin-like protein containing two distinct domains.";

Proc. Natl. Acad. Sci. U.S.A. 87:6798-6802(1990).

-I- SUBCELIULAR LOCATION: SECRETED.

-I- TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.

-I- SIMILARITY: TO PORCINE APOMUCIN.

-I- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SUBMAXILLARY MUCIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 903708
BHARGAVA A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGT 70
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PROSITE; PS01225; CTCK_2; 1.
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                                                                                                                                                                                                                                                                                                                  rgThrThrGluThrArgIleLeuSerGlyThrThrArgGlyArgSerGly
ACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCCGTTATGA
                      yrProGluThrThrValValAlaThrGlyGluGlnGlu...ThrGluThr
                                               ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATC
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                                                                      rThrSerLysSerAsnArgIleThrThrSerSerArgIlePro....T
                                                                                                                       LysGluAlaSerGluThrThrThrGlyProGlyIleSerThrThrGlySe
                                                                                                                                                                     {\tt alSerGlyArgValThrGlyValSerGluSerSerSerProGlyThrSer}
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seq_documentation_block:

ID NRK1_YEAST STANDARD; PRT; 1080 AA.

AC P38692;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE SERINE_THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-)

GN NRK1 OR YHR10ZW.
      seq_name: SwissProt_38:NRK1_YEAST
STRAIN-S288C / AB972;

MEDLINE; 94378003

JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,

DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,

DU Z., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,

KUCABA T., HILLIER L., MACRI C., MARDIS E., MENEZES S., MOUSER L

LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., WENEZES S., MOUSER L

NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.
                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete nucleotide VIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P24941; 1AQ1.
SGD; L0001276; NRK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 LysValAspIleTrpSerLeuGlyIleThrThrTyrGluIleAlaThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          732 CAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIGNATI D., WILCOX L.,
CAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTT
                                           ArgTyrLeuLeuPheArgAspLysAsnLysAsnLysTyrLysIleGluGl
                                                                                                                                                                                                                                                                                                                            LysGluPheIleAlaLeu......CysLeuAspGluAspProLys..
                                                                                                                                                                                                                                                                                                                                                                          GATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGG
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                                                                                           CACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGAT
                                                                                                                                                                                       TGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATT
                                                                                                                                                                                                                                                                                                                                                                                                                     leLysSerLysProProArgLeuGluAspArgSerTyrSerThrSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASES.
                                                                                                                                         leArgAlaHisLysAlaThrProThrSerIleLeuLysGluLeuIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S48944; S48944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U00059; AAB68860.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D29980; BAA06250.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00108; PROTEIN_KINASE_ST; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine/threonine-protein kinase; ATP-binding.
23 276 PROTEIN KINASE.
29 37 ATP (BY SIMILARITY).
52 52 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                . {\tt GluArgLeuSerAlaAspAspLeuLeuLysSerLysPheI}
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117061 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 6
Percent Identity: 21.531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Gaps:
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alignment_block:
US-09-323-427-5/rev x TUD_DROME
                                                                                         alignment_scores:
    Quality:
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                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      documentation_block:
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no require by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by a modified and this statement is not removed. Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOLUMBESKI G.S., BARDSLEY A., TAX F., BOSWELL R.E.; "Tudor, a posterior-group gene of Drosophila melanogaster, encodes novel protein and an mRNA localized during mid-oogenesis."; Genes Dev. 5:2060-2070(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366
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                                                                                                                                                              Developmental protein. SEQUENCE 2515 AA; 2
                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATERNAL TUDOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUD_DROME
                                                                                                                                                                                                 FLYBASE; FBgn0003891;
PFAM; PF00567; TUDOR;
                                                                                                                                                                                                                                   PIR; A41519; A41519
                                                                                                                                                                                                                                                       EMBL; X62420; CAA44286.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR
REGION OF THE DEVELOPING OOCYTE DURING THE EARLY TO MIDDLE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION
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                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                      90.00
0.552
44.414
                                                                                                                                                              285236 MW;
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                                                       Percent
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                                                       Gaps: 16
Identity: 19.074
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                      AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC
                                                           {\tt rAlaSerProProValValArgLeuThrThrLysAspLysArgSerLeuL}
                                                                                                                                                                                            GAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAA 491
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                                                                                                        TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA 441
                                                                                                                                                                                                                                  spAlaLeuLeuAspSerCys.....
                                                                                                                                                                                                                                                                                 GCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTG
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                                                                                                                                                                                                                                                                                                                      uProSerAlaIlePheGluLysAsnLysAlaLeuThrLeuThrThrPheA
                                                                                                                                                                                                                                                                                                                                                                A.....ACCGTTGATACTTTCT 591
                                                                                                                                                                                                                                                                                                                                                                                                             PheThrLeuIle...LysProValAlaGlu.....IleCysSerMetGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2142 ysIleTyrGluHisLeuGlnLysLeuValGlnAlaGluLeuLysLeuIle
                  EMBL;
                                                                                            the European Bioinformatics Institute. There are no rest use by non-profit institutions as content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     PANETTA R., GREENWOOD M.T., WARSZYNSKA A., DEMCHYSHYN L.L., DAY R., MIZNIK H.B., SRIKANT C.B., PATEL Y.C.;
"MOLECULAR cloning, functional characterization, and chromosomal localization of a human somatostatin receptor (somatostatin receptor type 5) with preferential affinity for somatostatin-28.";
Mol. Pharmacol. 45:417-427(1994).

-i- FUNCTION: RECEPTOR FOR SOMATOSTATIN-28. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBIT ADENYLYL CYCLASE RECEPTOR IS MEDIATED BY G PROTEIN EPROTEIN.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- TISSUE SPECIFICITY: PROMINENT IN THE PITUITARY AND SMALL INTESTINE. LOW LEVELS IN ISLETS AND SPLEEN. NOT DETECTED IN KIDNEY, PANCREAS, CEREBELLUM, OR CORTEX.

-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
SOMATOSTATIN RECEPTOR TYPE 5 (SS5R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'CARROLL A.-M., LOLAIT S.J., KONIG M., MAHAN L.C.;
"Molecular cloning and expression of a pituitary somatostatin receptor with preferential affinity for somatostatin-28.";
Mol. Pharmacol. 42:939-946(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 93125499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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                  L04535; AAA17029.1; -. U01152; AAC09011.1; -. X74828; CAA52825.1; -.
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GCRDB;

GCR_0514;

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alignment_block:
US-09-323-427-5/rev x SSR5_RAT
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                                                         171 oLeuLeuValPheAlaAspValGlnGluGlyTrpGlyThrCysAsnLeuS
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PROSITE; PS00237; G_PROTEIN_RECEPTOR;
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                                                                                                                    LysMetAlaSerAlaAlaValTrpValPheSerLeuLeuMetSerLeuPr
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erTrpProGluProValGlyLeuTrpGlyAlaAlaPheIleThrTyrThr
                             TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA 441
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coupled receptor;
family; Lipoprote;
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Gaps: 6
Percent Identity: 24.342
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PALMITATE (POTENTIAL).
A0DDD650 CRC32;
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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7 (POTENTIAL).
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6 (POTENTIA)
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alignment_scores:
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-!- FUNCTION: C-TERMINAL ALPHA-AMIDATION OF PEPTIDES.
-!- CATALYTIC ACTIVITY: PEPTIDYIGLYCINE + ASCORBATE + 0(2) =
-!- PEPTIDYL(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)O.

(THE PRODUCT IS UNSTABLE AND DISMUTATES TO GLYOXYLATE AND
CORRESPONDING DESGLYCINE PEPTIDE AMIDE).
-!- COFACTOR: COPPER, AND ASCORBATE.
-!- SUBCELLULAR LOCATION: SECRETORY GRANULES.
-!- SUBCELLULAR INCAMINGS TO THE COPPER TYPE II, ASCORBATE-DEPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE
(EC 1.14.17.3) (PAM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use by non-profit use of the long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eutheria; Primates; Catarrhini;
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TANAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
                                                ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
                                                                                                    AGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT
                                                                                                                                                        hrAsnThrValTrpLysPheThrLeuThrGluLysLeuGluHisArgSer
                                                                                                                                                                                                           CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT
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Align seg 1/1 to:
                                                                                      US-09-323-427-5/rev x CGE1_CHICK
                                                                                                                                                                                                                   Percent Similarity:
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01-0CT-1996 (Rel. 34, Cast sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
C1/S-SPECIFIC CYCLIN E1.
CCNET OR CCNE.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclin; Cell cycle; Cell division.
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE
-i- START) TRANSITION. INTERACTS WITH A MEMBER OF THE CDC2/CDK
PROTEIN KINASES FAMILY TO FORM MPF (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN E SUBFAMILY.
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Seq_documentation_block:
ID PHY3_AVESA STANDARD;
AC P06593;
AC 01-0AN-1988 (Rel. 06, Crea
DT 01-0AN-1992 (Rel. 21, Last
DT 15-JUL-1999 (Rel. 31, Last
DT 15-JUL-1999 (Rel. 32, Last
DT 01-MAR-1992 (Rel. 32, Last
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DE PHYYOCHROME A TYPE 3 (AP3)
CR APERSHEY H.P., BARKER R.F.,
RT MADLINE; 88185837.
RA HERSHEY H.P., BARKER R.F.,
RT MALLESTINE; 88185837.
RA MEDLINE;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name:
                                                                                                                                     MENDEL; 1305; AVESa; PhyA; 1.
PROSITE; PS00245; PHYTOCHROME_1;
PROSITE; PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HERSHEY H.P., BARKER R.F., IDLER K.B., MURRAY M.G., "Nucleotide sequence and characterization of a gene phytochrome polypeptide from Avena."; Gene 61:339-348(1987).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HERSHEY H.P., BARKER R.F., IDLER K.B., LISSEMORE J.L., QUAIL P.H.; "Analysis of cloned cDNA and genomic sequences for phytochrome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHYTOCHROME A TYPE 3 (AP3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WE amino-terminal structure of oat phytochrome.";

I Lett. 234:497-499(1988).

FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR PREGION. PHOTOCONVERSION OF PR IN ABSORBS MAXIMALLY IN THE FAR PREGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION
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          PF00360; phytochrome;
PF00512; signal; 1.
PF00989; PAS; 2.
PF01590; GAF; 1.
                                                                                                                                                                                                                                                                                                                                           X03242; CAAZ6999.1; -. M18822; AAA76820.1; -.
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141	179 TTGATTTACGTCACCGTGCACCTTCTGCAACATAATGGA	214 CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAG 180 ::::::::: ::: ::: ::: :: :: :: :: :: :: :: :: ::	230 GAACTGATATCAACAC 215 ::: 916 SerArgLysalaLeuLysasnThraspLeuAsnGluGluGlnMetLysG1 932	280 TCGTTTACTCAAGAAAGATCTGCAGAACCGGAGAATATCATTGATGTAC 231	324 AAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCCAACT 281	369TGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTT 325 :: ::: ::::::	406 CCAGATCAGTATTACCATTAAAGAACCAAATAGCGAA	450 CACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATG 407 ::: :: 834 GluLysAlaProPheGlyPhePheAspArgSerGlyLysTyrIleGluCy 850	500 TGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC	550 TGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATT 501 :::: ::: ::: :::	600 GATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGG 551 ::: ::::: ::::::: 794 AspLysMetLeuLeuGlyGluValPheAspSerSerAs 806	641 AGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTT 601 : :::::: ::: 778 nAlaAlaMetThr.LysLeuThrGlyTrpAsnArgAspGluValLeu 793	691 TTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGGTATCATTTGGTC 642 771 PheGlyTrp	Align seg 1/1 to: PHY3_AVESA from: 1 to: 1128	alignment_block: US-09-323-427-5/rev x PHY3_AVESA	alignment_scores: Quality: 86.50 Ratio: 0.618 Percent Similarity: 48.951 Percent Identity: 23.776		
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Page 17

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! P79991 xenopus laevis (afri ! O94829 homo sapiens (human). 4 ! O96440 leishmania chagasi.

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Sequence

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Sp_invertebrate:Q33115 1853.50 28

sp_invertebrate:Q39177 1363.50 28

sp_invertebrate:Q39277 725.50 11

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Database sequences: 225878
Database length: 69334122
Database length: 69334122
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        sp_invertebrate:097239
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-(q-/cgn2_1/USPTO_spoo1/US0933427/runat_14042000_170514_19920/app_query.fasta.
-(2-/cgn2_1/USPTO_spoo1/US09333427/runat_14042000_170514_19920/app_query.fasta.
-DB=SPTREMBL_12 -QEMT=fastan -SUFFIX=backtrans.rspt
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=4.000 -MINMATCH=0.100 -XGAPOP=10.000
-XGAPEXT=0.000 -GAPOP=4.500 -GAPEXT=7.000 -XGAPOP=10.000
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77 | Q24328 drosophila melanogaste

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sp_human:O94829
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
CUT-1-LIKE CUTICLIN PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIMINOUNI M., BAZZICALUPO P.; "cut-1-like genes of Ascaris Gene 193:81-87(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ascaris lumbricoides (common roundworm).
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Ascaridida;
Ascaridoidea; Ascarididae; Ascaris.
               AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG
                                                           CGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTT
                                                                                                                                                                                           GTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGG
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CUT-1-LIKE CUTICLIN PROTEIN.
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               (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 09,
                                                                          PRELIMINARY;
                Last annotation
                              Last sequence update)
                                             Created)
                                                                          PRT;
                                                                          389
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               update)
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alignment_block:
US-09-323-427-5/rev x Q19707
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RA BONETELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.,
RA BONETELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAITERER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAITERER N., LATREILLE P.,
ALIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA LIGHTNING J., LLOYD C., MCHURRAY A., SAUNDERS D., SHOWIKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VALOUN M., WATERSTON R.,
RATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., VALOUN M., WATERSTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., VALOUN M., WATERSTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., VALOUN M., WATERSTON A.,
WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., VALOUN M., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., VALOUN M., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., VALOUN M., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., WATERSTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., WATERSTON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., WATERSTON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., WATERSTON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.,
THE MEN J., ZONG M., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.,
THE MEN J., ZONG M., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.,
THE MEN J., ZONG M., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.,
THE MEN J., ZONG M., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.,
THE MEN J., ZONG M., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN M.,
THE MEN J., ZONG M., WEINSTOCK L., WILKINSON SPROAT J., WOHLD
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGA 1079
                            CTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGA
                                                                                                                                                       AACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAA
                                                                                                                                                                                                                                                                                                                                                                     alPheValThrThrThrValValValSerPheHisProGlnPheValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      u \verb|ProGluValGluCysGlyProThrSerIleThrValAsnPheAsnThrA|
                                                                                                                                                                                                                                                                                                                                                                                                  TTTTTGTAACAACAACTGTTGTTCATTTCGTTTCATCCATTATTTGTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oPheAspThrCysAsnValAlaArgThrArgSerLeuAsnProLysGlyV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCC
hrGlnValValProMetProIleCysLysTyrGluIleLeuAsnGlyGly
                                                                                                                        sThrValSerThrGlnIleGluValSerAspLeuThrThrAlaPheGlnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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Seq ID AC AC DT DT DT DT DT OC OC
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                                           O18479
O18479;
O1-JAN-1998
O1-JAN-1998
O1-NOV-1998
CUTICLIN-1.
                                                                                                             documentation_block:
O18479 PRELIMINARY;
MTCUT-1.
Meloidogyne artiellia.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                               383
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                                                                                                                                                                                                                                                        TGCCGTCATTATTACC.....ATTTCGTTTAAATTTCGTCCAAATC
                                                                                                                                                                              spLys
                                                                                                                                                                                                       AGAAG 4
                                                                                                                                                                                                                                                                                  HisIleSerValValThrValPheLeuGlyLeuThrVal.....PheVa
                                                                                                                                                                                                                                                                                                                                     luAsp.....
                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTGATTTACGTCACCGTGCACTTCTG.....CAACATAATGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgSerGlnLeuPheTyrGlnCysGlnIleSerIleThrValLysGluPro
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                                                                                                                                                                                                                                                                                                            AACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTT
                                                                                                                                                                                                                                                                                                                                                                                           ArgAlaGluLeuThrThrLeuGluValLeuGluGlyAsn....LeuPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rgValLeuLysLysArgSerAlaProValMetGluAsnIleLeuAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTACTCAAGAAAAGATCTGCAGAA...CCGGAGAATATCATTGATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAAT
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                                                         8 (TrEMBLrel.
8 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                       .SerPheArgGlnGluLeuCysIleSerSerPhe
                                                           05,
05,
05,
                                                        Last sequence update)
Last annotation update)
                                                                                     Created)
                                                                                                            PRT;
     Secernentea; Diplogasteria; Tylenchida;
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alignment_block:
US-09-323-427-5/rev x 018479
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Ratio: 4.042
Percent Similarity: 77.751
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MEDLINE; 97218031.

DE GIORGI C., DE LUCA F., DI VITO M., LAMBERTI F.;

"Modulation of expression at the level of splicing of cut-1 RNA
infective second-stage juvenile of the plant parasitic nematode
Meloidogyne artiellia.";

Mol. Gen. Genet. 253:889-598(1997).

EMBL; x96677; CAA65452.1; -.
                                                                                                                                                                     150
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                                                                                                                                                                                                                                                                                                                                                                                                                                            84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetArgLysLeuLeuPheAlaIleGlyValPheValAlaLeuAsnAlaIl
                                                 GGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCCATTCC
                                                                                                                                  CGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAAT
                                                                                                                                                                CCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTG
                                                                                                                                                                                                                                                                                                   TGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGA
                                                                                                                                                                                                                                                     TTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAA 724
                                                                                                                                                                                                                                                                                                                                                                                                       GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGT 824
                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt spSerCysAsnValAlaArgThr...AspAlaGluProLysGlyValPhe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProPheGluGlyHisValTyrValLysGlyLeuPheAspGlnAlaGlyCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCT....
                                 lyThrCysAspSerGluThrIleAspThrPheCysAlaValValHisSer
                                                                                                 uGlyGlnProIleGlnPheAlaThrIleAlaGlnGlnValTyrThrSerG\\
                                                                                                                                                                                                                                                                                                                                                                       sArgSerAspGluHisGlyArgGlnValAlaGlyIleGluLeuProPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  luIleGluCysGlyProThrSerIleThrValAsnPheAsnThrArgAsn
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                                                                                                                                                    q_documentation_block:
    Q9XVM7 PRELIMINARY;
    Q9XVM7;
    Q9XVM7;
    O1-NOV-1999 (TrEMBLrel. 12, Ld
    O1-NOV-1999 (TrEMBLrel. 12, Ld
    O1-NOV-1999 (TrEMBLrel. 12, Ld
 MEDLINE; 9
BURTON J.;
"2.2 Mb of
                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae;
                                                                                                                         F53F1.1 PROTEIN. F53F1.1.
                              SEQUENCE FROM N.A. MEDLINE; 94150718.
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 nucleotide
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Last sequence update)
Last annotation update)
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 sequence
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 from
                                                                                          Rhabditia; Rhabditida;
 chromosome
                                                                               Caenorhabditis.
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alignment_block:
US-09-323-427-5/rev x Q9XVM7
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINGRE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VANDERS D., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"2.1 Mc of contiguous nucleotide sequence from chromosome III of C.
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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EMBL; Z81088; CAB03124.1;
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hrCysThrTyrGlnIleLeuSerGlyGlyProPheGlyGluProValGlu
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LeuLeuCysLeuTyrArgGluSerGlnValThrValAlaAsnAsnIleSe
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                                               TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA
                                                                                                                                             TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA
                                                                                                                                                                                          {\tt rValAspGluIleSerThrIleSerTyrAsnValAsnLeuThrMetProTect} \\
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alignment_block:
US-09-323-427-5/rev
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Ratio:
Percent Similarity:
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O9XYU9;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CUTICULIN-1 (FRAGMENT).
Wuchereria bancrofti.
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Wuchereria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAMZY R., HELMY H., ADELY M., CURTIS K., WEIL G.;
"Wuchereria bancrofti L3 cuticulin-1 cDNA partial sequence.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. RAMZY R., HELMY H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315
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                                                                                                                               yAsnGlyAspLysValGluLeuLeuAsnAlaAspGlyCysAlaLeuAspL
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                                                       ysPheLeuLeuAsnAsnLeuGluTyrProThrAspLeuMetAlaGlyGln
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206 AA;
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4.064
86.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22602 MW;
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alignment_block:
US-09-323-427-5/rev
                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID 096775 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: sp_invertebrate:096775
                                      Align seg 1/1 to: 096775 from: 1
                                                                                                    Percent Similarity:
858 GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
                                                                                                                                                                                                                                                                                                                                                                             CUTICLIN (FRAGMENT).
CUT-1.
                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                             NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                    Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ012617; CAA10074.1; -.
                                                                                                                                                                                                                                             and Brugia malayi and, as in other nematodes, the cuticle.";
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
LEWIS E.K., HUNTER S.J., TETLEY L., PAVIA NUNES C.,
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae; Brugia.
                                                                                                                                                                                                                                                                                                                                                               Brugia malayi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134
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                                                                                                                                                                                                                                                                   "cut-1-like genes are present in the filarial nematodes Brugia pahangi
                                                                                                                                                                                                                                                                                   DEVANEY
                                                                                                                                                                                 SEQUENCE
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|lePheValIleValSerValAlaThrIleValAlaIleThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGCAAAACCTGCTGCAGCTGCGCAACTTTCGTTTTACTCAAGAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..TTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGT...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTG:::::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaAlaAlaSerArgGlnAlaAlaAlaPheArgValLeuLysLysArgAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rGlnGlyIleCysMetSerIleThrGlyPheThrLeuAlaGlyMetLeuI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spIleAsnGluGluPheThrSerLeuProAsnAlaLeuArgHisArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluAlaHisValTyrLysTyrAlaAspArgSerGlnLeuPheTyrGlnCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pValArgAspGluAsnIleValAspValArgThrAspLeuAsnAlaLeuA 134
                                                                                                              Quality:
Ratio:
                                                                                                                                                                                 127
127 AA;
                                                               x 096775
                                                                                                   662.00
5.296
98.425
                                                                                                                                                                                 14119
                                                                                                                                                                                 MW;
                                                                                                    Percent
                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                 3F738071 CRC32;
                                      6
                                                                                                 Identity:
                                      127
                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                               Gaps:
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                                                                                                    96
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                                                                                                    127
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808

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17

gValGlnCysPheTyrMetGluAlaAspLysThrValSerThrGlnIleG

34

17

ValIleSerPheHisProLeuSerValThrLysValAspArgAlaTyrAr AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG

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alignment_block:
                                                                           alignment_scores:
                                                                                                                       SQ
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                               Percent Similarity:
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Q21808 PRELIMINARY;
Q21808;
Q1-NOV-1996 (TrEMBLrel. 01
01-NOV-1996 (TrEMBLrel. 01
01-JAN-1999 (TrEMBLrel. 05
                                                                                                                                                                                           MEDLINE; 94150718.

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                       Nature 368:32-38(1994).
EMBL; Z49207; CAA89068.1;
SEQUENCE 290 AA; 33215
                                                                                                                                                                      "2.2 Mb of contiguous nucleotide sequence
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R07E3.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             558
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    luThrValAspThrPheCysAlaValValHisSerCysPheValAspAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValCysArgTyrGluIleLeuAspGlyGlyProThrGlyGlnProIleGl
                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last seq
(TrEMBLrel. 09, Last ann
                            654.50
3.306
69.965
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                                                                                                                         MW.
                       Length: 283
Gaps: 8
Percent Identity: 45.230
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
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                                                                                                                       441587FE
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                                                                                                                         CRC32;
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US-09-323-427-5/rev x Q21808
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:::|||||||||||:::|||
4 SerProArgGlyLeuPheLeuSerThrAsnValValValAlapheAsnPr
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                                                                                                                                                                                                                                                                                                          ThralailealaalaHisileGluTyrGlu.AspSerGluIleileSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTAAAGAACCAAATAGCGAA...TGTGTTCGACCACAATGTTCAGAAC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            snAlaPheLeuPheIleIleSerLeuValSerIleValHisValCys
                                                                                                                GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 185
                                                                                                                                                                                                                                {\tt spTyrIleIleProAsnAspAspIleIleSerLeuAsnTrpLeuGlnArg}
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                                                                                                                                                    AsnPhe.....AspMetArgIleSer....
                                                                                                                                                                                          AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT
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                                                                          ....GluLeuCysMetThrAlaIleGlyThrThrLeuLeuValPheLeuA 259
                                                                                                                                                                                                                                                                    roProArgArgArgSerAsnThrLeuProAlaProAspAspAsnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rValLysGluProGlyLeuAspTyrCysAspValProSerCysProAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lys \texttt{TyrAlaAspArgAspAsnMetTyrPheAspCysGlnIleSerIleTh}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lLeuAspGlySerProThrGlyProProValTyrPheAlaThrValGlyG
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                                                                                                                                                                                                                                                                                                                                                 .....CAAGGATTCGGAGCTGTTAAAAC
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                                    ... ACCGTGCACTTCTGC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
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seq_name:

sp_invertebrate:Q21540

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alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: Q21540
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-323-427-5/rev x Q21540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q21540 PRELIMINARY;
Q21540;
Q1-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1999 (TrEMBLrel. 1
M142.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
Q21540 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    1033 TACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATC
                                                                                                                                                                                                                                                                                                                                                                   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOMNEEN R., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SOUNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "2.2 Mb of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
EMBL; Z73428; CAA97806.1; -.
PFAM; PF00092; vwa; 1.
PRINTS; PR00453; VWFADOMAIN.
 795
                                310
                                                                                                                                                            278
                                                                                                                                                                                           945
                                                                                                                                                                                                                           261
                                                                                                                                                                                                                                        244 rThrLysGlnProPheGluGlyAsnValPheValMetAspHisTyrHisA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MCMURRAY A.;
                                                                                                                                                                                                                                                                                                                                                    GlyThrProGluIleIleCysGlyProAspArgIleGlyValLysAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity:
                                                ATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTT
                                                                                           rLeuAsnProLysGlyIlePheValGluValSerIleValPheMetPheH
                                                                                                                                                         GCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATC
                                                                                                                                                                                                                       spGluGluCysArgAlaGlyProGluLysPheProAspSerArgSerIle
TACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAAT
                            isSerLeuPheMetThrLysThrAspGlnThrValLysValGlnCysPhe
                                                                                                                            TCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTC
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Percent Identity:
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seq_documentation_block:
ID Q19053 PRELIMINARY;
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MEDLINE; 9415
WILSON R., AI
BONFIELD J.,
                                                                                        MCMURRAY
                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
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                                             SEQUENCE
                                                                           Submitted (OCT-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTTGCTAAATTAGTTTGGAATATCCAACAGATTTA...ATGGCTGGCCA
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| ValLeuLeuSerThrProAspTyrAspThrSerLeuArgLeuAlaThrLy
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                             94150718.
                                                                                       FROM N.A.
 AINSCOUGH
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J.
                R.,
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09,
CONNELL M., COPSEY
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BAYNES C. OPSEY T.,
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             c.,
                                                                           databases
 COOPER J., COULSON A.,
                BERKS
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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN SMALDON N., SMITH A., SOUNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; "2.2 MD of Contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
EMBL; Z66496; CAA91280.1;
SEQUENCE 484 AA; 53325
  194
                                         536 TTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG
                                                                                                                                                                                                                                                                                                                                                             128
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                                                                                                                                                                            TyrHisLysTrpThrCysValAlaGluLeuGluAsnValTyrCysMetLy
alIleAspAlaAsnGlyCysSerValAspGlyValIleLeuGlnAsnLeu
                                                                                      sValHisSerCysThrValTyrAspGlyGlnGlyGlyProProValThrV
                                                                                                                             TGTCCATTCCTGCTTTGTCGATGATGGT...AACGGTGATACTGTGGAAA
                                                                                                                                                                                                   TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGT
                                                                                                                                                                                                                                                                    luAla...GlyGlySerProIleLysTyrAlaArgIleGlyAspGlnVal
                                                                                                                                                                                                                                                                                                                GTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT
                                                                                                                                                                                                                                                                                                                                                                               TCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATG 684
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sThrargAsnSerPheAsnGlyLysValPheValLysGlyTyrValSerG
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                                                                                                                                                                                                                                                                                                                                                          uLeuGluSerGluThrGlnLeuProValCysArgTyrGluIleLeuAsnG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrLysLysValHisAsnHisValAspIleSerAlaLeuThrThrGlnLe
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Percent Identity: 45.020
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Seq_documentation_block:
ID 093532;
AC 093532;
AC 093532;
AC 093532;
AC 093532;
AC 093532;
AC 093532;
AC 093532;
AC 093532;
AC 093532;
AC 01-FEB-1997 (TrEMBLrel. 02
DT 01-JAN-1999 (TrEMBLrel. 02
DT 01-JAN-1999 (TrEMBLrel. 02
DT 01-JAN-1999 (TrEMBLrel. 02
DE F20D1.8 PROTEIN.

GN F20D1.8 PROTEIN.

OC Eukaryota; Metazoa; Nematoo
OC Rhabditina; Rhabditoidea;
RN [1]
RP SEQUENCE FROM N.A.
BURTON J.;
RN LSUBMITTED J.;
RN LSUBMITTED J.;
RN MEDLINE; 94150718.
RA WILSON R. AINSCOUGH R., AI
BONFIELD J., BURTON J., CO.
RA GRATON M., DEAR S., DU Z.
RA GRANDER A., GREEN P., HAW.
RA GRANDER M., KERSHAW J., KIRS'
RA GRANDER M., ESSHAW J., KIRS'
RA LIGHTMING J., LLOYD C., MCI
RA PARSONS J., PERCY C., RIFK,
RA PARSONS J., PERCY C., RIFK,
RA PARSONS J., PERCY C., RIFK,
RA PARSONS J., PERCY C., RIFK,
RA PARSONS J., PERCY C., RIFK,
RA PARSONS J., PERCY C., RIFK,
RA PARSONS J., PERCY C., RIFK,
RA PARSONS J., SMITH A., SONN,
RA THIERRY-MIEG J., THOMAS K.,
RA WATSON A., WEINSTOCK L., W.
RT "2.2 Mb of contiguous nucl.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL; Z78542; CAB01742.1;
SQ SEQUENCE 315 AA; 35785 J
                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-323-427-5/rev x Q93532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
    Quality:
    Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                              1152 CGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCC 1103
                          1052 CAATAACAATCTAATTTAATACACGTAATGCATTCGAAGGACATGTTTAT 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRY A., MCTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WEINSTOCK L., WILKINSON-SPROAT J., WOLLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
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EMBL; 278542; CAB01742.1;
SEQUENCE 315 AA; 35785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                41 nIleAspAsnGlyLeuGlnGlyGluProLeuIleArgCysGlySerGluS
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seq_documentation_block:
ID 022164
AC 022164;
DT 01-NOV-1996 (TrEMBLre
DT 01-NOV-1996 (TrEMBLre
DT 01-JAN-1999 (TrEMBLre
DE 104F8.4 PROTEIN.
GN 1704F8.4 PROTEIN.
GN Caenorhabditis elegar
OC Eukaryota; Metazoa; N
OC Rhabditina; Rhabditoi
RN [1]
RP SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     seq_name: sp_invertebrate:Q22164
                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rha
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                                                                                                                                                       (TremBLrel. 01, Created)
(TremBLrel. 01, Last seq
(TremBLrel. 09, Last ann
                                                                                                                                                                                                                                              PRELIMINARY;
                                              oda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
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Last annotation update)
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alignment_block:
US-09-323-427-5/rev x Q22164
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RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA WILSON R., BINGCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA GRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATENSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATENSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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EMBL; 266565; CAA91480.1; -.
SEQUENCE 384 AA; 43964 MW;
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| lalleAspValSerAsnLeuProThrGluSerValGlnSerAspLeuPro
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AGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG
                                            MetProThrCysSerTyrThrIleArgArgAspGlnLeuAspGlyProIl 176
                                                                                                                                                                                        AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG
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                                                                                                                                                                                                                                       aTyrHisIleArgCysMetTyrLysGluAlaAlaArgThrValThrAlaA
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Gaps: 9
Percent Identity: 31.218
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AC DT DT DT DT DE GN GN GN RN RN RR RR RR RR RR RR
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SEQUENCE FROM N.A. MEDLINE; 94150718. WHITE S.; "2.2 Mb.of contiguo
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O9XVN2;

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 12,
                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
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                                                                                               Rhabdītina; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                            alValValTyrHisArgTyrCysLysAsnGlu
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| etAlaTyrArgGluSerPheValPheLysPheAlaAspArgIleAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                               TTACCATTTCGTTTAAATTTCGTCCAAATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...LeuAspProGlnThrIleCysLeuAlaProLysLeuLeuValValAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luIleArgGlu.....
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                                                                                             Nematoda; Secernentea; Rhabditia; Rhabditida;
bidea; Rhabditidae; Peloderinae; Caenorhabditi
   nucleotide
                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                     PRT;
   sequence
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 from
   chromosome
                                                                                               Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1134 ACTACACTTATTGCATTGTCTTATTCG....ATTCCGGTTGACAATGG 1091
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BONFIELD J., BURTON J., CONNELL M., COPSEY J., COUPSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LOVD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., WATERSTON R.,
WATENSTON R., WATENSTON R.,
WATENSTON R., WALLNINGON SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
EMBL; 281086; CABO3116.1;
SEQUENCE 610 AA; 68585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 94150718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 yValValGlyLysProGluValPheCysGlyIleAspThrIleArgValL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HisProPhePheValThrGlyMetAspArgAlaPheSerIleArgCysPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hrLeuHisProArgGlyIleSerPheSerPheThrMetIleThrSerPhe
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                                                                                                                                                                                                 GAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e {\tt PheLeuGluSerIleLysGlyLeuAsnAlaGluIleAspValGlyThrL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTT
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TGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATA
                                                                                           HisLeuLysAsp...GlyTleGluGlyHisValLeuArgPheAlaGlnVa
                                                                                                                                                                                                                                                                                       eu \verb|AlaProGlnHisValAspGlnGluTyrSerLeuProValCysAlaTyr|
                                                                                                                                                                                                                                                                                                                                                                                            TCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAA
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Identity: 37.407
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Gaps:

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                                                                                                                                                                                                                                                                                                                                                                                                                       WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET J., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORRIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q93967 PRELIMINARY;
Q93967; Q94405;
01-FEB-1997 (TrEMBLrel. 02,
01-NOV-1998 (TrEMBLrel. 08,
01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                              Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. EMBL; Z81143; CAB03520.1; -. EMBL; Z75713; CAB03520.1; JOINED. EMBL; Z75713; CAB00057.1; -. EMBL; Z81143; CAB00057.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  elegans.
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                       LENNARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oGlnCysSer 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTATTACCATTAAAGAACCAAATAGCGAATGT......GTTCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isValPheLysTyrAlaAspLysValGlnLeuTyrPheThrCysThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uProGlnIleGluTyrGluHisGlyAlaIleSerAlaTyrThrAsnAlaH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATAATTTGGAATATCCAACAGAT...TTAATGGCTGGCCAAGAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATC
                                                                                                                                                                                                                                                                                                                                                                                        Mb of contiguous nucleotide sequence from chromosome III of
ans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_invertebrate:Q93967
Quality:
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                                                                                                          440 AA;
  477.50
                                                                                                             49299
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                          3F2BBBA2 CRC32;
Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400
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US-09-323-427-5/rev x Q93967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1005 TATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGAT 1106
CATTAAAGAACCAAATAGCGAATGT.....GTTCGACCACAATGT.
                                               LysPheAlaAspLysProGlyValTrpPhePheCysGlnValGlnMetCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgValLeuHisGlnTrpHisCysAsnAspGln.....MetTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pAlaGlyArgProAlaGlyAsnValIleGlnPheAlaArgValGlyGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTGGA...CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleProGlyCysThrTyrSerIleHisArgSerThrIleAspGluLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yAsnGlnLysThrArgLysProHisPheAspLeuGlnPheGlyAlaCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAA
                                                                                                     AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC
                                                                                                                                                       leArgTyrSerSerAspLeuGlnArgAlaTyrAlaGluSerSerValPhe
                                                                                                                                                                                                            TGGAATATCCAACAGATTTAATG...GCTGGCCAAGAAGCTCACGTATAC
                                                                                                                                                                                                                                                                  pValIleAspAspLysGlyCysProIleAspProIleLeuIleThrGlyI
                                                                                                                                                                                                                                                                                                                       AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATT
                                                                                                                                                                                                                                                                                                                                                                          ValLeuIleAsnAsnCysTyrValThrAspGlyPheGlyLysLysAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCCAGTATGCCGTTATGAAATT.....TTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               luLeuGlyValSerMetIleProThrThrGluLeuGluAlaArgHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrValValValSerPheHisProLeuPheIleThrLysValAspGlnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lyMetLysSerLeuArgSerValAspProArgGlyMetTyrTyrGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTCAAGTTGCC......GGAATTTCACTTCCATTTGATTCATGCA 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spGluIleArgIleTrpValLysThrArgLysIlePheAlaGlyArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eSerIleAspAsnGluIleIleGlyGluProAspIleGluCysLeuGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q93967 from: 1
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65.000
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489

217

392 250 539

200 589 187

170

153

715 137 765 120 815 103 865 70

956 53 1006

87

37

267

swetLysLys...HisGlyMetCysAspGlyIleThrProProSerCysG

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alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                             alignment_block:
US-09-323-427-5/rev x Q23097
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                                                                                                                                                                                                                                        Align seg 1/1 to: Q23097 from: 1
                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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Q23097 PRELIMINARY;
                                                                                                1077 CCAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACG 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                     WATSON A., WEINSTOCK L., WILKINSON-SPRUAT J., MURLUTAN, A., WEINSTOCK L., WILKINSON-SPRUAT J., MURLUTAN, A., 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
Rature 368:32-38(1994).
EMBL; 271267; CAA95850.1; -.
EMBL; 271267; CAA95850.1; -.
SEQUENCE 387 AA; 43212 MW; D127FF23 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Phahditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313
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                                       977 GTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCA 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILKINSON J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W01A8.3 PROTEIN. W01A8.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                64
  81
                                                                                                                                                            48
                                                                            rLysProPheArgGlyAsnIlePheValLysGlyArgAlaLysAspLysS
erCysArgGlnSerTyrAlaAsnAsnGlyThrAsnSerTyrSerLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGluGluLysAlaProSerSerArgArg.....LysThrTh
                                                                                                                                                          ProLysValIleCysAlaGluAsnAspLeuAlaLeuAspIleValThrSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCC
                                                                                                                                                                                                                                                                                                                                         476.00
2.235
59.167
                                                                                                                                                                                                                                                                                                                                         Percent Identity: 31.389
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                          to: 387
                                                                                                                                                                                                                                                                                                                                                                              Length:
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                                                                                                                   978
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  97
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	AlaProSarProPheCvsValProArgIesIesIesIProValIesPro	
œ	A JOHNA OO WALLELOUDE ALLELOLA WOLLOLLELOUDO LELA OO WOLLOLUDA OO WALLELOUDO	
335	ATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA	334
w	:: ::: euLeuValLeuAspProAlaAspArgGlyLe	
158	TAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACT	207
N		0 1
0 0	OCAGAGATATGATGATGTAGGAAGTGATATGAAGGAGGGGAGAGTATGTAGAAGGAGG	257
258	GCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT : : : : : Armon aa	307
303	uSerGluAlaSerGlyAspGly	295
308	GAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGC	351
294	::: ::: ::: CysGlnGluValThrProProAsnCysGlyValLysLy	278
352	AAATAGCGAATGTGTTCGACCACAATGT	383
384 278	GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG :: ::::: aspSerAsnGlnLeuTyrPheThrCysGlnIleArgLeuCysGlnLysG	261
6	spAlaSerLeuMetArgAlaHisAlaSerSerGlnValPheLys	4
	CAGATTTAATGGCTGGCCAAG	480
244	spPheAspGlyCysAlaThrAspProPheLeuLeuSerGluLeuSerTyr	228
481	GCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAAT	530
531 228	TG -	580 211
211	TGAAACC	198
9	yProAsnGlyProThrLeuThrTyrAlaAsnValGlyAspIleValF	വ
631	CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT:: :::	680
181	<pre>::: ::: :::::: SerMetValMetProLysCysGluTyrSerValArgArgAs</pre>	164
681	TCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGC	730
6	:: ::: :: ::: ::: LuIleValThrGlnAsnIleAspValSerMetIleProThrThrGluL	4
731	AACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTC	780
781 147	CCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGAT	830 131
w	nPheMetValThrValIleValSerPheHisProAl	-
831	TTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGT	877
878 114	TTTGATTCAATGCAATGTTGCGCGTACAGGATCTCTGAATCCACGTGGTAT :::	927 98

352

57

TTGATTGCTGCCGTCATTATTACCATTTCG

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SOOR REPARA
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us-09-323-427-5/rev x Q22680
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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Q22680 PRELIMINARY;
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                                                                                                                                                      1009 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG
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MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A. BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A. BONFIELD J., BURTON L., CONSTITUTION L., CONSTITUTION L., CONSTITUTION L., CONSTITUTION L., JOHNSTON L., JOHNSTON L., JOHNSTON L., JOHNSTON L., JOHNSTON L., JOHNSTON L., JOHNSTON L., JOHNSTON L., LIGHTNING J., CLUYD C., MIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I. SANALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I. SHOWNKEEN I. THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; "2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                  1059 CCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 1010
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Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                          959 GTGGACGT.....CAAGTTGCCGGAATTTCACTTCCATTT...GAT 922
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T22C8.7.
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                                                                                                               SValTyrValArgGlyPhePheProGlnThrValCysHisLeuAsnTyrC
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                                   ysThrArgLeuThrAsnArgProIleValMetAspLeuProPheArgGly
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Gaps: 11
Percent Identity: 37.282
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Peloderinae; Caenorhabditi
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285 ProlleLys
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                                         GCTGTTAAA 322
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                                                                                    snGlyCysGluGlyIleSerProProIleCysArgProMetAspLeuGly
                                                                                                                             ATAGC...GAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGA
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Title:
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Copyright (c) 1993 - 2000 Compugen Ltd
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45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_p13:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 45	C 44	C 43	c 42	41	c 40	w	38	37	. 36	ω	w	c 33	. 32	31	30	29	28	27	c 26	25	N	c 23	N	21	20	19	c 18	_	ш	c 15		<u> </u>	12	01.0		-	c 7				က (ယ (_	Result	
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ALIGNMENTS

KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	CEF22B5
HTG; Cuticulin; Elongation factor; GTP-binding ADP-ribosylation	Z50044.1 GI:899234	250044	Caenorhabditis elegans cosmid F22B5, complete sequence.	CEF22B5 25823 bp DNA	
r; G			2В5,		
TP-binding ADP-ribosylation			complete sequence.	INV 02-SEP-1999	

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MEDLINE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopta,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.,
Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
The true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bin/display?db=wormace&class=Sequence &object=F22B5
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small content of the specific or the specific or the specific or the specific content or the specific close once, or longer because we arrange for a small content or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the specific or the speci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The true left end of clone M05D6 is at 25723 in this sequence. The true right end of clone F14E5 is at 4610 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor; Phenylalanyl-tRNA synthetase; RNA binding Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighbouring submissions.
The true left end of clone F22B5 is at 24607 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F22B5.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence Z66523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabdītina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2 Mb of contiguous nucleotide sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z66523
                                                                                                                                                                                                                             comes from this
                                                                                                                                                                                                                                                                                                           /gene="F22B5.2"
join(411. .462,584. .663,745. .1127,1216. .1471)
/gene="F22B5.2"
                                    /protein_id="CAA90354.1"
/db_xref="GI:3876226"
                                                                                                                                                                                                               /note="similar to RNA binding protein; cDNA EST yk390d8, comes from this gene; cDNA EST yk499d6.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Caenorhabditis
/db_xref="SWISS-PROT:Q19706"
                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="F22B5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
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for a small
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VVTQFKVINKRVFKVADRKKWVKFGSCKGEPAGPQXATTYVAAEEVDMQFTRNRAGEQ
ILDVQEDKQTAKTTSREHCRHCKGNDHWSTHCPYKVMYCLDEEADADKDFDFKDBXNAM
MRPDGRQIDRNRSDENTCRVTNLPQEMNEDELRDLFGKIGRVIRIFIARDKVTGLPKG
                                                                                       complement(2833. .4393)
                                                                                                                               HSIKSHHWKIFSCCALSGDRLVQAMTWLCDDVGSRLFILD"
                                                                                                                                                          SEELKKLLGEERLAGASLLVLANKSDLPGAIDVNSIAQVIQMSSVYTSEKKCFLVLDL
                                                                                                                                                                                              EPTLGFDIKTVHFKDFQLNLWDVGGQKSLRSYWKNYFESTDALIWVVDSSDRERLLQC
                                                                                                                                                                                                                                                                                         /protein_id="CAA90353.1"
/db_xref="GI:3876225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F22B5.1"
join(1870. .2158,2209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAFVTFESRDDAARAIAELNDIRMYHMVLKVEWTRPSN"
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                                                                                                                                                                                                                         /db_xref="SWISS-PROT:Q19705"
/translation="MGFLKILRKQRAREREMRILILGLDNAGKTTLMKKFLDEPTDTI
                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                       note="similar to GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2387,2534.
                                                                                                                                                                                                                                                                                                                                                                                       ADP-ribosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2668)
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/db_xref="Sptrembl:Q19707"
/translation="MARYSLGLGLCLLVASVSAIPVDNNVEGEPEVECGPTSITVNEN
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TRNAFEGHVYVKGLFDOGECRNDEGGROVGGROVGCTSULTTAFOTCVVPMPICKYEILN
GGPTGEPVGFAYIGOGYYHKWTCDSETVDTFCAVVHSCTVDDGNGDTVQILDENGCAL
DKFLLNNLEYFDLMAGGAHYYKADRSQLEYYGOGYSITVKEENEEGARPTCSEPG
EGAVKQANQTAQFFRVLKKRSAPVMENILDVRAELTTLEVLEGNLPSSLTQAQALVAS note-"similar to cuticulin: CDNA EST EMBL:T01970 comes from this gene; CDNA EST CEESX90RB Comes from this gene; cDNA EST EMBL:T00412 comes from this gene; CDNA EST WA386c7.3 comes from this gene; CDNA EST YK386c7.3 comes from this gene; CDNA EST YK386c7.5 comes from this gene; CDNA EST YK504b12.3 comes from this gene; CDNA EST YK543g2.3 comes from this gene; CDNA EST YK543g2.3 comes from this gene; CDNA EST YK543g2.3 comes from this gene; CDNA EST YK652b8.3 comes from this gene; /protein_id="CAA90355.1" /db_xref="GI:3876227" /codon_start=1 s from this gene; cDNA EST

REIGEDSFRQELCISSFHISVVTVFLGLTVFVAIFITYMIVSRMMVPSDKMQSAC" /gene="F22B5.4"

join(9691. 9890,9940. .10234) /gene="F22B5.4" /note="cDNA EST yk304c8.3 comes yk304c8.5 comes from this gene; from this gene" from cDNA

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KaeiwldrsnskapwdwerlrdtywkmptvafdldgrtrkrcelmeQlQdemleaakk /protein_id="CAA90356.1" /db_xref="GI:3876228" /codon_start=1 this gene; cDNA EST EST yk594h3.3 comes

complement(10849. .12154) /gene="F22B5

complement(join(10849. .10984,11033. .11343,11397.
11578. .11832,11917. .12154))
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hes 633;
                                tgaacattgtggtcgaacacattcgctatttggttctttaatggttaatactgatctggca
                                                                                                                                                                                                                 CTGAGCAGTTTGGTTAGCTTGC-----TTAACTGCTCCAAATCCTTGTGGCTC
                                                                                                                                                                                                                                          agctgcagcaggttttgctgcggcaccacctgttttaacagctccgaatccttgtggttc
                                                                                                                                                                                                                                                                                                                  ACGGACATCAAGAATATTCTCCATTACTGGAGCGGATCTCTTCTTCAAAACTCTGAAGAA
                                                                                                                                                                                                                                                                                                                                             tcgtacatcaatgatattctccggttctgcagatcttttcttgagtaaacgaagttgcgc 288
                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAACACCATTTTGACAACTTACATTTCCTTCCAAAACTTCCAAAGTTGTGAGCTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      acgtaaatcaactggcaaagcttgattatcatcgctaatttcaagggtgttgatatcagt 228
        TTGATAGAAAAGTTGAGAACGATCAGCGTATTTGTAGACGTGAGCCTCTTGTCCAGCCAT
                                                                                                           AGAGCACGTTGGGCGAGCACACTCCTCATTTGGTTCCTTAACAGTAATGGAAATCTGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSNWDYLDEVDIIPKLPPNFDELRESKKWQERKEALEALLKVLT
/NERLSTKASTRELIGHLQWVLAKDANIOCQALAAKCIGKFATGLAKTSSFAGFLLP
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ROLDLVVPAKQPKGFIKAVVPVFGKLTGDADQDVREASLQGLGAVQRIIGDKNVKNLL
GDASSDEGKMKXIGETXEKSTASFAEEGAKNAPVABFTSSTPSASAASGDPSGGTATA
VVSGGAPVAEADPWDELDAFDVLSKWDDGFDTWIESKKWQERKEALEGLULTTANPS
LDPKANYGALVERLOKVLEKDANINVAALAANCITGIANGLRTKFQPFAVSVTPIIFE
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complement(join(12240.
13262. .13392,13465. ...
/gene="F22B5.6"
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join(15384. .15575,15622. .16479,16527. .17105,18608. .18694,
18794. .18946,18996. .19449,19497. .19843,20042. .20554,
20672. .21000,21677. .21812)
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LAQYHIIHESSNISWMLNSSRGKIVNENATWTHFGLTCVTTAFLCILTSLIIVDIL
FKTHETTFYVYVFMNIAVVACGLFVTGYLLGHLYVLIWFAKNSTIYSCROLGIGYTLITS
NSTGEEVRKLESAGCETAISSEFKNVFFDLLIQAVFIPLHILLTAFSWTFSGLYRPRW
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/db_xref="GI:3876232"
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/db_xref="GI:3876230"
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Pred. No. 4.1e-70;
0; Mismatches 233;
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Wilkinson-Sproat, J. and Wohldman, P.
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Caenorhabditis
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Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Culton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Yaughan, K., Waterston, R., Watson, A., Weinstock, L.,
                                                                                                                                                                                                                                                                                                          HTG; Cuticulin; Fork he Caenorhabditis elegans Caenorhabditis elegans
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Rhabditina; Rhabditoidea; Rhabditidae;
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IMPORTANT: This sequence is not the entire insert of clone C47G2. It may be shorter because we arrange for a small overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2 Mb o
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (27-APR-1995) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The true left end of clone T24F1 is at 34731 in this sequence. The true right end of clone T05B9 is at 12750 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neighbouring submissions.
The true left end of clone C47G2 is at 1 in this sequence. The true right end of clone C47G2 is at 6388 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368 (6466), 32-38 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence Z49912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 34831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end of this sequence (34731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mb of contiguous nucleotide sequence from chromosome III of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               graphical representation of this sequence and its analysis
15433. .17108
/gene="C47G2.2"
join(15433. .157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to cuticulin; cDNA EST EMBL:C10444 comes from this gene; cDNA EST eMBL:C12078 comes from this gene; cDNA EST yk262c12.3 comes from this gene; cDNA EST yk262c12.5 comes from this gene; cDNA EST yk265h3.5 comes from this gene; cDNA EST yk278g8.3 comes from this gene; cDNA EST yk278g8.3 comes from this gene; cDNA EST yk278g8.5 comes from this gene; cDNA EST yk278g8.3 comes from this gene; cDNA EST yk439e8.3 comes from this gene; cDNA EST yk439e8.5 comes from this gene; cDNA EST yk439e8.5 comes from this gene; cDNA EST yk439e8.5 comes from this gene; cDNA EST yk439e8.5 comes from this gene; cDNA EST yk583c11.3 comes from this gene; cDNA EST yk380a11.5 comes from this gene; cDNA EST yk380a11.5 comes from this gene; cDNA EST yk380a11.5 comes from this gene;
                                                                                                                                                                                                                                                          RNPFEGHVYVKGLYDQAGCRSDEGGRQVAGIELPFDSCNTARTRSLNPKGVFVSTTVV
ISFHPQFVTKVDRAYRIQCFYMESDKTVSTQIEVSDLTTAFQTQVVPMPVCKYEILDG
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                                                                                                                                                  GAVKQAGAGGAHAAAAPQAGVEEVQAAPVAAAAPVAAPVAAAAAAAPAVPRATLAQLRL
LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGICLTP
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join(2562. .2679,2992. .3217,3898. .4636,4687. .4878)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z49912
                                                                                                                                                                                                                           KFLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKDPGSECARPTCSEPQGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                           IGFASFLGIGTIVATALSATIFYVARPTSHKH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:6239"
/chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
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   .15770,16205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .34831) overlaps with the start of
   .16531,16772.
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gene CDS

ENSLMRLLKTDNFTLEDVLLNEFVVQESRYGKAELVQYITSRENMKALLELSLNPKIN TDLPMKQQYRLSFIASEILTIRGTDVFQKQIVTTEETRKCLVDFLNDKTPLNHLVAGF

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RVVYWSAQLLTWLILPLLQSYVTAGNFTILGK.RAAVINNALYXAIYSLCFLAILIYA
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DIEKLASEKSEAEENVKDIYKKVRVLFNSMKNDSNGQRRKVETILSKESDDVIDUFF
SRQVIDNAHLDESGPCSSAKLISLKKTIYAVGTLNATAQMKVLVDRALFLENLAFS
ESNGYKNLELSRNTCVPJGVRRFWYTRLOTFFCRILGIYTVPKMFFVLESCCTFFVVSY
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KGINTYLPICTILLCALHYYRGGAYULHNIGFDQFVEAEDMITNGGRSLVGIERN
RGINTYLPICTILLCALHYRRGAYULHNIGFDQFVEAEDMITNGGRSLVGIERN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(24417. .24975,25043. .25176,25237. .2552
25668. .25907,25967. .26054,26106. .26227,26277. .26608,
26681. .26785,26846. .26914))
/gene="C47G2.4"
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FEYYKEKPPAWONSIRHNLSLMDCFYKYAGFOONDGKGKYWALDDNCEDMEDNGSFLR
REKRYKKNSDTYHEMMSHHPWPEPPETLPOGMPEPPRMMHPMANIRMLFRACPH
MPAFFIPQNIDSQKILSMMASRIMPMDAPVSSGQKRTSSSSSPNENGSSAVSDKLSA"
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/gene="C47G2.
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                                                                                                                                                                                                                                                                                                                                                            codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                     from this gene; cDNA EST yk486d7.5 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oin(30076. .30134,30184. .30492,31050. .31274,31321. .31480,
11534. .31653,31701. .31835,31889. .32104,32160. .32570,
2639. .32935,32998. .33215,33263. .33651,33802. .34049)
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                                                                                                                                                                                                                                                                                                                                                                                                                            from this gene'
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CDS

BASE CO

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LOCUS
DEFINITION
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AUTHORS
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SOURCE
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Best Local
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C.elegans
M55997
                        Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 2310)
Sebastano, M., Lassan
                                                                                 cuticle protein; cuticlin C.elegans DNA.
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MOETLIAKIADNLIVEEGGPAEELYKKSALISASAKILEAFIKIWFYSNAPAQOLEEI
ERNLIEERHYSYGLMRECOMDUDYEHSYGDDERIVEGILANBLUNILOYLADIEAN
GSVWQPLLRLIIELCNTNCMSTHEKIAVAFRSLPFINLIKAAKMLPRASVLHCLLVKV
VILLLHSSFPCDELSPAAEYLLTEGGLIONIVDTATSENPGSSYACSGLRSFNONLGD
AINRAKKAGIEPHQKLLAILSADNTWTELEDIILLYNLKHRQMQHDFNDSSVVSSIRN
DSHGFNDSEEWTDASTKFAEMDATSSAKOAFSGTSSPEDNMQRFSDFSGGFDDTDE
BEFRKLGSERMSSSCAGISFTSPIKMPGEAEKTSEKASEPPSVVASTYPQOTNGNO
AFLEQEEGDGEWVWPTVPPLGETEVVTQTGHRPENMVDETAPDFSHLDMAPPKEDDM
WADDFSSFPTISFTAANASSSSSDAWFGSDIHLQGEASDWPLNNSHESKASDPVMVG
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nes 393; Conserv
                              catcagcatttagaatttccacagtatcaccgttaccatcatcgacaaagcaggaatgga
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ggcatactggcatcgggacaatttgagtttgaaaagcagttgtgatttcagatacctcaa
                                                                                            CGACGGCGCAGAAGGTGTCAGTGGTCTCAGAATCGCAAGTCCATTTGTGATAGACTTGTT
                                                                                                       caaccgcgcagaaagtatcaacggtttcagaatcgcatgtccatttatgataaactggct 641
                                                                                                                                                       CTTCTTCGTTAAGAATCTGAACGGTGTCGCCATTACCATCGTCAGTGCAAGAGTGAA
                                                                                                                                                                                                                                                                             TTTGGCATTGATAGAAGAGTTGGGAGCGATCGGCATATTTGTAGACGTGAGCTTCTTGGC
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/protein_id="AAAZ795.1"
/protein_id="AAAZ795.1"
/protein_id="AAAZ795.1"
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GGPSGQPIQFAIIGQQYYKKYPCDSETTDTFCAVVHSCTVDDGMDTYQLINLEGCAL
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FGAVKQAGAGGAHAAAAQAGVEEVQAAFVGAAFVAAAAAAAPAVPRATLAQLRL
LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGISSTP
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567 c 433 g
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join(1186. .1920,1971.
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join(1186. .1920,1971.
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/strain="N2"
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                                                                                 agctccgaatccttgtggttctgaacattgtggtcgaacacattcgctattttggttcttt
                             CAATACTCTAAATGCAGCAGCTTGTCGTGATGCAGCTGCAACCACTTGCGCGTTTTAAT
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                                                                                                                                           TAACAATGATGATCGATGACGTAGCGCATTTGGTAATGAGGTAAACTCTTCATTTATATC
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Ramzy,R., Helmy,H., Adely,M.,
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                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAD28743.1"
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1112 c 128 g 236 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Wuchereria bancrofti"
/db_xref="taxon:6293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="cuticulin-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="L3 larvae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to Ascaris lumbricoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    country="Egypt:
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Ascaris l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Timinouni,M. and Bazzicalupo,P. cut-1-like genes of Ascaris lum Gene 193 (1), B1-87 (1997) 97390131
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-OCT-1996) GA3, I.I NA 80125, Italy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nemato
Ascaridoidea; Ascarididae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ascut-1) gene, complete cds U73005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Timinouni, M. and Bazzicalupo, P.
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lumbricoides
          /product="CUT-1-like cuticlin protein precursor"
/protein_id="AAB66646.1"
/protein_id="AAB66446.1"
/db_xref="GI:1657625"
/translation="MCRAVSFLALFGLAAAIPVDNGVEGEPEIECGPTSITVNFNTRN
PEGHAYVKGLYDQEGCRSDEGGRQVAGISLPFDSCRVVARTRSLNPRGIFVTTTVVIS
FHPLFITKVDRAYRVQCFYMEADKTVSTQIEVEEITTAFQTIVPMFVCRYEILDGGP
TGQPTQFATICQQVYHKWTCDSETVDTFCAVVHSCFVDDGSGDTIQILNEEGCALDKY
LLNNLEYPTDLMAGGEAHVYKXADRSQLFYQCQITITIKEPNSECPRTTCSEPQGFGA
                                                                                                                             /note="cuticlin gene; ASCUT-1; proteins of other nematodes" /codon_start=1
VRPGGSIAPKKQRRCQLRLIKKSGGDYDNTLDVRTDFSALDISDRDEALPMDLRHRAF
                                                                                                                                                                                      join(882.
                                                                                                                                                                                                  /gene="ascut-1"
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/note="site of transplicing by
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/product="CUT-1-like
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X96677
Biologia Molecolare, Via Orabona 4, 70126, Bari, ITALY 2 (bases 1 to 2584)
De Glorgi,C., De Luca,F., Di Vito,M. and Lamberti,F.
Modulation of expression at the level of splicing of cut-1 RNA
                                        Submitted (15-MAR-1996) C. De Giorgi, Dipartimento di Biochimica Biologia Molecolare, Via Orabona 4, 70126, Bari, ITALY
                                                                                                                         Eukaryota; Metazoa; Nematoda; Secernentea; Diplogasteria; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae;
                                                                                                                                                    Meloidogyne artiellia.
Meloidogyne artiellia
                                                                                  1 (bases 1 to 2584)
De Giorgi,C.
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5064. .5070
/gene="ascut-1"
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join(930. .954,2851. .3239,3583. .4083,4499. .4690)
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No. 7.7e-49;
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Matches 581; Conserv
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CTTCGTTCAAAATTTGCACGGTGTCCCCATTGCCATCATCCACCACACAGCTGTGCACAA
                   cagcatttagaatttccacagtatcaccgttaccatcatcgacaaagcaggaatggacaa
                                                                                  CAGTCAAATCGGTTGGGTATTCCAAGTTGTTGAGCAAGAACTTGTCCAGGGCACAGCTTC
                                                                                                     ccattaaatctgttggatattccaaattatttagcaaatatttatcaagagcacatccat
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/protein_id="CAA55452.1"
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TVVLSFHPOEVTKVDBAYRVQCFYMEADKTVSAQLEVSEITTQFOTQVVPMPVCKYEI
LEGAALGQPIQFATIAQQVYTSGTCDSETIDTFCAVVHSCVVDDGNGDTVQILNEGSC
ALDKFLLNNLEYPTDLTAGQEAHVKYADRSQLEYQCG13TIKEPHSECARPKCAEP
SGENAVKVGAGGAGAPPPAAAAAATPPPAAAPPAPIAPAIPARPKGLEGALRLRK
RRAAPGEQVLDVRTEFNALDISDKPFNLPAHIRHHHLMENLSAEPQRRFIYQGGQQV
CMSSFRANHLRYGHCNGCSHWWVHSTYCLFIVVFFSNEIK"
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join(<467. 943,1139.
/gene="Mtcut-1"
467. 2052
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/db_xref="taxon:42426"
/clone_lib="lambda7-2(1)"
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<467. .943
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                                                                                                                                                                                                                                                                                                                                                                                                                    AGACGAACACTCCTTTGGGTT----CAGCATCAGTGCGGGCAACATTGCAAGAGTCGAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTGAGCATCTTAAACGTTGGGTAAGGAAGCAAAATGTTGAAATTAAACCACTCGATT 1008
                   cut-1-like genes are present in the pahangi and Brugia malayi, and, as components of the cuticle
                                                                 Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 637)
Lewis, E., Hunter, S.J., Tetley, L., N
 Mol. Biochem. Parasitol. 99339397
                                                                                                             Brugia malayi
                                                                                                                                                         Brugia malayi cut-1 gene,
AJ012617
                                                       Devaney, E.
                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
                                                                                                                          Brugia malayi.
                                                                                                                                  cut-1 gene; cuticlin.
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Direct Submission
Submitted (06-NOV-1998) Devaney
University of Glasgow, Bearsden
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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/protein_id="CAA10074.1"
/protein_id="GAA10074.1"
/db_xref="GI:3858955"
/db_xref="SPTREMBL:096775"
/translation="VISFHPLSVTKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFQT
QIVPMPVCRYEILDGGPTGQPIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGN
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/gene="cut-1"
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/db_xref="taxon:6279"
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Pred. No. 4.5e-35;
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                                                                                                         GAAATTACA
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Brugia pahangi
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AJ012618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Filarioidea; Onchocercidae; Brugia. 1 (bases 1 to 358)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cut-1 gene; cuticlin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99339397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis, E., Hunter, S.J., Tetley, L., Nunes, C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 358)
                                                                                                                                                                                                                                                            110
                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA10075.1"
/db_xref="GI:3970656"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(<1. .191,350. .>356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(<1. .191,350. .>356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Brugia pahangi"
/db_xref="taxon:6280"
                                                                                                                                                                                                                                                                                                                                    /gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                  "UNADGCALDKYLLNNLEYPTDL
                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:096776"
/translation="PIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
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                                                                                                                                                                 Score 156.6; DB 3
Pred. No. 4.7e-27;
0; Mismatches 24
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                                                                                                                                                                                               DB 34;
                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANI
                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone F53F1. The true right end of clone M04G12 is at 21759 in this sequence. The start of this sequence (1..101) overlaps with the end of sequence Z81103. The end of this sequence (39379..39478) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bin/display?db=wormace&class=Sequence &object=F53F1
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both dye primer and dye terminator reaction, from distinct subclones.

Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the conte
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Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonfield, J., Burton, J., Connell, M., Copsey, T., Copper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, Fulton, L., Gardner, A., Green, P., Hillier, L., Junston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Tinkhanian, T. Ilovd, C., McMurray, A., Mortimo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burton, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 39478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence AL021448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the specified clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 Mb of
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                                                                             complement(join(14923. 16033. 16271,16318. ...
                                                                                                                                                                                                              complement(14923.
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .39478
note="predicted using Genefinder; similar
                                           /gene="F53F1.
                                                                                                                                                                        /gene="F53F1.1"
                                                                                                                                                                                                                                                              /clone="F53F1"
                                                                                                                                                                                                                                                                                                /chromosome="\
                                                                                                                                                                                                                                                                                                                                       /organism≃"Caenorhabditis elegans"
/db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson, K., Baynes, C., Berks, M., Connell, M., Copsey, T., Cooper, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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er,L., Jier,M.,
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CDNA EST EMBL:D72018 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C12451 comes from this gene; cDNA EST EMBL:C12451 comes from this gene; cDNA EST EMBL:C10189 comes from this gene; cDNA EST EMBL:C10189 comes from this gene; cDNA EST yk506b3.3 comes from this gene; cDNA EST yk437e9.3 comes from this gene; cDNA EST yk437e9.5 comes from this gene; cDNA EST yk311h10.3 comes from this gene; cDNA EST yk311h10.3 comes from this gene; cDNA EST yk311h6.5 comes from this gene; cDNA EST yk300g2.3 comes from this gene; cDNA EST yk300g2.3 comes from this gene; cDNA EST yk300g2.3 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk314b3.5 co
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join(17396. .175
18339. .18524)
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eesloslotdyidmylvhypkndsdnddvnnaeyrkiayevleeakaagkvrsigvs
eesloslotdyidmylvhypkndleyhphfariploxyckekniffqafsslarhepkl
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/note-"similar to aldehyde reductase; cDNA EST yk473d8.5
comes from this gene; cDNA EST yk473d8.5 comes from this
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/gene="F53F1.4"
join(21582...21670,21781...22009)
/gene="F53F1.4"
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GKNFPPCCNQVEYHPHFTREELKNYCKSEGIFFQAFSSLARHNETLLSSEIITRLAEK
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                                                                                              25572. .26408
/gene="F53F1.5"
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/db_xref="GI:3877460"
/db_xref="SPTREMBL:P91998"
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IILI KEDSFCMVVHTCS VDDGRGETS FLIDS NGCSIDK FLLS NLEY PGNLLAGQEAH V
join(25572. .25660,25850. .26408)
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CDS

Phote = "predicted using Geneifinder; similar to cuticilin; cDNA EST SMBL:07107 comes from this gene; cDNA EST CEEEN060F comes from this gene; cDNA EST CEEEN060F comes from this gene; cDNA EST SMBL:071280 comes from this gene; cDNA EST SMBS:071280 comes from this gene; cDNA EST SMBS

Query Match 9.3%; Score 107.4; DB 34; Length 39478; Best Local Similarity 61.7%; Pred. No. 2.1e-15; Matches 171; Conservative 0; Mismatches 106; Indels 0; Gaps

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                                                                                                                                                                                                                                                                                                                   current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone E04D5.
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Caenorhabditia; Rhabditida; Rhabditida; Rhabditida; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 3136)
2 Anderson K Ravnes.C. Berks,M.,
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Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
The true left end of clone ZK673 true right end of clone T09F3 is
                                                                                                                      neighbouring submissions.
The true left end of clone E04D5 is at 1
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Wilkinson-Sproat,J. and Wohldman,P.
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6750. .6930,7003. .7283,7337. .8179,8228. .8326)
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ETHFESPKELWEVRWRPMTGYNKFAIKELTKTDKMAAGLPIRKKDASHPLNNVPAGAV
RQAGAYIPPHLRKPLGGGSAGPPSAAAPTPGNQNQRPAQPRANGNGNAPQPFRPQOS
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VEKGATHALSSEPAENHVAVVVPAVGSTPAKRVRYKSESFPVYGNRTFFKSDKAVM
TWNQRGOSLILASVEVDKTNOSYCEOSLYLINIGSGESVVVPLEKKGPIYAAKWNE
NGREFAVCYGYMPAKVTFYNPRGVPIFDTIEGPRNDVFYNAFGNIVLICGFGNIAKGK
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CDNQVTRVFEIATNKEILCVELKRTRKILFSPKDNFLLTFEPWAVYGPKTAENQKPEP
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/gene="E04D5.1"
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/db_xref="taxon:6239"
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                                                                                                                                            .31536) overlaps with the start of
.10028,
32. .11629,
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/protein_id="CAA91282.1" /db_xref="GI:3875454"

codon_start=

10089. .10283,1 11691. .11718))

/db_xref="Sptrembl:019055" /translation="Megenleyadihstippkceklkirvflsbnaqkhlegfflkyp /translation="Megenleyadihstippkceklkirvflsbnaqkhlegfflkyp /translation="Megenleyalipplathatolmtcleyklkirvflylkkhlegfflyhk /tvpvfflakvvqfaipfililitferylmtctekkregitfqvltlslsfrkafsai

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27861 AAGTTCAGCAACGCAAGTCCATTTGTGATAGACTTGATCTCCGATTCGAGCGTACTTAAT 27802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 acattcgctatttggttctttaatggtaatactgatctggcattgatagaaaagctgtga 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tocal Similarity 56.18; hes 179; Conservation
                                                                                                                                                                                                                                                                                                                                                                                      tggttgaccggttggtcca 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agtatcaccgttaccatcgtcgacaaagcaggaatggacaaccgcgcagaaagtatcaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGATTCTGAAGGATCACCCCATCTACAGAACATCCATTGGCATCAATGACAGTTACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caaattatttagcaaatatttatcaagagcacatccat---cagcatttagaatttccac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggtttcagaatcgcatgtccatttatgataaactggctgaccaatgatagcaaattgaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTCCACCTTGTCCATCATAAACCGTACATGAGTGAACTTTCATACAGTACACATTCTC 27862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGTCAGCAAATTTGAAGACTGGTGCGAGTTTTCCAGCTGTCAAGTCAGAGGTGTACTC
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Caenorhabditis elegans cosmid F53B6, complete sequence
281086
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28158. .28410,28491. .28811,29092. .29213)
/gene="E04D5.3"
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5592 c
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YPYDSHESGYPTRPANYPVASSRYPIPTTQAPASYPSSPAPPPPGADIDNGYPEPQPI
YIAETPENAYDGIVGFNDTEQPFTTSAAYTEDGVYSRLIKRNVVESTEQINASNKKRP
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/translation="Wpsrlawkelkgggepevycetasisllektrnnsfngkvevkgy
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vsepscmtvgdgktghreevrhdscgverkgeingvvisatviisehsieitkidrav
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xhkwtcvaelenvycmkvhsctvydgqggppvTvIDangcsvdgvIlqnleytsblta
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LILLCLLFATTVVVFIVIVQKQRQILAQTAFFKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA91280.1"
/db_xref="GI:3875452"
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/translation="MWSINLTVHIILLVTFSVSHVVTTAVTKATGETTVRGAGQDLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA91281.1"
/db_xref="GI:3875453"
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                                                                                        32412 bp
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Pred. No. 7.8e-10;
0; Mismatches 137
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REFERENCE
AUTHORS
TITLE
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IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small content of the specific or the specific or sequence overlapping sections once, or longer because we arrange for a small content of the specific or longer because we arrange for a small content of the specific or longer because we arrange for a small content of the specific or longer because we arrange for a small content of the specific or longer because we arrange for a small content of the specific or longer because we arrange for a small content of the specific or longer because we arrange for a small content of the specific or longer because we arrange for a small content of the specific or longer because we arrange for a small content or longer because we arrange for a small content or longer because we arrange for a small content or longer because we arrange for a small content or longer because we arrange for a small content or longer because we arrange for a small content or longer because we arrange for a small content or longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we are longer because we longer because we are longer because we are longer because
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence Z81523.

The true left end of clone F32H2 is at 32306 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The start of this sequence (1. .105) overlaps with the end of sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Johnston, L., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Riffen, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Wateston, R., Watson, A., Weinstock, L., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neighbouring submissions.
The true left end of clone F53B6 is at 1 in this sequence. The true right end of clone F53B6 is at 5116 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor associated protein; Thrombospondin like. Caenorhabditis elegans. Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is not the entire insert of clone F53B6 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://webace.sanger.ac.uk/cgi-
bin/display?db=wormace&class=Sequence &object=F53B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Wilson, R., Ainscough, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 32412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end of this sequence (32306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cuticulin; Human platelet tetraspan antigen like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 (6466), 32-38 (1994)
                                                                                                                               platelet-endothelial tetraspan antigen
                                                                                                                                                                                                                                                      1480. .3649
/gene="F53B6.1"
join(1480. .1638,1707. ..
3205. .3308,3430. .3649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:1627952
/protein_id="CAB03120.1"
/db_xref="GI:3877452"
                                                                                                                                                                                                                   /gene="F53B6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="F53B6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis
                                                                                        codon_start•1
                                                                                                                                                                       'note="predicted using Genefinder; Similarity to Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secernentea; Rhabditia; Rhabditida; ditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                      .1946,2437. .2628,2969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .32412) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baynes, C.,
                                                                                                                                    (SWLPET3_HUMAN)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berks, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initiation
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BASE COUNT ORIGIN

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RESULT 11 CEF53B6

DEFINITION

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/note="predicted using Genefinder; similar to thrombospondin like; cDNA EST EMBL:214404 comes from this gene; cDNA EST EMBL:2171 comes from this gene; cDNA EST yk195c9.3 comes from this gene; cDNA EST yk195c9.5 comes from this gene; cDNA EST yk28697.3 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk353h1.3 comes from this gene; cDNA EST yk353h1.3 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMSRTVECVAVNPISSAPIKLPMSECQDOEQPKLFESCEVRSCPLQEDSKLSEDEAPY
QMRYGDMYQCSASCLGGKQKAALKCIQYSTGKSYQWSQCDARRAPPEKSBPCNOHPCP
PFWLTSKYSDCSMSCGSTARRSVK-KAQTVSKTDGADAHIVLAEDDRCHEKKPQETETC
NVVACPATWYSSLNKRHNKIKLNKLKTAQWTECSRSCDSGERRRQVWCEIRDSRGKTQ
NVVACPATWYSSLNKRHNKIKLNKLKTAQWTECSRSCDSGERRRQVWCEIRDSRGKTQ
RRPDVECDANTKPQTVEVCSFGGCSRPELLSNRVFEQNAEQKKLTLGIGGVATLYQGT
SIKIKCPAKREDKKIYMKKNGKKIKHNDAHIKYSANGHLVPHARMEDAGVYECFTDB
GGNVTLNEKYRDFPASRVDLAPKPQIPSTKNRQRVQVSKEDVLREQASVLHKMNVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKCSYTVVFLLFYLLIASPHVDALSWAAWSPWSSCTKTCGGGVS
ROLRRCLTSKCSGESVRFKVCAOKTCESKSRLARDTICGGEEIVSRGOCEVVCRSRLI
ROLRRCDDGTPCQAATSRAVCSKGSCQIVGCDGLISSSFREDACGVCGGRGOTCDN
GKFIMRVDSGTYACASNCDDIVDWSGAGRSIASTSQPIVVCVNAITGRVVPEKLCAD
LIKVSEEYTACASNCADIVDWSGAGRSIASTSQPIVVCVNAITGRVPPEKLCAD
LRPKVEARPCPHLICPSRWMAADWTECVPHCGEGTRKREVYCVGTAHNVTVHVPDTFC
ENGTRPAAEENCVSTSCGRWEAGKWSKCTASCGGGVRRRHVACVGGSDCDEGGRPRQE
TTCYAGIPCSIATNSLDWNDRAYLDGNTFGSMDNHNWQAPRLVAGEWSTCSSTCGTG
                                                                                                                                                                                                                                                                                                                    comes from this gene; cDNA EST yk193h3.5 comes from this gene; cDNA EST yk411f5.3 comes from this gene; cDNA EST yk411f5.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(19892. .20022,20241. .20283))
/gene="F53B6.8"
                                                                 SSKAKHSKRSSKSSKKGTSGKSGKGSSKRGGKSSKSSKSKKVKTATTSGSQVSTVSAA
TGVSDKQSNSSKSSRKSSKSSKSRKNRRLDSDAQKKMEKSGKSGKVALIPKTQQTTGS
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/db_xref="G1:3877449"
/translation="MAITSRGOPFRKSKCDQSIDNKNQFEVLKEEARVCASIARTRML
/translation="MAITAFCAKNRKTVHAKNKNKNKNKSSKSRKSTRGASKSGKSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21609. .21818))
/gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(20516. .20602,20648. .20953,20999. .21424,
21609. .21818))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(20516. .21818)
/gene="F53B6.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKSAIGEEGRKKNOLLKRDFSKLANPLSEFSLYREOPD70FLKNRKIKNVDQDSRLFSLLEKYIFHSLSINLTIYLKALHFQTRVFPFKSFPHFNTLKFTFQTKWALIGISAYGARGRLIKFSYIV7ALISILFSISCICYGIWLLARRSQYAELVSPSLYVDVGRILVFISILSILSILNYLICFYAIFKEMRCFVTSCAVASIVIAVMLIIGGCIGLN
YRVNPVYGFAEPRSSVKIDVLRLNGEQKTDKLVLLTANANGSTNPHEAFANQAEHREN
                                      QVGHSLAEEVNSIKHSKEMNVAPAKLQYQTLGGVNQIELKNTSNERKAYKIKCSDNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGYYQSNYWGKRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIKLFHSCDSLEVRQKCCSTCTFVERKKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCVWISSGRPAGRNCEQMRRPHSARACVADEPLPPCMPTASALYQRDASCQDQSRFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCRFTNGTSVDIQHCDITNRPATTMDCPNQNCKAEWRTSDWGSCSSECGTGGVQLRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GETRNVDNSTCESLASVRPPETRPCHREDCPRWEASQWSECSSQRCVSSMLAQKRRNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEALLTAPNDEKAREQLRKYGNELVARWDIGHWSECRQKTCHVAGYQARGISCKVTFH
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/db_xref="GI:4008366"
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                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB54255.1"
/db_xref="GI:5824510"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="predicted using Genefinder; cDNA EST yk193h3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MDFGILLVFLMAVAGTFAGISVSFSHSHEFPRHGLLGGGGFNPY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=
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29798 TGCCTCCGCATATTGCATGCTCCAATTGGAATTG 29831
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                                                                                                                                                                                                                                                                                                                                                                                  722 atttgagtttgaaaagcagttgtgatttcagatacctcaatctgtgcactaactgtttta 781
                                                  gtacgcgcaacattgcatgaatcaaatggaagtg 935
                                                                                                              GGATGAAACGAGGTGATCATTGTGAAGGAAAATGATATTCCACGTGGATGCAGTGTTCGT
                                                                                                                                                                 ggatgaaacgaaatgacaacagttgttgttacaaaaataccacgtggattcagagatcgt
                                                                                                                                                                                                                            ATTGACTCGAGGAAGAAACATCGAATACTGAATGCTCGATCCATTCCCGTCACAAAGAAT
                                                                                                                                                                                                                                                                               tcagcttccatgtaaaagcattgtactcgatatgcacgatcaactttggtaacaaataat 841
                                                                                                                                                                                                                                                                                                                                           AATTGATTTAATACTTCAGAGTTAACATACCCAACATCAATTTCCGCGTTCAATCCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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/protein_id="cab03118.1"
/protein_id="cab03118.1"
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/translation="MSRESPVSLAQLVEREPLIKKFDPDIERGQIVSTYGRGLINAGIFPN
CYPRGPMEXYHPYDMMEPKLCLSYTTINIDPALLSYROMLPTNEQEMLLSPRAFFNE
EVECSPDMKSVQTAFELIKGLGLSYTTINIDPALLSYROMLPTNEQEMLLSPRAFFNM
GYPINIQYLPSQGFIRAENIEDYNLRIQAFFKKNIAKIEQKQVVVISDNVMVDLTRNE
HVETVDDIILQCIKRPTCQMNFISLKKGBAQIMDSPILPLTKSLYLVKPFYWTDVPLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="minlslfivktvytfywvvlekvqlhsfkqyvvalrfesvqfknp
PILLLIYNRIFLQSITILILLSTSSCFEIQNGVVGKPEVFCGIDTIRVKVNTEHPFN
GRIYVDGESDKQHCVQHSADAHSSPQEFTIPIGACNMRRQRTLHPRGISFSFTMITSF
HPFFYTGMDRAFSIRCFFLESIKGLNAEIDVGTLAPQHVDQEYSLPVCAYHLKDGIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(27666.
/gene="F53B6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="TTT Lys K-trNA; predicted using trNAscan-SE-1.11; preliminary prediction; similar to trNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MILSDQNFLQTQWKEPQTAQSKNTESKCEFHGNSNEVKPIGSLN
GQSIAQCRIHTEKTVFIVKGGEQARMEENEIYAIETFGSTGKGYFHDDMETSHYMKNF
ELADEKIPLRLQKSKGLLNLIDKNFATLAFCRCWIDRLGETKYLMALKGKCSYSTASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(27666. .27862,27919. .27959,28076
28905. .29001,29330. .29417,29467. .29606,29648.
30107. .30301,30478. .30589))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYPNHPELNON"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(26258. .26342,26501. .2
27153. .27288,27334. .27459)
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/gene="F53B6.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycoprotein (SW:I2A6_RAT)"
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/gene="F53B6.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQIEYEHGAISAYTNAHVFKYADKVQLYFTCTVQLCYKHDGGCEGITPPQCSGHSHGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVLRFAQVGQKVTHVWRCDQDASHVYGILIHSCYADDGHGNKFELVDDRGCSTDPFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMLILTLFTDRWMAMVGACILQSFAGKIIGKRANLLLNLII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB03116.1"
/db_xref="GI:3877448"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="predicted using Genefinder; similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="F53B6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F53B6.t1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F53B6.t1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F53B6.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.4%;
59.3%;
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51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74.8; DB 34; Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 32412;
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MEDLINE
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AUTHORS
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KEYWORDS
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CER07E3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bin/display7db-wormace&class=Sequence &object=R07E3
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTIONS THIS sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone R07E3. The true right end of clone F41E7 is at 36774 in this sequence. The start of this sequence (1. .115) overlaps with the end of sequence Z68106.

The end of this sequence (39633. .39736) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lioyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted (05-MAY-1995) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
On Nov 21, 1995 this sequence version replaced gi:798823.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans cosmid R07E3, complete sequence 249207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cottage, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z49207.1 GI:1067021
HTG; ADP,ATP carrier protein; Cuticulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 39736)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submission
                                                     /note="Serine and threonine rich protein, Carboxyl terminus is glycine rich; cDNA EST EMBL:COB296 comes from this gene; cDNA EST yk259b4.5 comes from this gene; cDNA EST yk574h3.3 comes from this gene; cDNA EST yk574h3.3 comes from this gene; cDNA EST yk597h8.3 comes from this
                                                                                                                                                                                                                             5080. .8873

/gene="R07E3.6"

/gene="R07E3.6"

join(5080. .5246,5409. .5769,5826. .5942,6381. .6905,

6955. .7075,7125. .7448,7495. .7787,7831. .7980,8037.

8222. .8405,8470. .8873)
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                                                                                                                                                                                                             /gene="R07E3.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:6239"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                        /clone="R07E3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-SEP-1999
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/translation="MIFLVEWFLITLLIFLAVTGKTLGLREYYUNTLVYIFEWGATUN
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TVSVLVDDTLDE ITAGNEAVIEDQVTNRESSAAGLÆNNLLSRTKYSFHFENWQLTLLW
IAGFNERYYULVPCRIALFGLAIVLMIYSTSIIGLVPNAKVRKELURROCMFLMCHRIYS
RAFSSVIRFHDKENRANKGGIALVLMITSPIDLVPNAKVRKEGIONNTSVMMEKKGS
RAFSSVIRFHDKENRANKGGIANTSPIDLFWNLSCHUFTERGEAGDRAKVWDRMREHVNDENKLPIILFPEGTCINNTSVMMEKKGS
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RQSEFAMAEYNGIRDCISKIRLEQGAMALWRGNGAGVARCLPNHTLNFAFRDIYRNTL
LKNVDRNESEGKFLAGTFVSGGLGGATTLFMLYPFDPARTRLALDVKKDGSRKYKGMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(17917. .18025,18074. .18331
18604. .18751,18800. .18877,18947. .19072))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EBITTTTKAPTTTTQSTTTTTQLPTTTTTEPTTTTTVDPLAENEELEKQAIEVM KSLDDERI JOAENVEYOKKOENAAKRINNELKMMOKAREKNKPHKETTTSLAT EORKTTTIVASSTETSSTVTTDATEATTTAPTTTVATTTKKRSNIPEAEDOELET EORKTTTIVASSTETSSTVTTDATEATTTAPTTTVATTTKKRSNIPEAEDOELET AEKTTTKVTEDGPITTEFPEYIKKRNAIVGIKTLTPAQLEAAINAKPIPSSASEASAPSNIPETSAAPAAAPVALPEDIAPPGIALPGCITDOISOGFMEYOASSIVEDMRPILG SILVEGESQLAREILMPGILK SILVGESSASRARAASVRYZEKYKTPUIRDIMADGYSENSLVGFESQLAREILMPGILK SILVGESSASRARAASVRYZEKYKTPUIRDIMADGYSENSLVGFESQLAREILMPGILK KILVGSSASRARAASVRYZEKYKTPUIRDIMADGYSENSLVGFESQLAREILMPGILK KILVGESSASRARAASVRYZEKYKTPUIRDIMADGYSENSLVGFESQLAREILMPGILK KILVGESSASRARASVRYZEKYKTPUIRDIMADGYSENSLVGFESQLAREILMPGILK KILVGESSASRARASVRYZEKYKTPUIRDIMADGYSENSLVGFESQLAREILMPGILK KILVGESSASRARASVRYZEKYKTPUIRDIMADGYSENSLVGFESQLAREILMPGILK KILVGESSASRAGARASVARIANAVATENSLVGFESQLAREILMPGILK KILVGESTAREILMPGILK 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22011. .22170,22220.
23254. .23259))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="R07E3.3"
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AQISITTSGMVCYPLDTVRRSMMMQSGKQIKQYTSTKDCWKTLYKKDGINGFYRGALT
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MLEEKSSDILNIMQGISEEERDELLKQIDEQDDEEEMIRKISSLKPKFKIGDHDADEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA89072.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="cDNA EST yk278a10.3 comes from this gene; cDNA EST yk278a10.5 comes from this gene; cDNA EST yk486f8.5 comes from this gene; cDNA EST yk603d8.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(11510. .11773,12101. .12476,12528. .1282
13402. .13542,13587. .13696,13745. .13863,13912. .14026,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "IDFSFFSSNRKKL"
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EGYEQGRDGVKTTFHGDSGVMTGGGHSAPTFDYLNMPSESFGLAPVAPPAPPPPPATQ
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EHVSTTPEESITENTTAEVPASTASTKDTKLSVKIRSEDEKREEDKLSDDEKPNYMKK
LEEIYKKEEELVERELAEMSVAEIFEKEVVIKTTKVTFTSTTTEIPTTTTTEEATTTT
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LKKIAMRNNPKYNAPSRSSFTIPPPTFKAEDLDMNKLKRGKGDSIINEKMLTLLLPRV
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/db_xref="GI:3878959"
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                      acattcgctatttggttctttaatggtaatactgatctggcattgatagaaaagctgtga 426
caaattatttagcaaatatttatcaagagcacatc 521
                                                                                                                       TCTATCGGCATATTTGTATACGTGGGCTTCCCTTCCCGCCATCAGGTCTGTGGGATACTC
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/db_xref="GI:3878958"
/db_xref="SFTRMBL:Q21810"
/translation="MMAISLEKREDDERAPISHVEHHPLAGNHCSEHACREQKRENLQK
RHLYLFTIWLMFIIFVVPLFTKLQAEKVSRRAHTNERGIQNIAKEYIAYTEKFDKSYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(29470...29618,30123.
30963...31067,31117...31252))
/gene="R07E3.7"
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VEAAWAIAHGEKRNLSEQTLLLDCDLVDNACDGGDEDKAFRYIHRNGLANAVDLPYVAH
RQNGCAVNDHWNTTRIKAAYFLHHDEDSIINWLVNFGPVNIGMAVIQPWRAYKGGVFT
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complement(join(26570. .26749,26841. .26917,27073.
27330. .27855,27863. .27958,28006. .28071,28119. ..
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SDYIIPNDDIISLNWLQRNFDMRISELCMTAIGTTLLVFLNAFLFIISLVSIVHVCCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA89073.1"
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/db_xref="SFTRMBL:021813"
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/gene="R07E3.1"
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/db_xref="GI:3878962"
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64.5%;
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Pred. No. 7.2e-06;
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RESULT 13
CEY39A1_3/c
WPCOMMENT
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AUTHORS
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ORGANISM
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CEM142/c
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Fragment Name
CEY39AL 0
CEY39AL 1 11
CEY39AL 2 21
CEY39AL 3 31
CEY39AL 4 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATACGTGGTAGGGTTTCGTGGCGAGACGCAGAGAAGTATCGTAGTCCGGAGTTGAGAGA 82130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGAACACTGTTGTGAT 81873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccggttggtccaccatccaaaatttcataacggcatactggcatcgggacaatttgagtt 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAATGCATTCCCATCTATGATATACACTTTCACCGAGAGTTGCAAAACGGACTATTGGG 81950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTATCCACATAGCAAGAGTGAACTAACATTCCGAAAGTGTCCTTATCAGCACCCTCCACT 82010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tatacgtg---agcttcttggccagccattaaatctgttggatattccaaattatttagc 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATTTCAGACATAGTGTTATTTGACACTGATATTGTAGTACCGGGCGGTCCGCGTACTTA 82190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tcatcgacaaagcaggaatggacaaccgcgcagaaagtatcaacggtttcagaatc----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCACCGCGTCTAGGCCACAACCATTCGAATCAAGAATATCCACTCTATCACCGTAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaatatttatcaagagcacatccatcagcatttagaatttccacagtatcaccgttacca 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197;
                                                    Wilson, R., Aliscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry Mangel, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                              HTG; Cuticulin; Homeobox protein EVX1 like Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans cosmid M142, complete
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                                        2 Mb of
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                                    contiguous nucleotide
(6466), 32-38 (1994)
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200001
300001
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210000
310000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419585
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                                      sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANI
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                                                                                                                                                                                                                                                                                              Caenorhabditis.
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                                                                                                                                                                                              Jier, M.,
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REFERENCE
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because we arrange for a small converte because 
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on Nov 4, 1996 this sequence version replaced gi:1370039.
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the entire insert of clone M142. The true right end of clone C44B9 is at 5059 in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  available information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end of this sequence (36203.
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/gene="M142.2"
join(8540. .8572,9335. .9416,9468. .9679,10373. .10721,
10772. .10974,11033. .11175,11871. .12501)
/gene="M142.2"
                                                                                                                                                                                           /db_xref="SPTREMBL:Q21540"
/translation="MRPIPYDISLSITSFLSLILICSANPIDNGLVDSELIHECVTHK
/translation="MRPIPYDISLSITSFLSLILICSANPIDNGLVDSELIHECVTHK
AVEVILLLDASGSIGDDTFKKOLFSRAHILASRLNISEDGSHMALIQXAETPKLEFSLG
OFNHPTOLEMAIQRIEYQSGATNTGQALRLTLEKGLQGARPGIPKVAIVITDGQSQDD
VSEPSQLLRDADVMVXAIGVTNLVNVHOLHQMYGNPVRVFTVESFEQLDRALADSLTW
SMCKTEFREJPEICGFDRIGVKASTKOPFBEONVFVMDHYHDEECRAGPEKFPDSRS
IGLTVPFFSACNVHRYRSLNPKGIFVEVSIVFMFHSLFMTKTDQTVKVQCFYMEADKHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SWISS-PROT:Q10658"
/translation="MKAEQQQGSIAPEPSQMPRPPPVTEQAITTEAELLAKNQI
TPNDVLALPGITQGFLCSPSANVYNIEETKFQIRDLDTEHVLEEIAKPENETEENLQA
QAESARYVRYRFAPNFLKLKTVGATVEFKVGDVPITHFRMIERHFFKDRLLKCFDFEF
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GVGTIDVFTDSVTVLEQEPACQQVTTYSFRFSISTNQKIENS"
                                          DKDTFGMLVHSCYVDNGYGDRVDILDSNGCGLDAVLLSTPDYDTSLRLATKPYHVFKY
ADRPVLQFQCQITLCLKYDGGCEGITPPQNCKKLPGEDGHHHHHHPEKRRKLVRRLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"cDNA EST yk258al.3 comes from this gene; cDNA EST yk258al.5 comes from this gene; cDNA EST yk532all.3 comes from this gene"
                                                                                                                                                      TVPLSVSMITTVFREQIYQMPQCAYTLRKGAPDGPIVRFATLGESVYHRWECIEVEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA97806.1"
/db_xref="GI:3878735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFCMPNSRNNCEHIYEFPQLSQQLMDDMINNPNETRSDSFYFVENKLVMHNKADYSYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA97807.1"
/db_xref="GI:3878736"
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/gene="unc-119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="predicted using Genefinder; similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/clone="M142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36306)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in this sequence. The the end of sequence
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for a small
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DLRKMPKEERROYILQAEVPGGMGGGPGGSGGAEAGRIGGLHPLYSQIDETGRSISRT
MPKDMSHNSPOTPPKQPROKRYQMGIPPNRMCYSSDAPPTIPSHQQQPPQFFNSQHL
PQRFRGGRQRGAPPPPPQPMPMLIGYDMPGAPMQADPPILTADGQMVNGTPQRVVIM
QSPTHLPGGPVVMIPQQQMVPPPQSKMTPVGGPMGPMTPSIPVQVPPNTMMTATSP
TGSV1YPAASPPGPPHTIMIQSIGVPKRKSNFLKIVRKISFFLNFYDFFLILRKLKK
EXKGADIEFFEKIKSTDFKKYPSSTSKTDGNMFPMFDRGSGGWWGPCTMLRESGADA
EQLLAKRYEILKRLQASEDDDDPEDGGIGHVSYVASSVLDDRMDHPLTMIPVPTID
LPAIPISFANMFTESETWTMIGEMYQNNFRAPSLTAPSSNQPMNVNASASATVQAECEN
RKILDFPLKYRKMTLMFEKVSTCFHYTLKDYMVFVYLNTLMFSKRAPRRRARATIPQ
RKILDFPLKYRKMTLMFEKVSTCFHYTLKDYMVFVYLNTLMFSKRAPRRRRARATIPQ
RKILDFPLKYRKMTLMFEKVSTCFHYTLKDYMVFVYLNTLMFSKRAPRRRRARATIPQ
                                                                                                                                                                                                                                                                                                                                                                                               MIEIILSIQSNTHVSSQLWSAVRARGCQFLGPAMQDDVLRLILMTLETGECIARKNLV
MYVVQTLASDYPQVSKTCVGHVVQLLYRASCFWVLKRGESSLWGLKEEERTYESLRR
EHBSGIVQLAFESGGLRIGPDQWSALLYADQSHRSHMQSIIDKLOSKNSYQGGVEELA
LAGSQTSMLVPAYRYFLTQVIPCLEFFAGIEHEDTSMRMIGDALHQIRILLKLHCSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAPTGQGGQWQEVLCCSICNRHFNETFLPVSLICGHVICRKCAE
KPENQTKPCPHDDWKTTHSPSEYPNNVALLSVIFPRKQCMTLSGAVSEAEKRVDQLSI
QIAKFFREADSERGCTVSSREISRTLQRKVLALLCYQWREVDGRLKTLKMCRGISERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(34039. .34101,34448. .34750,35530. .36306,
299276.1:105. .698,299276.1:1364. .1566,299276.1:1666. .1772,
299276.1:4495. .2795,299276.1:3714. .3928,
299276.1:4056. .4104,299276.1:5846. .5958,
299276.1:6478. .6729,299276.1:7169. .7338)
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join (34039. 34101,34448. 34750,3530. 36306,

Z99276.1:105. .688.Z99276.1:1364. .1566.Z99276.1:1666.

Z99276.1:2495. .2795.Z99276.1:3714. .3928,

Z99276.1:6478. .679.Z99276.1:5846. .5958,

Z99276.1:6478. .6729.Z99276.1:7169. .7338)
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/translation="maschltashvalescerfaraktegpeagnnbyngtryterl
tremainkyhkiriskehlescerfaraktegpeagnnbyngtryterl
tremainkyhkiriskehlescerfaraktegpeagnnbyngtryterl
DKTLGELTPNLMKSPAISIRGQAYLQLKRTIPDTCWCGEDIRVLGLVLVHKPYEVSD
VTKDAKATGFDESRAESAVLQVQKILSKPMTEYTARALDLFTLGAIVANYSSSEMSDT
VTKDAKATGFDESRAESAVLQVQKILSKPMTEYTARAPLDFTLGAIVANYSSSEMSDT
DDIPQLSADTIAALSMYGABQOEKTEQLQSGTIEKIDEDWQLSQFWYDDETSRKLVAE
GVAAALEGSEARPARIGCVSSPTLVKFFHETEEYKTGQIQLTLFEFDDRFGLKFPTEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"similar to Zinc finger, C3HC4 type (RING finger); CDNA EST EMBL:D67323 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA97810.1"
/db_xref="GI:3878739"
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31500. .31763,32933. .33043)
/gene="M142.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:045962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="M142.
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                                                                                     COMMENT
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                                                                                                                                                                      AUTHORS
TITLE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11891 CGGAACACTGTTGTGAT 11875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500
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                                             Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, predictions from Genefinder (P. Green, U. Washington), and ot
                                                                                                                                                                                                                                                                                                                                                       Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Catreille, P., Lightning, J., Lloyd, C., Komuray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 36069)
Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans cosmid 2K265, complete sequence.
                                  available information
                                                                                                                                                                                                                                                                                                      elegans
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                                                                                                                                                                                          Dobson, R.
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Similarity 52.0%;
                                                                                                                                                                      irect Submission
                                                                                                                                                                                                                                                                                                                                .2 Mb of contiguous nucleotide
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  graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          b
                                                                                                                                                                                                                                                                          (6466),
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Pred. No. 7.8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       φ
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                                                                                                                                                                                                                                                                                                                                   chromosome
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IMPORTANT: This sequence is not the entire insert of clone ZK265. It may be shorter because we arrange for a small overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The true left end of clone T01G9 is at 35964 in this sequence. The true right end of clone T02E1 is at 4168 in this sequence. The start of this sequence (1. .110) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighbouring submissions. The true left end of clone ZK265 is at 1 in this sequence. The true right end of clone ZK265 is at 2412 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The end of this sequence (35964. .36069) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://webace.sanger.ac.uk/cgi-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHDYNIKKRVTVGGHTIGADVFKLPNESFEPSKVSTLEDMIHDYFKRTGNIIRRSVRI
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VGEVLDRLAEETQLNREQMNCFALFVYSESMSLQLQPDSLI DGKLKVDKWNTT I RKLV
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COMPLEMENT (8777. .13818)
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                                                                                                                                                                                                                        agatacctcaatctgtgcactaactgttttatcagcttccatgtaaaagcattgtactcg
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                         tacaaaaataccacgtggattca 893
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TTSTTSTTTTEKNSFFLYDAKLKPVLSTKTYIYKFEFSIKCQNVFISNIYFRPTTA
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SEICVFCIRRVVILDKNPVGGRLKLRKAKKKNCYGLVTEDCPTHAVGCRIRAKKDHIE
WYELSRLYDRNQLVCVYPEEYKSMTGCMRKPSGSIRCWCGGRENCNDPETSRDLVEAF
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29467. .2931,29755. .29902,29982. .30024,30072. .30293,
30599. .30709,30782. .30854,30908. .30989,31418. .31619)
//gene="ZKZ65.7"
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20-AUG-1998 (first entry)
DNA encoding a N-acetylglucosamine-6-phosphate deacetylase.
Staphylococcus aureus protein; ribozyme; antisense sequence; control;
Staphylococcal gene; regulatory element; bacterial gene expression;
vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
toxic shock syndrome; ss.
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                                                                                                                                                                         S. aureus coding sequence SEQ ID NO. 45.

S. aureus infection; diagnosis; therapy; central nervous system disorder; upper respiratory tract infection; othicis media; bacterial tracheitis; acute epiglottitis; thyroiditis; empyema; lung abscess; splenic abscess; cardiac infection; infective endocarditis; secretory diarrhoea; ulcer; retroperitoneal abscess; cerebral abscess; blepharitis; conjunctivitis; keratitis; endophthalmitis; preseptal cellulitis; orbital cellulitis; darcryocystitis; epiddymitis; intrarenal abscess; perinephric abscess; toxic shock syndrome; impetigo; folliculitis; cutaneous abscess; cellulitis; wound infection, bacterial myositis; septic arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a Staphylococcus aureus protein, that, based on homology with an Escherichia coli protein, is believed to be a N-acetylglucosamine-6-phosphate deacetylase. The present sequence was obtained from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequence is also useful as a source of regulatory elements for the DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                               X33788
X33788;
                                                                                                                                                                                                                                                                                                                         25-JUN-1999 (first entry) S. aureus coding sequence S. aureus infection; diagn
                             14-SEP-1998; U18987.
12-SEP-1997; US-058710.
(SMIK) SMITHKLINE BEECHAM CORP
                                                                                                                         Staphylococcus
                                                                                                                                                              osteomyelitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black MT, Burnham MK, Hodgson JE, Knowles DJC, Pratt JM, Reichard RW, Rosenberg M, Ward JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. aureus coding sequence SEQ ID NO. 8.

S. aureus infection; diagnosis; therapy; central nervous system disorder; upper respiratory tract infection; otilis media; bacterial tracheitis; upper respiratory tract infection; otilis media; bacterial tracheitis; acute epiglottitis; thyroiditis; empyema; lung abscess; splenic abscess; cardiac infection; infective endocarditis; secretory diarrhoea; ulcer; retroperitoneal abscess; cerebral abscess; blepharitis; conjunctivitis; keratitis; endophthalmitis; preseptal cellulitis; orbital cellulitis; keratitis; epididymitis; intrarenal abscess; perinephric abscess; toxic shock syndrome; imperigo; folliculitis; cutaneous abscess; collulitis; wound infection; bacterial myositis; septic arthritis;
                                                                                                                                      Burnham MKR, Lonetto MA, WPI; 99-229138/19. P-PSDB; Y05308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus WO9912557-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X33781 standard; DNA; 1182
X33781;
25-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Staphylococcus aureus polynucleotides Claim 21; page 90-91; 102pp; English.
This sequence represents a S. aureus polynucleotide of The invention also relates to the polypeptides encoded
                                                New isolated Staphylococcus aureus polynucleotides Claim 20; Page 65-67; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The polypeptides can be used for the treatment or prevention of The polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polypeptide or polynucleotide can also be used to diagnose of the polynucleotide or polynucleotide can also be used to diagnose or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleotide or the polynucleo
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                                                                                                                                                                                                                                                                                                                                       12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                             14-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           products can
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aureus polynucleotide of the invention
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CC related to their expression. The polypeptides and vectors containing them cc can also be used in immunisation methods. The products can be used for treating infection, e.g. infections of the upper respiratory tract, (e.g. otitis media, bacterial tracheitis, acute epiglottitis, cc thyroiditis), respiratory (e.g. empyema, lung abscess), cardiac cc (e.g. infective endocarditis), gastrointestinal (e.g. secretory cc diarrhoea, splenic abscess, retroperitoneal abscess), central nervous csystem (CNS) (e.g. cerebral abscess), eye (e.g. blepharitis, cconjunctivitis, keratitis, endophthalmitis, preseptal and orbital cc (e.g. epididymitis, intrarenal and perinephric abscess, toxic shock csyndrome), skin (e.g. impetigo, folliculitis, cutaneous abscesses, ccllulitis, wound infection, bacterial myositis), bone and joint cc (e.g. septic arthritis, osteomyelitis), or Helicobacter pylori cc infections, (e.g. causing stomach cancer, ulcers and gastritis). The products can also be used for treating in-dwelling devices and wounds. Sequence 1182 Bp; 416 A; 174 C; 257 G; 335 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus contig SEQ ID #33. Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-1999 (first entry)
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               5881.
/*tag=
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53.2%;
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            the sequence lare included to given in the sequence 1.5940
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the sequence listing in the specification. They
are included to maintain the nucleotide numberi-
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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bases represent a line of
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(BUJA/) BUJARD H. Bujard H, Pan W, S WPI; 98-240088/21

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V35363
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Best Local
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09-APR-1998.
02-OCT-1997;
02-OCT-1996;
                                                                                                                                                                                                      23-SEP-1998 (first entry)
P. falciparum gp190 DNA.
gp190; malaria; MSP-1; merozc
monoclonal antibody; passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents one of 5.91 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM), read-only memory (RAM), sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used
                                                                                                                                                                                                                                                                                                        V35363 standard;
V35363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the computer readable medium.

Sequence 7563 BP; 2584 A; 1028 C; 1476 G; 2229 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-S.aureus
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Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch
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05-JAN-1996; US-009861
                                                                                                                                                                                     Plasmodium falciparum
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Pred. No. 3.2;
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Claim 2: Fig 1; 51pp; English.

The sequence encoding the P195 protein of Plasmodium falciparum (N50530) and a peptide comprising at least one of its epitopes (see P50777) are claimed. Also claimed is a vaccine for inducing immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the new DNA sequence, together with a carrier.

Sequence 5760 BP; 2565 A; 630 C; 725 G; 1840 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP-154454-A.
11-SEP-1985.
21-FEB-1985;
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26-SEP-1984; GB-024340.
21-FEB-1985; GB-004429.
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                                                                                                                                                                                                                                                                                          Cloned
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hes 123;
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for expressing the protein
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23; Conservative
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216. .5179
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04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                          A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                               WPI; 99-045171/04.

WPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides and for the detection of Enterococcus and for the develop products for the detection of Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis genome contig SEQ ID NO:217. Enterococcus faecalis; contig; detection; Enterocovaccine; attenuation; computer readable medium; ds
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X13154;
                         polypeptides encoded by the Enterococcus faecalis nucleotide secan be used in vaccines to prevent or attenuate an Enterococcal
Sequence
                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                              use in vaccines
                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9850555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis
                                                                                                                                                                                                                                                              infection
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                 infection.
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23; Conservative
                                                                                                                                                                                                                                             Page 1103-1107; 2084pp;
8395
B₽;
                                                                                                                                                                                                                                                                            for prevention or attenuation of Enterococcus
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Pred. No. 4
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1692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcal infection;
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Best Local Similarity
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Enterococcus faecalis.
W0985055-A2.
12-NOV-1998; U08985.
04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
116-MAY-1997; US-046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 1617-1618; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be used in vaccines to
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atcataaagacctttcacataaacatgtccttcgaatgcattacgtgtattaaaattgat 1044
                                                                                                                                                                                                                                                                                                           tgttgttacaaaaaataccacgtggattcagagatcgtgtacgcgcaacattgcatgaatc 924
                                                                                                                                                                                                                                                                                                                                                                                                TAGTAAATCTGGATGACTACGGCTTACAAAAACTTGTGGGCCCTTTTGAATTGTTTTCAAC 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                    tactcgatatgcacgatcaactttggtaacaataatggatgaaacgaaatgacaacagt 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTTACGATTTCAACAATTCCATCATAAACTTCTGGAATTTCTTGTTCAAAAAGMCGTTT 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gatttcagatacctcaatctgtgcactaactgttttatcagcttccatgtaaaagcattg 804
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                                                                                                           TTGTTTTGATAAGACTGCTTCGATTTTACCTAAGTTTACATAAATATAACGACGATCTTG 1128
                                                                                                                                                                         aaatggaagtgaaattccggcaacttgacgtccaccttcatcattacggcaaccttcttg
                                                                                                                                                                                                                                                       ACGTGATACGTAAACTTTAAYCCGAYCATGCGGTTGGTAAAATTCATTTGGCATTTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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faecalis; contig; detection; Enteroco-
enuation; computer readable medium; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Pred. No. 2
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Mismatches

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Query Match
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Matches 88
                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding interleukin-1 receptor accessory protein used for therapeutic modulation of II-1 activity Claim 2; Fig 1; 95pp; English.

This cDNA clone codes for human interleukin-1 receptor accessory molecule (III-R ACM) (see W53897), a new member of the immunoglobulin superfamily that forms a complex with type 1 III-R and which has higher affinity forms of III-1 than the receptor itself, suggesting that the known high and low affinity forms of III-R are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAR-1998.
26-AUG-1996;
26-AUG-1996;
                                                                                                          Nucleic acid fragments are useful as diagnostic probes and primers, for isolation of II1-R AcM-encoding genomic sequences, for in situ hybridisation to determine chromosomal localisation of the gene, for chromosome identification and for identifying mutations that
                                                                                                                                                                         and recombinant vectors are claimed. Also claimed are isolated nucleic acid molecules encoding epitope-bearing portions (see W53898-915) of ILI-R ACM. Recombinant ILI-R ACM can be used to identify IL-IR agonists and antagonists useful for therapeutic modulation of IL-1 activity, and to raise specific antibodies.
                                                                                                                                                                                                                                                                     in fact the receptor with or without II1-R AcM, respectively.
The 2155 bp sequence is present in clone HMEEJ52 (deposited as ATCC 97666) derived from microvascular epithelium (no details of isolation given). Recombinant expression in Escherichia coll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signal transduction; infection; so rheumatoid arthritis; therapy; ds
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Human interleukin-1 receptor accessory molecule cDNA
                                                                              might be linked to disease. Sequence 2155 BP; 709
                                                                                                                                                                                                                                                         mammalian and insect cells is described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; W53897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME
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                3.0%;
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              Score 34.6;
Pred. No. 3
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                                                                                                                                                                                                                                                         Recombinant host cells
                               DB 1;
                                                                                 433
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                                                                               <u>ن</u>
                               Length 2155;
                                                                                 584
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PT anti-S.aureus vaccines
PS Claim 1; Page 544-549; 3271pp; English.
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC saureus in a sample. S.aureus is implicated in numerous human diseases,
CC sincluding cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC cand their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer readable medium; vaccine; S.aureus infection; immunodetectio cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
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Barash SC, Choi GH, Dillon PJ,
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05-JAN-1996; US-009861
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence".
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Query Match Best Local

Similarity

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Score 34.6; Pred. No. 8

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DВ

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04-MAY-1998;
14-NOV-1997;
16-MAY-1997;
16-MAY-1997;
                                   Claim 1; Page 615-626; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and from identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis ancleotide sequences
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Sequence 9062 BP; 27
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                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
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                                                                                                                                                   Enterococcus faecalis genome contig SEQ ID NO:859.

Enterococcus faecalis; contig; detection; Enterococca

vaccine; attenuation; computer readable medium; ds.

Enterococcus faecalis.

WO985055-A2.

12-NOV-1998.
14-NOV-1998.
16-NAY-1997; US-066009.

R 16-NAY-1997; US-044031.
16-MAY-1997; US-04655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                              HUMAN GENOME SCI INC. SC. Dillon PJ, Kunsch
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it into
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Pred. No. 18;
0; Mismatches
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RESULT 15
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ID T36122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                      08-AUG-1996;
31-JAN-1996;
31-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                               Caries; antigen I/II; genetic immunisation; Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                     T36122;
26-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        S. mutans antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2022-2024; 2084pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can be used in vaccines to prevent or attenuate an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3549 BP;
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                                                                                                                                                                                                                        GB-001826.
                                                                                                                                                                                                                                     G00207
                                                                                                                                                                                                                                                                        sequence (vqvsrkglvryfyrskmvkrflklstsiqwtl) that differs from amino acids 618-650 given on page 46 of the specification"
                                                                                                                                                                                                                                                                                                               /transl_except= 2001 .2049
/note= "bases 2001-2049 code for an amino acid
                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       I/II gene.
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                                                                                                                                                                                                                                                                                                                                                                                                           epitope;
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Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                           tooth decay; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   faecalis genome
hich are primary
er-based system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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(W02098), a 185 kDa cell surface protein at least partly responsii for S. mutans adhesion to teeth. The I/II antigen includes a series of overlapping T-cell, B-cell and adhesion epitopes. Fragments (see also T35111-21) of the gene can be used to produce recombinant polypeptides (W02087-97) carrying such epitopes for use in vaccines for immunisation against dental caries. The DNA

can also

themselves

эd

used as

nucleic acid

A Streptococcus mutans gene (T36122) codes (W02098), a 185 kDa cell surface protein at

Page 46-49; 63pp;

English.

for I/II antigen

responsible

Disclosure;

adheres

to tooth

in

competition

with

Streptococcus

mutans

antigen

(UNME-) UNITED MEDICAL Kelly C, Lehner T; WPI; 96-371434/37.

δı

DENTAL SCHOOLS GUYS

P-PSDB; W02098

Nucleic acid encoding polypeptide for prevention or treatment of dental caries - which stimulates T or B cell response, and/or

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Search completed: April 16, 2000, 04:47:46 Job time: 10165 sec
                                        В
                                                    Qγ
                                                                      В
                                                                                   δÃ
                                                                                                    В
                                                                                                                  Qy
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                                                                                                                                                                                                         SS
                                                                                                                                                                 Query Match 2.9%; Score 34.2; DB 1; Length 4865; Best Local Similarity. 49.2%; Pred. No. 5.7; Matches 90; Conservative 0; Mismatches 93; Indels 0; Gaps
                                                                                                                                  vaccines.
Sequence 4865 BP;
                                        1428 ATC 1426
                                                 559 atc 561
                                                                                                                                                                                                         1687 A;
                                                                                                                                                                                                         967 C;
                                                                                                                                                                                                         953 G;
                                                                                                                                                                                                         1258 T;
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Result
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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        32.6
32.4
32.4
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
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length: 1000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-323-427-5
1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/fCTUS9_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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        GenCore version (c) 1993 - 2000
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US-08-559-303B-7
US-07-781-034-4
US-07-781-03-8-4
US-08-764-100-17
US-08-764-100-14
US-08-764-100-20
US-08-789-478-1
US-08-789-478-1
                       US-08-597-236-1
US-08-746-682A-1
US-08-742-003-1
US-08-322-760A-1
US-08-322-760A-1
US-08-468-405-7
US-08-468-405-7
US-08-638-596-1
US-08-635-066-1
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US-08-425-069-1
US-08-317-844B-
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Compugen Ltd
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838.958 Million cell updates/sec
Sequence 705, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 19, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Seq
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	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6
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ALIGNMENTS

COUNTRY: USA ZIP: 22313-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UMMER: US/07/772,087 FILING DATE: 19911008 CLASSIFICATION UMBER: 29,768 REJING LARGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION UMBER: 29,768 REFERENCE/DOCKET NUMBER: 16754/115 CHCO TELECOMMUNICATION UNBER: 16754/115 CHCO TELECOMMUNICATION UNBER: 10704/115 CHCO TELECOMMUNICATION UNBER: 10704/115 CHCO TELECOMMUNICATION UNBER: 10704/115 CHCO TELECOMMUNICATION UNBER: 10754/115 CHCO TELECOMMUNICATION UNBER: 10754/115 CHCO TELECOMMUNICATION UNBER: 10754/115 CHCO TELECOMONICATION UNBER: 10 ; Sequence 1, Application US/07772087 ; Patent No. 5275945 GENERAL INFORMATION: STRAIN: 164A-1 FEATURE: NAME/KEY: CDS LOCATION: 716..1849 OTHER INFORMATION: /product= "mature protein of the p APPLICANT: HSIAO, Humg-Yu APPLICANT: FODGE, Douglas W. APPLICANT: LALONDE, James J. TITLE OF INVENTION: ALKALINE P TITLE OF INVENTION: DETERGENT MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE: NUMBER OF SEQUENCES: E CITY: Alexandria STATE: Virginia STRANDEDNESS: TOPOLOGY: STREET: ADDRESSEE: linear double ALKALINE PROTEASES STABLE IN HEAVY-DUTY Suite 500 LIQUIDS

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-07-772-087-1
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5182210-9
                                                                                   RESULT 3
5352450-1/c
;Patent No. 5352450
; PATENT ROGA, TOSHIHIKO;OKAHASHI, NOBUO;TAKAHASHI, ICHIRO;SHIBUYA, KOJI;OHTA, HIROTAKH
;SHIBUYA, KOJI;OHTA, HIROTAKH
;TITLE OF INVENTION: METHOD FOR PREPARING VACCINE FOR DENTAL
;CARIES AND VACCINAL COMPOSITIONS FOR DENTAL CARIES USED AS NASAI
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; APPLICANT: BINNS, MATTHEW M.;BOURSNELL, MICHAEL;CAMPBELL, JOAN I.A.;TOMLEY, FIONA M.
TITLE OF INVENTION: FOWLDOX VIRUS PROMOTERS; NUMBER OF SEQUENCES: 22
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Best Local 9
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Best Local Similarity 52.9
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 29-MAY-199
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LOCATION:
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Local Similarity 55.6%;
les 85; Conserva+:...
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                                                                                                                                                                                                                                            aagtactcaatttactgtaataagatgtttcta 9172
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1022..1846
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716..1021
NUMBER: US/07/529,602
29-MAY-1990
                                                                                                                                        TOSHIHIKO; OKAHASHI, NOBUO; TAKAHASHI, ICHIRO
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Pred. No. 2.2;
0; Mismatches
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PCT-US96-05320A-705
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Best Local Similarity
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                 ZIP: 20003-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                APPLICATION NUMBER: 08/476,102
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1528
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TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                   APPLICATION NUMBER: POFILING DATE: April22, CLASSIFICATION:
                                              NAME: Eric K. Steffe
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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United States of America
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United States of America
Johns Hopkins University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamilton O. Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    720 Rutland Avenue
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                                       1488
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705:

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LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
PCT-US96-05320A-705
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Best Local Similarity 56.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/
PRIOR APPLICATION DATA:
PILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
                TELEFAX: 312-913-0002 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Chicago
CITY: Chicago
CITY: Illinois
"SATE: IISA
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-11996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                               TELEPHONE: 312-913-0001
                                                                                                              FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DEMIRJIAN, David
APPLICANT: CASADABAN, Malcolm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 TATGTCAAAGCCAAAAAGTGCGGTGAAATTTGCATTTTATACGGCA 186
                                                                                   REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,963-E
                                                                                                                                                      APPLICATION NUMBER: US 60/001,995 FILING DATE: 01-AUG-1995
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/019,580 FILING DATE: 12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                            US/08/781,802
10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stable Biocatalysts for Ester Hydrolysis 12
                                                                                                                                                                                                                         US 60/009,704
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Pred. No. 2.4;
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Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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OTHER INFORMATION: open reading frame; other possible start codons ATG/met4;
OTHER INFORMATION: TTG/leu7; GTG/val8; GTG/val15; GTG/val36; ATG/met62"
FEATURE:
                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIAN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Yu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2846 TCAATCTGCTGCTATTTTCTTCACCATATGGACGTTATTCAAAAACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2666 GATCCACTCTATTTATGCCCTCTACAGGGTTACAAAACAATTCTTTTGTAACTATATAAA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2606 TCTGATTAACAAGAATATTTGTGGCGCGAAACAGCCGCGGGTTTCCTTCTCCTCCCCTCTT 2665
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LOCATION:
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STRANDEDNESS: SIR
                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 22046
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                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTTCCATCTGTCTGAGAGTCAAATGGTCGTCTCACCAAGTTAACTTGTTAATGAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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197..1699
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197..1699
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Pred. No. 6.5;
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                                                                                                                                                            Version #1.25
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REFERENCE/DOCKET NUMBER: 1447-106P TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)

(703) 205-80 03) 205-8050

205-8000

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Best Local 9
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                                                                                                                                                                                                                                                                                         APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A 7
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRO
                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & STREET: 301 No. 5989894th Washington CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1674 TTGTCCAGCACCTTGTCCACCTAATCCTCCTTGTCCAGCACCTCCAGCTGCTGCTGCTGC 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1614 TGCACCTGCACCTTGTCCACCTAATCCTCCTCGACCAGAACCTTGGCTTCCAAGTCCTCC 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
AUTHORS: Xu, Ming
AUTHORS: Lewis, Rando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 accacctgttttaacagctccgaatccttgtggttctgaacattgtggtcgaacacattc 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 ttctgcagatcttttcttgagtaaacgaagttgcgcagctgcagcaggttttgctgcggc 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..2154
OTHER INFORMATION:
OTHER INFORMATION:
APPLICATION NUMBER: US/0 FILING DATE: 04-OCT-1994
                                                                                                                                                               COUNTRY:
                                                                                                                                                                                    STATE:
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nes 65; Conserv
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DATE: Sept.-1990

RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE: Structure of a protein superfiber: TITLE: drafline silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                22046
                                                                                                                                                             Virginia
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
7120-7124
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                   US/08/317,844B
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Pred. No.
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                                                                                                                                                                                                                      Street
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                                                                                                                                                                                                                                                                                             AND A TRANSFORMED AND PRODUCTS THERE
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RESULT 8
US-08-559-303B-72/c
; Sequence 72, Applicatio
; Patent No. 5824501
; GENERAL INFORMATION:
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; PAGES: 7120-7124
; DATE: Sept.-1990
; RELEVANT RESIDUES IN SEQ ID NO: US-08-317-844B-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 241-130
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1674 TTGTCCAGCACCTTGTCCACCTAATCCTCCTTGTCCAGCACCTCCAGCTGCTGCTGCTGC 1615
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                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                             APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA APPLICANT: GRODEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: N
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
REGISTRATION NUMBER: 28,9
CURRENT APPLICATION DATA:
                                                                                                                          COTTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1..2154
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 accacctgttttaacagctccgaatccttgtggttctgaacattgtggtcgaacacattc 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 ttctgcagatcttttcttgagtaaacgaagttgcgcagctgcagctaggttttgctgcggc 312
                                                                                                                                                     STREET:
                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-105P
                                                                                                                COUNTRY:
                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Xu, Ming AUTHORS: Lewis, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                     10016
                                                                                                                                     NEW YORK
                                                                                                                                                                                                                                                                                                                                                 Application US/08559303B
                                                                                                                                                                      90 PARK AVENUE
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                                                                                                                   U.S.A.
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                                                                  INCH 1.44 Mb STORAGE DISKETTE
                                                                                                                                                                                                                        METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME 78
                                                                                                                                                                                        ROTHSTEIN & EBENSTEIN
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Best Local Similarity 44.4
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/07781034 Patent No. 5442050
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TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 72:
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TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                   APPLICANT:
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LENGTH: 4437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    932 agtgaaattccggcaacttgacgtccaccttcatcattacggcaaccttcttgatcataa 991
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                                                                            COUNTRY: UZIP: 02173
                                                                                                              STREET: Two Mil:
CITY: Lexington
STATE: Massachu
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                                                                                                                                                                       ADDRESSEE:
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                                                                                                                Massachusetts
                                                                                                                                                   Two Militia Drive
                                                                                              USA
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                                                                                                                                                                     Hamilton,
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                                                                                                                                                                                                                          Molecular Cloning of Antigens Shared By Rat- and Human-Derived Pneumocystis Carinii
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Pred. No. 12
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
PNGTH: 1189 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08328
FILING DATE: 19920930
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER: MGH91-02A
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/781,034
FILING DATE: 19911018
FILING DATE: 30-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 18-OCT-1991
                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                ZIP: 02173
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                                      30-SEP-1991
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                                                     US 07/768,166
                                                                                                           US 07/781,034
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REGISTRATION NUMBER:

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TELEFAX: (617) 861-9540
TELEX: 951794
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, App...
Sequence 17, App...
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Best Local Similarity 51.0%;
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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HYPOTHETICAL: NO
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                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            STREET: 975 Cal:
                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                                                                                                                          Floppy disk
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                         APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION UMMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY,AGENT INFORMATION:
NAME: NO. 5773700ris, Allen E.
RECISTRATION NUMBER: 34,490
REPERENCE/DOCKET NUMBER: 137-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 354-3592
TELEPHANE: (415) 857-1125
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: van Grinsven J., r
APPLICANT: De Haan, Petrus T
APPLICANT: Gielen L., Johann
                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc
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LENGTH: 3414 base pair
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                TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 06-DEC-1996
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                              COMPUTER:
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nes 77; Conserv
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Pred. No. 12;
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                                                                                                                                                                                                                                                                              Version #1.25
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                         FILING DATE:
FILING DATE:
17-MAR-1993
APPLICATION NUMBER: US 08/03/1-
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773700715, Allen E.
REGISTRATION NUMBER: 34,490
REGISTRATION NUMBER: 137-1061
TELECOMMUNICATION 19070RMATION:
"PRIRPHONE: (415) 354-3592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uuery Match 2.7%;
Best Local Similarity 50.3%;
Matches 77; Conservative
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INFORMATION FOR SEQ ID NO:
               TELEFAX: (415) 857-11
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                           CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US/08/214,064
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gielen L., Johannes J.
APPLICANT: Peters, Dirk
APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/01 FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: CA
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o. 5773700
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975 California Avenue
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De Haan, Petrus T.
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Pred. No. 1:
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US-08-764-100-20
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Best Local Similarity 50.3%;
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                                                                         TELEFAX: (415) 857-112
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     APPLICATION NUMBER: US 08/032
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 920601
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5773700ris, Allen E
REGISTRATION NUMBER: 34,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 354-3592
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goldbach, Robert W
TITLE OF INVENTION: Improvement TITLE OF INVENTION: Compounds
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APPLICATION NUMBER: U
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APPLICANT: Peters, Dia
APPLICANT: Goldbach, F
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CITY: Palo Alto
                                                                                                                                                           REFERENCE/DOCKET NUMBER:
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                            STRANDEDNESS:
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           TOPOLOGY:
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                                       : 4970 base pairs
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De Haan, Petrus T.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 14
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APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
TITLE OF INVENTION: DISSASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
APPLICATION NUMBER: US 60/035,022

FILING DATE: 10-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
TELEPAX: (919) 541-8689
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
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PRIOR APPLICATION DATA:
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1 Similarity 50.3%;
77; Conservative
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T: 3054 Cornwallis Road
Research Triangle Park
No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08989478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                     UMBER: US 60/035,021
10-JAN-1997
                                                                                                                                                                                                                                                                                                                      UMBER: US 60/034,382
27-DEC-1996
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LENGTH: 5655 base pairs
TYPE: nucleic acid
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OTHER INFORMATION:
FEATURE:
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LOCATION: 4271..4474
OTHER INFORMATION: /
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              aaacgaaatgacaacagttgttgttacaaaaat 879
                                                                   | ttccatgtaaaagcattgtactcgatatgcacgatcaactttggtaacaaataatggatg 846
AAAATTAATTAAAAGAAAACTATTTCATAAAAT 1486
                                                    TAGAAGATAAAAAATTATATCAGATTGATTCAATTAAATTTTATAATAATATCATTTTAA 1453
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Description AII11196 SWOV3MCA1 AA701731 SWOV3MCA1

Minimum Maximum

larva cDNA

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Genes expressed in molting L3 la
Unpublished (1997)
On Sep 12, 1996 this sequence va
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Bio
Department of Biological Science
                                                                                                                                                                                      Onchocerca volvulus.
Onchocerca volvulus.
Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
1 (bases 1 to 665)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
Department of Biologic
College, Northampton,
Tel: 4135853826
Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
AII11196
AII111196.1 GI:3510080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AII11196 665 bp mRNA EST 31-AUG-1998 SWOV3MCA1232SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCA1232 5',
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                          TGGACCACATTCAATTTCTGGTTCACCTTCTACACCGTTATCAACCGGAATAGCAT
                                                                                                                                                                                                                                451;
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Seq primer: pBluescript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3; were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="SWOv3MCA1232"
/clone_lib="Onchocerca volvulus molting L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
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/db_xref="taxon:6282"
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                                                                                                                                                                            Matches 431;
                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                     562
                                                                actggttgaccggttggtccaccatccaaaatttcataacggcatactggcatcgggaca 721
                                                                                                                               ggtttcagaatcgcatgtccatttatgata--aactggctgaccaatgatagcaaattga 661
atttgagtttgaaaagcagttgtgatttcagatacctcaatctgtgcactaactgtttta
                                                                                                             GGTTTCAGAATCACATGTCCATTTATGGTAACACTGGGTTGACCAATGGTAGCAAATTGA 563
                                                ACAGGTTGTCCGGATGGTCCACCATCAAGAATTTCATATCGGCATACAGGCATCGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA701731 628 bp mRNA SWOV3MCA11445K Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCA1144 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           College, Northampton, MA, Tel: 4135853826
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
On Sep 19, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S Genes expressed in molting L3 larvae of Onchocerca volvulus
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AA701731
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1 (bases 1 to 628)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 4135853786
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                                                                                                                                                                                                                                                                            181
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                            The library is available from Dr. slustigm@nybc.org)."
a 121 c 125 g 201 t
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/db_xref="taxon:6282"
/clone="sWOv3MCA1144"
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(SL96MLW-OvmL3)"
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1997 this sequence version
                                                                                                                                                                                           32.1%;
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                                                                                                                                                                          Score 372.2; DB 37; Pred. No. 9.3e-90; 0; Mismatches 78;
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from Dr. Sara
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AA618895/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcattacgtgtattaaaattgattgttattgaagttggtccacattcaatttctggctca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tcatcattacggcaaccttcttgatcataaagacctttcacataaacatgtccttcgaat 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405188
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                       College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes expressed in molting
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                                                                                                                                                                                                                                                                                                                                                                                 genome@smith.edu
           // note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
                                                                                                                                                                                                          /clone="SWmL3CO1879"
/clone_lib="Onchocerca volvulus
(SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                  /organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                    /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                      dev_stage="molting L3"
culture,
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and converted to double-stranded
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KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGGATTACGAGTATTAAAGTTGACAGTAATTGATGTTGGACCACATTCAATTTGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417;
1 (bases 1 to 639)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797212.
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                        AI322117 639
SWOV3MCAM12G08SK
                                                                                                                                                           Onchocerca volvulus
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                        Onchocerca volvulus.
                                                                                                                                      Filarioidea; Onchocercidae;
                                                                                                                                                                                                                                                      AI322117.1
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(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM12G08 5',
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                                                                                                                                                                                                                                                      GI:4056268
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                                                                                                                                                                                                                                                                                                                                                                 639 bp
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                                                                                                                                           Onchocerca.
                                                                                                                                                           Secernentea; Spiruria; Spirurida;
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
Tel: 4135853826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The library is available from slustigm@nybc.org)."

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/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Un1-ZAP XR;
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Pred. No. 4.2e-86;
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  gcacatccatcagcatttagaatttccacagtatcaccgttaccatcatcgacaaagcag 574
                                                                         tcttggccagccattaaatctgttggatattccaaattatttagcaaatatttatcaaga 514
                                                                                                                                                   ATACTAATCTGGCATGGATAATAAATCTCAGATCGATCAGCGTATTTATAAACATGAGCT 550
                                                TCTTGGCCAGCCATTAGATNTGATAGATATTCCAAATTGTTGAGTAAATACTTGTCCACA 490
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SWOV3MCAM02C01SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM02C01 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 College, Northampton, MA, 01063, USA Tel: 4135853826
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Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Oct 30, 1997 this sequence version replaced gi:2160807.
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/lab_host="XLI-Blue MRF/"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of 0. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
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a 106 c 138 g 178 t 1 others
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/db_xref="taxon:6282"
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                                                                                                                                                                                                           Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                 Unpublished (1997)
On May 5, 1995 this sequence version replaced g1:797827
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA585626 776 bp mRNA EST 30-DEC-199/
SW3D9CA349SK Brugia malayi L3 molting-day 9 larva cDNA
(SAW97MLW-BmL3d9) Brugia malayi cDNA clone SW3D9CA349 5', mRNA
                                                                                                                                      Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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Brugia malayi
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(bases 1 to 776)
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(SAM97MLW-BmL3d9)"
/dev_stage="third stage larvae, nine
/lab_host="E. coli XL1-Blue MRF'"
                                                                                     /organism="Brugia malayi"
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SWOV3MCAM02A04SK Onchocerca volvulus
(SU906MLM-OvmmL3) Onchocerca volvulus
                                       Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 537)

Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lus
Genes expressed in molting L3 larvae of Onchocerca vo
Unpublished (1997)
                                                                                                                                                                                              Onchocerca volvulus.
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steven A. Williams
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
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primer: pBluescript SK.
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/db_xref="taxon:6282"
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                    ttccatgtaaaagcattgtactcgatatgcacgatcaacttttggtaacaaataatggatg 846
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Nilliams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797124
Contact: Steven A. Williams
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The library is available from Dr. Šara Lustigman (email: slustigm@nybc.org)."
106 c 111 g 181 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in culture, and converted to double-stranded CDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
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/lab_host="XL1-Blue MRF'"
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(SL96MLW-OvmL3)"
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/clone="SWOv3MCAM12A04"
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Steven A.
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larvae, 13, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-2ap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Maniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome@smith.edu
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Xho I; Filarial nematode parasite of humans. Third-stage
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/strain="Kumba, Cameroons"
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                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="molting L3"
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                                                                                                                                           Onchocerca volvulus

Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spiruria

Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 531)

1 (bases 1 to 531)

Williams, S.A., Lizotte-Waniewski, M., Laney, S., Lustigman, S., Williams, S.A., Lizotte-Waniewski, M., Geisel, S., Jost, S., Kucaba; Hillier, L., Allen, M., Bwles, L., Geisel, S., Jost, S., Kucaba; Martin, J., Steptoe, M., Theising, B., White, Y., Wylie, T., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chapperlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S.,
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367; Conserv
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Scienc
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                 AA901444 531 bp mRNA EST LATVE CINC. SMOV3MCAM03B05 Onchocerca volvulus molting L3 larve cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone onch17 5' similar TR:Q93115 Q93115 CUT-1-LIKE CUTICLIN PROTEIN PRECURSOR.;, mRNA
                                                  Molecular Parasitology
                                                                                    Unpublished (1998)
On Jan 19, 1998 this sequence
                                                                                                                      Underwood, K. and Marra, M. Molecular Parasitology OvmL3
                                                                     Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                 Onchocerca volvulus.
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les 75;
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please reference the Williams lab clone id -
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The library was constructed by Sara Lustigman and Michel
Lizotte-Waniewski in the Laboratory of Dr. S.A.Williams.
library is available from Dr. Sara Lustigman email
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 0000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
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On May 9, 1995 this sequence version replaced gi:802401
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SWOV3WCA691SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO691 5', mRNA
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Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On May 9, 1995 this sequence Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S Genes expressed in molting L3 larvae of Onchocerca volvulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 1026 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Voctor: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Voctor: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, 13, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture mRNA was isolated from approximately down molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture mRNA was isolated from approximately day 5 in culture mRNA was isolated from approximately considered management of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the 
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/clone_lib="Onchocerca volvulus molting L3
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MB3D6AA4G10T3 Brugia malayi day 6 post-infection third stage SAW96MLW-BmL3d6 Brugia malayi cDNA clone 3D6AA4G10 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +44 131 650 6760 Fax: +44 131 670 5450
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Brugia malayi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes expressed in day six post-infection, third stage larvae of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blaxter, M.L., Waterfall, M., Daub, J.,
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/dev_stage="third stage larvae, six days after infection"
/lab_host="p. coli XL1-Blue"
/note="vector: lambdaZapII (UniZap XR); Site_1: Eco R I
(5' end); Site_2: Xho I (3' end); Brugia malayi is a
lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi isolated
from the peritoneal cavity of jirds six days after
infection. The mRNA was converted to double stranded cDNA
using reverse transcriptase and oligo(dT) followed by
RNASE H and DNAPOl I. The library had 2 x 10E5 independent
recombinants and average insert size was 900 base pairs.
The library was constructed by Michelle Lizotte-Waniewski.
The library is available from The Filarial Genome Project
Resource Center: contact Dr. S.A. Williams, Clark Science
Center, Smith College, Northampton, MA 01063 USA phone +1
413 585 3826 fax +1 413 585 3786 email genome@smith.edu."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Brugia malayi"
/strain="TRS Labs"
/db_xref="taxon:6279"
                                                                                                                                                                                                                                                                                                                                                                                    /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Brugia malayi day 6 post-infection third stage
larvae SAW96MLW-BmL3d6"
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REFERENCE
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hes 301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On May 9, 1995 this sequence version replaced gi:802407 Contact: Steven A. Williams Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 466)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWOv3MCA758SK Onchocerca volvulus molting L3 la (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone
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Pred. No. 4.2e-62;
"Mematches 53;
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clone SWmL3CO758 5', mRNA
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VERSION KEYWORDS

ACCESSION

LOCUS

SOURCE

ORGANISM

Onchocerca volvulus.
Onchocerca volvulus

COMMENT

Smith College Molecular Parasitology

Biological Sciences, Clark Science Center, Smith

Department of Biological Sciences

Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae Unpublished (1997)
On Sep 12, 1996 this sequence version Contact: Steven A. Williams

version

Laney, S. and Lustigman, S. of Onchocerca volvulus replaced gi:1405277.

REFERENCE

(bases 1 to 459)

Eukaryota; Metazoa; Nematoda; Secernent Filarioidea; Onchocercidae; Onchocerca.

Secernentea;

Spiruria;

Spirurida;

AUTHORS TITLE JOURNAL

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RESULT 14
AA618952/c
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AA618952.1
EST.
                                                                                AA618952 459 bp mRNA EST 12-NOV SWOV3MCA2020SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3C020
                                          AA618952
                                                            sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reverse transcriptase and oligo(dT) followed by RNase H and DNA pol 1. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle library was constructed by Sara Lustigman and Michelle library was constructed by Sara Lustigman and Michelle library is available from Dr. Sara Lustigman (email: Slustigment)."

The library is available from Dr. Sara Lustigman (email: slustigment) savailable from Dr. Sara Lustigman (email: slustigment). 3 g 144 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
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                      GI:2522828
                                                                                                                                                                                                                                       89
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Pred. No. 1.1e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atcaactttggtaacaaataatggatgaaacgaaatgacaacagttgttgttacaaaaat 879
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCACGTGGATTTAACGAACGTGTACGTGNTACATTACAGGAATCAAACGGAAGTTCAAT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCAACTTTTGTCACAAACAATGGATGGAATGAGATGACAACAACTGATGTGACAAAAAT 314
                                                                                                                                                                                                                                                                              CACGTATACANGTCCTTCAAATGGATTACGAGTATTAAAGTTGACAGTAATTGATGTTGG
                                                                                                                                                                                                                                                                                                                                                           SWOv3MCA318SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO318 5', mRNA
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Fax: 4135853786
                  AA625010
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AA625010.1
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2 others
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/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Onchocerca volvulus molting L3 larva (SL96MLW-OvmL3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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83.9%;
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Pred. No. 2.1e-60;
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Matches 305; Conserv
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                    atttccacagtatcaccgttaccatcatcgacaaagcaggaatggacaaccgcgcgcagaaa
                                                                                                                                                                                                                                                          AATTCCACCTTATCACCGTTACCATCATCAACGAAGCATGAATGTACAACAGCACAGAAT 76
                                                                                                         GCAGCTGCAGCACCATTTCGTGANCGAACTGCTCCAAATCCTTGTGGTTCTGCACAT 316
                                                                                                                                                                                                                                                                                                                                                                    gcaggttttgctgcggcaccacctgttttaacagctccgaatccttgtggttctgaacat 355
                                                                                   GTTGGATATTCCAAGTTGTTGAGCAAATATTTGTCCAAAGCACAACCATCAGCATTTAAT 136
                                                                                                                                                                         AACAGTTGTGATCGATCCGCATATTTGTAGACGTGAGCCTTCTTGTCCAGCCATTAAATCA
                                                                                                                                                                                               Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On May 9, 1995 this sequence version replaced gi:802391 Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes expressed in molting Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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Onchocerca volvulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Filarioidea; Onchocercidae; Onchocerca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // Care Poetor: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Nho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mANA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
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/db_xref="taxon:6282"
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/lab_host="XL1-Blue MRF'"
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Pred. No. 1e-59;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 395;
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5.1.4_p5_4578 Compugen Ltd. GenCore version (c) 1993 - 2003 Copyright

sw model using search, nucleic OM nucleic

4, 2003, 09:12:27; Search time 1 Seconds (without alignments)
4.131 Million cell updates/sec April ö

Run

Title: Perfect score:

1 atgatgattcgtcttattgc......ttcgtccaaatcagaaggca 1161 us-10-054-562a-3 Sequence:

Scoring table:

IDENTITY_NUC Gapoxt 0.0

1 seqs, 1779 residues Searched:

Total number of hits satisfying chosen parameters:

sed Minimum DB Maximum DB

length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1 summaries

us-10-054-562a-1:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	
១	. 1161 100.0 1779 1 us-10-054-562a-1
DB	<u> </u>
Length	1779
Match	100.0
Score	1161
NO.	7
	No. Score Match Length DB ID Description

ALIGNMENTS

RESULT 1 us-10-054-562a-1

Gaps ö Length 1779; Indels ö DB 1; ; Score 1161; 1; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 100.0%;
Matches 1161; Conservative 0;

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1 ATGATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCG 60 ð g

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240 GAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGAT 347 181 ö -**Q**

TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTTGTAACAACA 241 ò

466 407

1126 1020 1186 1080 1140 1306 1006 1066 886 946 840 480 540 900 992 99 780 900 960 420 646 706 826 GTGTCATTTCGTTTCATCCATATTTGTTACCAAAGTTGATCGTGCATATCGAGGTACAA TGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACA ACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT ACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGAT TIGCTAAATAATTIGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAA CCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAA GATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGA CAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCA GTTGTCATTTCGTTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAA 647 1001 1067 1127 1187 1247 1307 361 421 587 707 827 721 781 947 841 1021 1081 1141 301 467 527 481 541 601 167 661 887 901 961 셤 ô ద ò 용 ò 셤 ò g ò g ò g ò 요 . 8 8 ģ . <u>a</u> . 8 유 ò g à ద ò 9 à 요 õ

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